

## FEATURES

## source

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 ORIGIN

Query Match 80.9%; Score 1310.4; DB 6; Length 2528;  
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 AUTHORS  
 TITLE  
 JOURNAL  
 Submitted (25-JUL-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 Contact: MGC help desk  
 Email: [gcaps-remail.nih.gov](mailto:gcaps-remail.nih.gov)  
 Tissue Procurement: ATCC/DCTD/DNP  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
 http://www.systemsbio.org  
 contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)  
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia

## REMARK

## COMMENT

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 AX362255 1524 bp DNA linear PAT 15-FEB-2002  
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 ACCESSION AX362255  
 VERSION AX362255.1 GI:18694585  
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 SOURCE human.  
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 REFERENCE 1  
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Matanabe, C.K., and Wood, W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same  
 JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;  
 Genentech, Inc. (US)  
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 Location/Qualifiers  
 BASE COUNT 321 a 433 c 435 g 335 t  
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 ACCESSION AX319944  
 VERSION AX319944.1 GI:17901491  
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1  
 AUTHORS Galvin, K.A. and Rudolph-Owen, L.A.  
 TITLE Methods and compositions for the diagnosis and treatment of  
 cardiovascular and tumorigenic disease using 4941  
 Patent: WO 0181634-A 3 01-NOV-2001;  
 Millennium Pharmaceuticals, Inc. (US)



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AUTHORS	Baker,K.P., Desnovers,L., Gerlitsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smlth,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0193983-A 15 13-DEC-2001; Genentech Inc. (US) Location/Qualifiers 1. 1524 /organism="Homo sapiens" /db_xref="taxon:9606"		
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JOURNAL			
FEATURES	source		
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Matches 1384; Conservative	0; Mismatches 0; Indels 1; Gaps 1		
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LOCUS			
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VERSION	AC079773.8 GI:15145561		
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SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 129676)		
JOURNAL	Sulston, J.E. and Waterston, R.		
MEDLINE	Toward a complete human genome sequence		
PUBMED	Genome Res. 8 (11), 1097-1108 (1998)		
REFERENCE	9847074		
AUTHORS	2 (bases 1 to 129676)		
TITLE	Shah, N., Meyer, R., Boyer, E. and Dignan, G.		
JOURNAL	The sequence of Homo sapiens BAC clone RP11-258B17		
REFERENCE	Unpublished (2001)		
AUTHORS	3 (bases 1 to 129676)		
TITLE	Waterston, R.H.		
JOURNAL	Direct Submission		
PUBMED	Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA		
REFERENCE	4 (bases 1 to 129676)		
AUTHORS	Waterston, R.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA		
REFERENCE	5 (bases 1 to 129676)		
AUTHORS	Waterston, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA		
COMMENT	On Aug 9, 2001 this sequence version replaced gi:14488388. ----- Genome Center Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu/gsc Contact: saplens@watsn.wustl.edu ----- Summary Statistics Center project name: H_NH0258B17 ----- NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.  MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis		

[illegible]

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 DEFINITION Sequence 203 from Patent EP1067182.  
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 VERSION AX136281.1 GI:14272687  
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 ORGANISM Homo sapiens  
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 Mammalia; Eultheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1890)  
 AUTHORS Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and  
 Hayashi, K.  
 TITLE Secretory protein or membrane protein  
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AUTHORS	Kwakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Ito, R., Otsuki, T., Saito, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kluch, H., Kanda, K., Wagatsuna, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K. and Isogai, T.									
TITLE	NEDO human cDNA sequencing project									
REFERENCE	Unpublished									
AUTHORS	Isogai, T. and Yamamoto, J.									
TITLE	Direct Submission									
JOURNAL	Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team) ; 2-6-7 Kazusa-Kametani, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.									
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:51:07 ; Search time 4118.22 Seconds

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	1373	84.8	1524	6 AX358762	AX358762 Sequence
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6	1310.4	80.9	2528	6 AX362255	AX362255 Sequence
7	789.2	48.7	826	6 AX319944	AX319944 Sequence
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15	413.4	22.6	444	6 AX150120	AX150120 Sequence
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23	54.8	3.4	125020	9 AF429315	AF429315 Homo sapi
24	54.2	3.3	3917	10 AB017027	AB017027 Mus muscu
25	52.4	3.2	1254	6 E11480	E11480 cDNA encodi
26	52.4	3.2	1257	6 AX280911	AX280911 Sequence
27	52.4	3.2	4131	9 HSNENURA	X70070 H. sapiens m
28	50.4	3.1	7218	6 E6494	E6494 Sequence 14
29	50.4	3.1	1140	6 E37240	E37240 Novel phys
30	50	3.1	1140	6 E63120	E63120 Peptide der
31	50	3.1	1148	9 AF100206	AF100206 Macaca mu
32	50	3.1	1583	9 HS003642	HS003642 Human G pro
33	50	3.1	1754	9 BC032688	BC032688 Homo sapi
34	50	3.1	1801	9 HSHG110RP	X89271 H. sapiens m
35	50	3.1	1872	6 AR107256	AR107256 Sequence
36	50	3.1	1872	6 AR194356	AR194356 Sequence
37	50	3.1	125020	9 AF429315	AF429315 Homo sapi
38	50	3.1	169216	2 AC090238	AC090238 Homo sapi
39	50	3.1	171744	9 AP001786	AP001786 Homo sapi
40	48.4	3.0	3248	9 AK097232	AK097232 Homo sapi
41	48.2	3.0	7218	6 I66494	I66494 Sequence 14
42	47.4	2.9	99437	2 AC103419	AC103419 Rattus no
43	47.4	2.9	167929	2 AC128436	AC128436 Rattus no
44	46	2.8	289	6 AR162089	AR162089 Sequence
45	46	2.8	289	6 AR166614	AR166614 Sequence

#### ALIGNMENTS

RESULT 1  
AK094501  
LOCUS  
DEFINITION  
AK094501 1832 bp mRNA linear PRI 15-JUL-2002  
Homo sapiens cDNA FLJ37182 fls, clone BRAZ2001350, weakly similar  
to Homo sapiens Gz-selective GTPase-activating protein (RGS20)  
mRNA  
ACCESSION  
AK094501  
VERSION  
AK094501.1 GI:21753575  
KEYWORDS  
oligo capping; fls (full insert sequence).  
SOURCE  
Homo sapiens alzheimer cortex cDNA to mRNA, clone 11b-BRAZ2  
clone: BRAZ2001350.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1

Prod. No. is the number of results predicted by chance to have a

APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James:  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC30  
CURRENT APPLICATION NUMBER: US/10/172,039A  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 156  
LENGTH: 2680  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-172-039A-156

Query Match 1.4%; Score 23; DB 6; Length 2680;  
Best Local Similarity 100.0%; Pred. No. 0.057;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619  
Db 2655 TGTAAAAA 2677

RESULT 45  
US-10-145-016A-156  
Sequence 156, Application US/10145016A  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James:  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC32  
CURRENT APPLICATION NUMBER: US/10/145,016A  
CURRENT FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 156  
LENGTH: 2680  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-145-016A-156

Query Match 1.4%; Score 23; DB 6; Length 2680;  
Best Local Similarity 100.0%; Pred. No. 0.057;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619  
Db 2655 TGTAAAAA 2677

Search completed: November 8, 2002, 02:03:49  
Job time : 106.231 secs



```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C40
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-165-353-156
```

```
Query Match 1.4% Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAAAAAAAAAAAAAAAAAA 1619
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677
```

```
RESULT 43
US-10-170-481A-156
Sequence 156, Application US/10170481A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C53
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-170-481A-156
```

```
Query Match 1.4% Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAAAAAAAAAAAAAAAAAA 1619
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677
```

```
RESULT 44
US-10-172-039A-156
Sequence 156, Application US/10172039A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

```

: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James:
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2630PIC56
: CURRENT APPLICATION NUMBER: US/10/162,522A
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-162-522A-156

Query Match          1.4%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677

RESULT 41
US-10-165-038A-156
: Sequence 156, Application US/10165038A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerltsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
```

```

: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James:
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2630PIC29
: CURRENT APPLICATION NUMBER: US/10/165,038A
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-165-038A-156

Query Match          1.4%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677

RESULT 42
US-10-165-353-156
: Sequence 156, Application US/10165353
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerltsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
```

```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC39
CURRENT APPLICATION NUMBER: US/10/143,031A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remainig Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-143-031A-156
```

```
Query Match 1.4%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAA 1619
DB 2655 TGTAAAAA 2677
```

```
RESULT 39
US-10-145-092A-156
Sequence 156, Application US/10145092A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geiber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC45
CURRENT APPLICATION NUMBER: US/10/145,092A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remainig Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-092A-156
```

```
Query Match 1.4%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAA 1619
DB 2655 TGTAAAAA 2677
```

```
RESULT 40
US-10-162-522A-156
Sequence 156, Application US/10162522A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geiber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

```
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C79
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 227
LENGTH: 2136
TYPE: DNA
ORGANISM: Homo Sapien
US-10-125-923A-227
```

```
Query Match 1.4%; Score 23; DB 6; Length 2136;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 2061 TGTAAAAAAAAAAAAAAAAAAAA 2083
```

```
RESULT 37
US-10-145-087A-156
Sequence 156, Application US/10145087A
```

```
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

```
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C47
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-087A-156
```

```
Query Match 1.4%; Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677
```

```
RESULT 38
US-10-143-031A-156
Sequence 156, Application US/10143031A
```

```
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
```

US-10-145-129A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;  
 Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619

DB 1974 TGTAAAAA 1996

RESULT 34  
 US-10-125-923A-53

Sequence 53, Application US/10125923A  
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P3430R1C79  
 CURRENT APPLICATION NUMBER: US/10/125, 923A  
 CURRENT FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 10/052586  
 PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059263  
 PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266  
 PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120  
 PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063121  
 PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063486  
 PRIOR FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540  
 PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541  
 PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544  
 PRIOR FILING DATE: 1997-10-28

Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 612

SEQ ID NO 53  
 LENGTH: 1998

TYPE: DNA  
 ORGANISM: Homo Sapien

US-10-125-923A-53

Query Match 1.4%; Score 23; DB 6; Length 1998;  
 Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619

DB 1974 TGTAAAAA 1996

RESULT 35

US-10-165-353A-136

Sequence 136, Application US/10165353A  
 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Bolstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paonli, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630P1C40  
 CURRENT APPLICATION NUMBER: US/10/165, 353A  
 CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450  
 PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632  
 PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641  
 PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649  
 PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791  
 PRIOR FILING DATE: 1998-03-12

Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 624

SEQ ID NO 136  
 LENGTH: 1998

TYPE: DNA  
 ORGANISM: Homo sapiens

US-10-165-353A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;  
 Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619

DB 1974 TGTAAAAA 1996

RESULT 36

US-10-125-923A-227

Sequence 227, Application US/10125923A  
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.



US-10-170-481A-136

Query Match 1.4%: Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 0.058;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 30

US-10-172-039A-136

; Sequence 136, Application US/10172039A  
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C30  
; CURRENT APPLICATION NUMBER: US/10/172.039A  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 624  
; SEQ ID NO 136  
; LENGTH: 1998  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-172-039A-136

Query Match 1.4%: Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 0.058;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 31

US-10-145-016A-136

; Sequence 136, Application US/10145016A  
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C52  
; CURRENT APPLICATION NUMBER: US/10/145.016A  
; CURRENT FILING DATE: 2001-10-18  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 624  
; SEQ ID NO 136  
; LENGTH: 1998  
; TYPE: DNA  
; ORGANISM: Homo sapiens



US-10-165-038A-136

Query Match	1.4%;	Score 23;	DB 6;	Length 1998;
Best Local Similarity	100.0%;	Pred. No. 0.058;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1597	TGTAACAAAAA	1619
Db	1974	TGTAACAAAAA	1996

RESULT 28  
US-10-165-353-136

1 GENERAL INFORMATION:  
 2 APPLICANT: Ashkenazi, Avi  
 3 APPLICANT: Baker Kevin P.  
 4 APPLICANT: Botstein, David  
 5 APPLICANT: Deenoyers, Luc  
 6 APPLICANT: Eaton, Dan  
 7 APPLICANT: Ferrara, Napoleon  
 8 APPLICANT: Flivaroff, Ellen  
 9 APPLICANT: Fong, Sherman  
 10 APPLICANT: Gao, Wei-Qiang  
 11 APPLICANT: Gerber, Hanspeter  
 12 APPLICANT: Gerritsen, Mary E.  
 13 APPLICANT: Goddard, Audrey  
 14 APPLICANT: Godowski, Paul J.  
 15 APPLICANT: Grimaldi, J. Christopher  
 16 APPLICANT: Gunney, Austin L.  
 17 APPLICANT: Hillan, Kenneth J.  
 18 APPLICANT: Kljavin, Ivar J.  
 19 APPLICANT: Kuo, Sophia S.  
 20 APPLICANT: Napier, Mary A.  
 21 APPLICANT: Pan, James;  
 22 APPLICANT: Paoni, Nicholas F.  
 23 APPLICANT: Roy, Margaret Ann  
 24 APPLICANT: Shelton, David L.  
 25 APPLICANT: Stewart, Timothy A.  
 26 APPLICANT: Tumas, Daniel  
 27 APPLICANT: Williams, P. Mickey  
 28 APPLICANT: Wood, William I.  
 29 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 30 ACIDS  
 31 TITLE OF INVENTION: Acids Encoding the Same  
 32 FILE REFERENCE: P2630P1C40  
 33 CURRENT APPLICATION NUMBER: US/10/165.353

```

; PRIOR FILING DATE: 1998-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 624
; SEQ. ID NO. 136

```

US-10-165-353-136

Query Match	1.48;	Score 23;	DB 6;	Length 1998;
Best Local Similarity	100.0%;	Pred. No. 0.058;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1597	TGTAATAAAAAAAAAAAAAA	1619
Db	1974	TGTAATAAAAAAAAAAAAAA	1996

RESULT 29  
US-10-170-481A-136  
; Sequence 136, Application US/10170481A

```

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC53
CURRENT APPLICATION NUMBER: US/10/170,481A

```

```

; PRIOR FILING DATE: 1998-03-12,
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 624

```

US-10-145-092A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. NO. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 26

US-10-162-522A-136

Sequence 136, Application US/10162522A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C56

CURRENT APPLICATION NUMBER: US/10/162,522A

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/074450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

Remaining prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 624

SEQ ID NO 136

LENGTH: 1998

TYPE: DNA

ORGANISM: Homo sapiens

US-10-162-522A-136

Query Match 1.4%; Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. NO. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 27

US-10-165-038A-136

Sequence 136, Application US/10165038A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C29

CURRENT APPLICATION NUMBER: US/10/165,038A

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/074450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

Remaining prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 624

SEQ ID NO 136

LENGTH: 1998

TYPE: DNA

ORGANISM: Homo sapiens

US-10-145-087A-136

Query Match 1.4%: Score 23; DB 6; Length 1998;

Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619

DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 24

US-10-143-031A-136

Sequence 136, Application US/10143031A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC39  
CURRENT APPLICATION NUMBER: US/10/143,031A  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 136  
LENGTH: 1998  
TYPE: DNA  
ORGANISM: Homo sapiens

US-10-143-031A-136

Query Match 1.4%: Score 23; DB 6; Length 1998;

Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619

DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 25

US-10-145-092A-136

Sequence 136, Application US/10145092A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC45  
CURRENT APPLICATION NUMBER: US/10/145,092A  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 136  
LENGTH: 1998  
TYPE: DNA  
ORGANISM: Homo sapiens

```
; FILE REFERENCE: PAL31PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 457
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-457

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1689;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 1654 TGTAAAAAAAAAAAAAAAAAAAA 1676

RESULT 21
US-10-260-046-19
; Sequence 19, Application US/10260046
; GENERAL INFORMATION:
; APPLICANT: Dhugga, Kanwarpal S.
; TITLE OF INVENTION: Manipulation of Plant Polysaccharide
; FILE REFERENCE: 1296
; CURRENT APPLICATION NUMBER: US/10/260,046
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/325,614
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Zea mays
US-10-260-046-19

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1740;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 1711 TGTAAAAAAAAAAAAAAAAAAAA 1733

RESULT 22
US-10-264-237-890
; Sequence 890, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAL31PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 890
; LENGTH: 1765
; TYPE: DNA
; ORGANISM: Homo sapiens
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```
US-10-264-237-890

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1765;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 1739 TGTAAAAAAAAAAAAAAAAAAAA 1761

RESULT 23
US-10-145-087A-136
; Sequence 136, Application US/10145087A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertschen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C47
; CURRENT APPLICATION NUMBER: US/10/145,087A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 136
; LENGTH: 136
; TYPE: DNA
; ORGANISM: Homo sapiens
```

FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1078)..(1078)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-264-237-563

Query Match 1.4%; Score 23; DB 6; Length 1092;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
Db 1037 TGTAAAAAAAAAAAAAAAAAAAA 1059

RESULT 16  
US-10-264-237-40/c  
; Sequence 40, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 40  
; LENGTH: 1326  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (912)..(912)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-264-237-40

Query Match 1.4%; Score 23; DB 6; Length 1326;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
Db 54 TGTAAAAAAAAAAAAAAAAAAAA 32

RESULT 17  
US-10-264-237-995  
; Sequence 995, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 995  
; LENGTH: 1539  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-264-237-995

Query Match 1.4%; Score 23; DB 6; Length 1539;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
Db 1509 TGTAAAAAAAAAAAAAAAAAAAA 1531

RESULT 18  
US-10-264-237-1007  
; Sequence 1007, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 1007  
; LENGTH: 1571  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-264-237-1007

Query Match 1.4%; Score 23; DB 6; Length 1571;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
Db 1539 TGTAAAAAAAAAAAAAAAAAAAA 1561

RESULT 19  
US-09-602-472A-1  
; Sequence 1, Application US/09602472A  
; GENERAL INFORMATION:  
; APPLICANT: Bidney, Dennis L.  
; APPLICANT: Hu, Xu  
; TITLE OF INVENTION: Sunflower Disease Resistance Genes  
; FILE REFERENCE: 35718/200630  
; CURRENT APPLICATION NUMBER: US/09/602,472A  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/140,876  
; PRIOR FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1593  
; TYPE: DNA  
; ORGANISM: Helianthus annuus  
US-09-602-472A-1

Query Match 1.4%; Score 23; DB 5; Length 1593;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
Db 1571 TGTAAAAAAAAAAAAAAAAAAAA 1593

RESULT 20  
US-10-264-237-457  
; Sequence 457, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```

; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 114
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-114

Query Match
Best Local Similarity 1.4%; Score 23; DB 6; Length 574;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA1619
DB 551 TGTAAAAA573

RESULT 12
US-10-264-237-1055
; Sequence 1055, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 1055
; LENGTH: 785
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (74)..(74)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1055

Query Match
Best Local Similarity 1.4%; Score 23; DB 6; Length 785;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA1619
DB 734 TGTAAAAA756

RESULT 13
US-10-264-237-687
; Sequence 687, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-687
```

```

; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 687
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-687

Query Match
Best Local Similarity 1.4%; Score 23; DB 6; Length 1001;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA1619
DB 974 TGTAAAAA996

RESULT 14
PCT-US02-33408-5/C
; Sequence 5, Application PC/TUS0233408
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: HAYASHI, Yasunori
; TITLE OF INVENTION: NR3B Receptor Subunit Compositions and Related Methods
; FILE REFERENCE: M00656, 70068, MO
; CURRENT APPLICATION NUMBER: PCT/US02/33408
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US 60/344,545
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 5
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Rattus norvegicus
PCT-US02-33408-5

Query Match
Best Local Similarity 1.4%; Score 23; DB 1; Length 1040;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA1619
DB 42 TGTAAAAA20

RESULT 15
US-10-264-237-563
; Sequence 563, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 563
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (57)..(57)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-563
```

```

US-10-266-131-1361/c
; Sequence 1361, Application US/10266131
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Murine Polynucleotide Tags and
; FILE REFERENCE: Lex-0030-USA
; CURRENT APPLICATION NUMBER: US/10/266,131
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/09/611,675
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/143,878
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 2908
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1361
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(286)
; OTHER INFORMATION: n = A,T,C or G
US-10-266-131-1361

```

```

Query Match          1.4%; Score 23; DB 6; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAA...1619
DB 24 TGTAAAAA...2

```

```

RESULT 8
US-09-907-907A-31
; Sequence 31, Application US/09907907A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Leszczynska, Magdalena
; TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESENCE A
; FILE REFERENCE: A34584-A-PCT-USA (070050,1664)
; CURRENT APPLICATION NUMBER: US/09/907,907A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US 09/243,277
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-907A-31

```

```

Query Match          1.4%; Score 23; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAA...1619
DB 290 TGTAAAAA...312

```

```

RESULT 9
US-10-240-425-758/c
; Sequence 758, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.

```

```

; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 758
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF1675419
US-10-240-425-758

```

```

Query Match          1.4%; Score 23; DB 6; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAA...1619
DB 23 TGTAAAAA...1

```

```

RESULT 10
US-10-240-425-525/c
; Sequence 525, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF162104
US-10-240-425-525

```

```

Query Match          1.4%; Score 23; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1597 TGTAAAAA...1619
DB 52 TGTAAAAA...30

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RESULT 11
US-10-264-237-114
; Sequence 114, Application US/10264237
; GENERAL INFORMATION:

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US-10-125-923A-215

## Query Match

Best Local Similarity 1.5%; Score 24; DB 6; Length 1337;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAACAAAAA 1619

DB 1298 GTGTAACAAAAA 1321

## RESULT 3

US-10-266-829-15

Sequence 15, Application US/10266829  
GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 29 Human secreted proteins

FILE REFERENCE: P2041P1

CURRENT APPLICATION NUMBER: US/10/266,829

PRIOR FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: 09/756,168

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: PCT/US00/19735

PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: 60/145,220

NUMBER OF SEQ ID NOS: 146

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 15

LENGTH: 2057

TYPE: DNA

ORGANISM: Homo sapiens

US-10-266-829-15

Query Match 1.5%; Score 24; DB 6; Length 2057;  
Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAACAAAAA 1619

DB 1907 GTGTAACAAAAA 1930

## RESULT 4

US-10-240-425-1530/C

Sequence 1530, Application US/10240425  
GENERAL INFORMATION:

APPLICANT: Williams, Amanda

APPLICANT: Bolland, Joseph F.

APPLICANT: Lord, Reginald V.

APPLICANT: Alvarez, Chris

APPLICANT: Wetzel, Jwe C.

APPLICANT: Scherf, Dwe

TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue

FILE REFERENCE: 44921-5026

CURRENT APPLICATION NUMBER: US/10/240,425

PRIOR FILING DATE: 2002-09-30

PRIOR APPLICATION NUMBER: PCT/US01/09847

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 60/193,446

NUMBER OF SEQ ID NOS: 1588

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 1530

LENGTH: 2305

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. X06374

US-10-240-425-1530

Query Match 1.5%; Score 24; DB 6; Length 2305;

Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAACAAAAA 1619

DB 1626 GTGTAACAAAAA 1603

## RESULT 5

US-09-513-999C-20982

Sequence 20982, Application US/09513999C  
GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59,US2 REG

CURRENT APPLICATION NUMBER: US/09/513,999C

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 20982

LENGTH: 102

TYPE: DNA

ORGANISM: Homo sapiens

US-09-513-999C-20982

Query Match 1.4%; Score 23; DB 5; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.065;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAACAAAAA 1619

DB 73 TGTAAACAAAAA 95

## RESULT 6

US-09-907-907A-23

Sequence 23, Application US/09907907A  
GENERAL INFORMATION:

APPLICANT: Fisher, Paul B.

APPLICANT: Leszczynska, Magdalena

TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESENC

FILE REFERENCE: A34584-A-PCT-USA (070050,1664)

CURRENT APPLICATION NUMBER: US/09/907,907A

PRIOR FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: US 09/243,277

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 23

LENGTH: 198

TYPE: DNA

ORGANISM: Homo sapiens

NAME/KEY: unsure

FEATURE:

LOCATION: 21

OTHER INFORMATION: a or c or g or t

US-09-907-907A-23

Query Match 1.4%; Score 23; DB 5; Length 198;  
Best Local Similarity 100.0%; Pred. No. 0.064;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAACAAAAA 1619

DB 160 TGTAAACAAAAA 182

## RESULT 7

Best Local Similarity 99.98; Pred. No. 0;  
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 GGCACCTTTTCCGAGATGTTCTTCTTCACAGCTTTGCGCTGCAAAATCCAGTGTACCA 60  
141 GGCACCTTTTCCGAGATGTTCTTCTTCACAGCTTTGCGCTGCAAAATCCAGTGTACCA 200

61 GTGTGAAGAATTCACGTGAACACAGACTGCTCTCCCGAGTTCAATTGTGAATTCAC 120  
201 GTGTGAAGAATTCACGTGAACACAGACTGCTCTCCCGAGTTCAATTGTGAATTCAC 260

121 GGTGAACCTTCAAGACATGTCTCAGAAAGATGTGAGCAAAATGCGCGGATCATGTA 180  
261 GGTGAACCTTCAAGACATGTCTCAGAAAGATGTGAGCAAAATGCGCGGATCATGTA 320

181 CCGCAAGTCTCTGATCATCTACGCGCTCTCTCATCTGCGCTCTCCCGGATACAGTCTT 240  
321 CCGCAAGTCTCTGATCATCTACGCGCTCTCTCATCTGCGCTCTCCCGGATACAGTCTT 380

241 CTGCTCTCCCGAGGAAATCTCAATCTGATCTGATCTGCTGCAACACCTCTCTTTGTA 300  
381 CTGCTCTCCCGAGGAAATCTCAATCTGATCTGATCTGCTGCAACACCTCTCTTTGTA 440

301 CCGGCGCAAGGCGCCAGAAAGGGAAGTTCTGCTCGGCGCTCAGAGCGGATCCGCGAC 360  
441 CCGGCGCAAGGCGCCAGAAAGGGAAGTTCTGCTCGGCGCTCAGAGCGGATCCGCGAC 500

361 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTGCGCACATGCTGAGCTGAAGAGATG 420  
501 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTGCGCACATGCTGAGCTGAAGAGATG 560

421 CCACCCCTCTCTGATGTTCTTCCAGCCCTCGCCCGCAACCCCGACCTCCCTGATGTA 480  
561 CCACCCCTCTCTGATGTTCTTCCAGCCCTCGCCCGCAACCCCGACCTCCCTGATGTA 620

481 GTTCTCTCTGCTGCTCTTTTATTTCTGGGTAGGAGCGGAGATCCGTCTCTTTTGT 540  
621 GTTCTCTCTGCTGCTCTTTTATTTCTGGGTAGGAGCGGAGATCCGTCTCTTTTGT 680

541 CCGTGTGAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTAATTCAGCTGAT 600  
681 CCGTGTGAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTAATTCAGCTGAT 740

601 TTTCAGTATGATCTGAAGAGAGGTGAGTGAAGTTCACCCCATGCTGTGTATAC 660  
741 TTTCAGTATGATCTGAAGAGAGGTGAGTGAAGTTCACCCCATGCTGTGTATAC 800

661 CCGAGTCAAGGCGCGAGCTGCGAGATCACTCTTAAGAGTCACTGAGTGGCATCTGCC 720  
801 CCGAGTCAAGGCGCGAGCTGCGAGATCACTCTTAAGAGTCACTGAGTGGCATCTGCC 860

721 TTTTGTAAAGCTTCCATGTCATTCATCCGATGAGGCGCATTTTGTGAGACTGCAGA 780  
861 TTTTGTAAAGCTTCCATGTCATTCATCCGATGAGGCGCATTTTGTGAGACTGCAGA 920

781 GTGAGAGTGAAGTTTCTTAGGGCTGAGGCGCAAGTTCACACTCAAGGCTCCCTGCTTG 840  
921 GTGAGAGTGAAGTTTCTTAGGGCTGAGGCGCAAGTTCACACTCAAGGCTCCCTGCTTG 980

841 ACATTCAAATCTCATGCTCTGAAAACCATTTCTCTGAGAGAAATGGCTGGTTGGCGC 900  
981 ACATTCAAATCTCATGCTCTGAAAACCATTTCTCTGAGAGAAATGGCTGGTTGGCGC 1040

901 CTGAGTTGGGCTTAGTACTCGAGACTCAATGACTGGAGTCTAGACTGGGCTCGGCT 960  
1041 CTGAGTTGGGCTTAGTACTCGAGACTCAATGACTGGAGTCTAGACTGGGCTCGGCT 1100

961 CGCTCTGAAGAGCTTTAAGAAAATCTTCTCAGTTCTCTTCTGAGAGAGCTGCGCGGG 1020  
1101 CGCTCTGAAGAGCTTTAAGAAAATCTTCTCAGTTCTCTTCTGAGAGAGCTGCGCGGG 1160

1021 ACGGAAAGAGAGCGGCGCTGCAAAAGCGGCGCTGAGGCTGAGTGGCATGTA 1080

Db 1161 ACGGAAAGAGAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGAGTGGCATGTA 1220  
Qy 1081 CCGGAGAGCGCTTCTCTGTTGGCTGTCAGAGCGGCGGACAGACACCTTGC 1140  
Db 1221 CCGGAGAGCGCTTCTCTGTTGGCTGTCAGAGCGGCGGACAGACACCTTGC 1279  
Qy 1141 ACGAACCACCGGCAATGCTGCGAGAGACACCTGTACAGAGAGCGGTTGATGACCGAG 1200  
Db 1280 ACGAACCACCGGCAATGCTGCGAGAGACACCTGTACAGAGAGCGGTTGATGACCGAG 1339  
Qy 1201 CTGAGTGAAGAAACCTCTCCGAGAGAGGAGAGATCATGTACGCGCGGAAGTACAG 1260  
Db 1340 CTGAGTGAAGAAACCTCTCCGAGAGAGGAGAGATCATGTACGCGCGGAAGTACAG 1399  
Qy 1261 CTGCTCCAGTCTGCTGCTGGGTTTGGCGCAGCATGATCTCCGAATCTGTTGGCATC 1320  
Db 1400 CTGCTCCAGTCTGCTGCTGGGTTTGGCGCAGCATGATCTCCGAATCTGTTGGCATC 1459  
Qy 1321 CAGCATACGCGCAATGTCACAAATCAAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1380  
Db 1460 CAGCATACGCGCAATGTCACAAATCAAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1519  
Qy 1381 AGAGA 1385  
Db 1520 AGAGA 1524

RESULT 2  
US-10-125-923A-215  
; Sequence 215, Application US/10125923A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C79  
; CURRENT APPLICATION NUMBER: US/10/125,923A  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
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; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Remaining Prior Application data removed - See file Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 215  
; LENGTH: 1337  
; TYPE: DNA  
; ORGANISM: Homo Sapien



923

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: PRIOR FILING DATE: 1999-08-17
: PRIOR APPLICATION NUMBER: 60/151733
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: PRIOR FILING DATE: 1999-12-07
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: PRIOR FILING DATE: 1999-12-07
: PRIOR APPLICATION NUMBER: 60/169835
: PRIOR FILING DATE: 1999-12-07

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Query Match 78.1% Score 1264: DB 42: Length 1524:
Best Local Similarity 99.9% Pred. No. 9.6e-234:
Matches 1384: Conservative 0: Mismatches 0: Indels 1: Gaps 1:

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QY 1 GGCACCTTTTGGGATGTTCTTCTGCTCCAGGCTTTGGCGTGAATCCAGTGTACCA 60
Db 141 GGCACCTTTTGGGATGTTCTTCTGCTCCAGGCTTTGGCGTGAATCCAGTGTACCA 200
QY 61 GTGTGAAGATTCAGCTGAAACAAGACTGCTCTCCCGAGTTCAATGTGAATTCAC 120
Db 201 GTGTGAAGATTCAGCTGAAACAAGACTGCTCTCCCGAGTTCAATGTGAATTCAC 260
QY 121 GGTGAAGCTTGAAGCATGTCTCAAGAAAGATGTAGAGCAAGTCCGGGATCATGTA 180
Db 261 GGTGAAGCTTGAAGCATGTCTCAAGAAAGATGTAGAGCAAGTCCGGGATCATGTA 320
QY 181 CCGCAAGTCTGTGATCATGAGGCGCTGTCTCATGCTCTCCGGGTACAGTCTT 240
Db 321 CCGCAAGTCTGTGATCATGAGGCGCTGTCTCATGCTCTCCGGGTACAGTCTT 380
QY 241 CTGCTCCCCAGGAACTGAAGTCAATGTTGCATGAGCTGTGCAACACCCCTTTGTA 300
Db 381 CTGCTCCCCAGGAACTGAAGTCAATGTTGCATGAGCTGTGCAACACCCCTTTGTA 440
QY 301 CGGGCCAGAGGCCCAAGAAAGGGGAGTTGCTGCGGCGCTCGAGGCGAGGCTCCGAC 360
Db 441 CGGGCCAGAGGCCCAAGAAAGGGGAGTTGCTGCGGCGCTCGAGGCGAGGCTCCGAC 500
QY 361 CACCATCTCTGTTCTCAAAATAGCCCTTCTCGGCACTGTGAAGCTGAAGAGATG 420
Db 501 CACCATCTCTGTTCTCAAAATAGCCCTTCTCGGCACTGTGAAGCTGAAGAGATG 560
QY 421 CCAGCCCTCTGCTGATGTTCTTCCAGCCCTGCGCCCAACCCCACTCTCTGAGTGA 480
Db 561 CCAGCCCTCTGCTGATGTTCTTCCAGCCCTGCGCCCAACCCCACTCTCTGAGTGA 620
QY 481 GTTCTTCTGGGTGCTCTTATTTCTGGGTAGGGAGGGGAGTCCGTTCTCTTTGTT 540
Db 621 GTTCTTCTGGGTGCTCTTATTTCTGGGTAGGGAGGGGAGTCCGTTCTCTTTGTT 680
QY 541 CCGTGCATTAATGAAGAGCTCGTAAAGCTTGAATTAATTAATTAATTAATTAAT 600
Db 681 CCGTGCATTAATGAAGAGCTCGTAAAGCTTGAATTAATTAATTAATTAATTAAT 740
QY 601 TTTTCAATGATGTTGAAGAGAGGTGAGTGAAGTTCACCCCATGTTGTGTAC 660
Db 741 TTTTCAATGATGTTGAAGAGAGGTGAGTGAAGTTCACCCCATGTTGTGTAC 800
QY 661 CGGAGTCAAGGCCAGGCTGGAGAGTCAAGTCTTAGAAGTCACTGAGTGGGATCTGCC 720
Db 801 CGGAGTCAAGGCCAGGCTGGAGAGTCAAGTCTTAGAAGTCACTGAGTGGGATCTGCC 860
QY 721 TTTTGAAGGCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 780
Db 861 TTTTGAAGGCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 920
QY 781 GTGAGAGTGAAGCTTTCTTAGGGCTGAGAGGCCAGTTCCCACTGAAGCTCCCTGCTTG 840

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Db 921 GTGAGAGTGAAGCTTTCTTAGGGCTGAGAGGCCAGTTCCCACTGAAGCTCCCTGCTTG 980
QY 841 ACAATTAATTAATGATGCTCTGAAACCAATTCCTGACAGAGATGGCTGGTTGCGCC 900
Db 981 ACAATTAATTAATGATGCTCTGAAACCAATTCCTGACAGAGATGGCTGGTTGCGCC 1040
QY 901 CTGAGTTGGGCTCTAGTGAAGTCAAGTCAATGAGTGAAGTGAAGTGAAGTGAAGT 960
Db 1041 CTGAGTTGGGCTCTAGTGAAGTCAAGTCAATGAGTGAAGTGAAGTGAAGTGAAGT 1100
QY 961 CGCTCTGAAGAGTCTTAAAGAAATCTTCTCAATTTCTCTTGAAGAGACTGGCGCGGG 1020
Db 1101 CGCTCTGAAGAGTCTTAAAGAAATCTTCTCAATTTCTCTTGAAGAGACTGGCGCGGG 1160
QY 1021 ACGGGAAGCAACAGGCGCTGCAACAAGCGGCGCTGTGCGGTGGAGTGGCATGTA 1080
Db 1161 ACGGGAAGCAACAGGCGCTGCAACAAGCGGCGCTGTGCGGTGGAGTGGCATGTA 1220
QY 1081 CCGCAGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1221 CCGCAGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
QY 1141 ACGAACAACCCGGAAGTCTGCGAGACACCTGTACAGAGCGGTTGATGACCGAG 1200
Db 1280 ACGAACAACCCGGAAGTCTGCGAGACACCTGTGTACAGAGCGGTTGATGACCGAG 1339
QY 1201 CTGAGGTAGAAAGGTCCTCGAAGAGGAGAGATGATGATGATGATGATGATGATG 1260
Db 1340 CTGAGGTAGAAAGGTCCTCGAAGAGGAGAGATGATGATGATGATGATGATGATG 1399
QY 1261 CTGCTCAGTGTGCTTGGGTTGGCGGAGCCATGATCTCGAATCTGTTGGGCATC 1320
Db 1400 CTGCTCAGTGTGCTTGGGTTGGCGGAGCCATGATCTCGAATCTGTTGGGCATC 1459
QY 1321 CAGCATACGCGCATGTACACATCAGCCCTGGCAGACAGAGAGAGAGAGAGAG 1380
Db 1460 CAGCATACGCGCATGTACACATCAGCCCTGGCAGACAGAGAGAGAGAGAGAG 1519
QY 1381 AGAGA 1385
Db 1520 AGAGA 1524

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Job time : 3659.06 secs

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 PRIOR APPLICATION NUMBER: 60/146963  
 PRIOR FILING DATE: 1999-08-03  
 PRIOR APPLICATION NUMBER: 60/149320

TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-218-631-15

Query Match 78.1% Score 1264; DB 42; Length 1524;  
Best Local Similarity 99.9%; Pred. No. 9,6e-234;  
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 1 GGCACATTTTTCGAGATTTCTTCTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA 60
DB 141 GGCACATTTTTCGAGATTTCTTCTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA 200
OY 61 GTGTGAAGAATTCACGTGACACAGACTGCTCTCCCGAGTTCAATGTGAATGGAC 120
DB 201 GTGTGAAGAATTCACGTGACACAGACTGCTCTCCCGAGTTCAATGTGAATGGAC 260
OY 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGAAATGATGAGCAAAATGCCGGATATGTA 180
DB 261 GGTGAAGCTTCAAGACATGTGTGAGAAAGAAATGATGAGCAAAATGCCGGATATGTA 320
OY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTGCCGGGTACAGTCCCT 240
DB 321 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTGCCGGGTACAGTCCCT 380
OY 241 CTGTCTCCCGAGGAAACTGACATCACTGTTGCATCACTGTGCAACACCCCTCTTTGTA 300
DB 381 CTGTCTCCCGAGGAAACTGACATCACTGTTGCATCACTGTGCAACACCCCTCTTTGTA 440
OY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 360
DB 441 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 500
OY 361 CACCATCTCTGTTCTCAAAATAGCCCTCTTCGCGACACTGCTGAACCTGAAGAGATG 420
DB 501 CACCATCTCTGTTCTCAAAATAGCCCTCTTCGCGACACTGCTGAACCTGAAGAGATG 560
OY 421 CCAGCCCTCTCTGCAATGTTCTTCCAGCCCTCGCCCAACCCCACTCTCTGAGTGA 480
DB 561 CCAGCCCTCTCTGCAATGTTCTTCCAGCCCTCGCCCAACCCCACTCTCTGAGTGA 620
OY 481 GTTCTCTGAGGTCCTTTTATCTGGGTAGGAGCGGGAGTCCGTCTCTTTTGT 540
DB 621 GTTCTCTGAGGTCCTTTTATCTGGGTAGGAGCGGGAGTCCGTCTCTTTTGT 680
OY 541 CCTGTCAAAATTAAGAGAGCTCGTAAAGCAATCTGAATTAATTCAGCTGACTGAAT 600
DB 681 CCTGTCAAAATTAAGAGAGCTCGTAAAGCAATCTGAATTAATTCAGCTGACTGAAT 740
OY 601 TTTTCAGTATGTAAGAGAGAGGAGTGAAGTGAATGACCCCACTGCTGTGTAAC 660
DB 741 TTTTCAGTATGTAAGAGAGAGGAGTGAAGTGAATGACCCCACTGCTGTGTAAC 800
OY 661 CGGAGTCAAGGCGCAGAGTGCAGAGTCACTGCTTAAGAGTGAAGTGGGCAATCTGCC 720
DB 801 CGGAGTCAAGGCGCAGAGTGCAGAGTCACTGCTTAAGAGTGAAGTGGGCAATCTGCC 860
OY 721 TTTTGTAAAGCTCCAGTGTCCATTCCTCATGATGGGGCATAGTTGAGACTGAGAG 780
DB 861 TTTTGTAAAGCTCCAGTGTCCATTCCTCATGATGGGGCATAGTTGAGACTGAGAG 920
OY 781 GTGAGAGTGAAGTGTCTTAAAGGCTGAGAGGCGCAGTTCCCACTCAAGGCTCCCTGG 840
DB 921 GTGAGAGTGAAGTGTCTTAAAGGCTGAGAGGCGCAGTTCCCACTCAAGGCTCCCTGG 980
OY 841 ACATTCAAACTTCATGCTCTGAAAAACATCTCTGCGAGCAAGATTTGGCTTCCGCG 900
DB 981 ACATTCAAACTTCATGCTCTGAAAAACATCTCTGCGAGCAAGATTTGGCTTCCGCG 1040
OY 901 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGAGTTAGACTGGGGCTCGGCT 960
DB 1041 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGAGTTAGACTGGGGCTCGGCT 1100
OY 961 CGCTCTGAAAAGTGTGAAGAAATCTTCTGATGTTCTTGACAGAGACTGCGCGGG 1020

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DB 1101 CGCTCTGAAAAGTGTGAAGAAATCTTCTAGTTCCTTCCAGAGACTGCGCGCGG 1160
OY 1021 ACAGGAGAGCAACAGGCGCTCTGACAAAGCGGCGCTGTGTGGTGTGAGTCCGATGTA 1080
DB 1161 ACAGGAGAGCAACAGGCGCTCTGACAAAGCGGCGCTGTGTGGTGTGAGTCCGATGTA 1220
OY 1081 CGCGAGGCGCTTCTGCGGTGTGCGTGTGCTGACGACAGCGGCGACACGACCTTGC 1140
DB 1221 CGCGAGGCGCTTCTGCGGTGTGCGTGTGCTGACGACAGCGGCGACACGACCTTGC 1279
OY 1141 ACAGAACCCCGCAAACTGCTGCGAGAGACACCTGTACAGAGAGCGGTTGATGACCGAG 1200
DB 1280 ACAGAACCCCGCAAACTGCTGCGAGAGACACCTGTACAGAGAGCGGTTGATGACCGAG 1339
OY 1201 CTGAGGTGAGAAAACGCTCTCGAGAGAGGAGAGATCATGTACGCCGGAAGTAGAC 1260
DB 1340 CTGAGGTGAGAAAACGCTCTCGAGAGAGGAGAGATCATGTACGCCGGAAGTAGAC 1399
OY 1261 CTGCTCCAGTGTGCTTGGGTTGGCCGACGACATGATCCGGAATCTGTTGGGCATC 1320
DB 1400 CTGCTCCAGTGTGCTTGGGTTGGCCGACGACATGATCCGGAATCTGTTGGGCATC 1459
OY 1321 CAGCATACGGCCAAATGTCACAAATCAGCCCTGGGCGACAGAGGAGGAGAGAC 1380
DB 1460 CAGCATACGGCCAAATGTCACAAATCAGCCCTGGGCGACAGAGGAGGAGAGAC 1519
OY 1381 AGAGA 1385
DB 1520 AGAGA 1524

```

RESULT 45  
US-10-218-765-15

Sequence 15, Application US/10218765

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Geriltsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3530P1C19

CURRENT APPLICATION NUMBER: US/10/218,765

PRIOR FILING DATE: 2002-08-12

PRIOR FILING DATE: 2002-10-11, 480

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

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PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31



Query Match 78.1%; Score 1264; DB 42; Length 1524;  
 Best Local Similarity 99.9%; Pred. No. 9,6e-234;  
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 GGGAACTTTTGGGAGTGTCTCTGCTTCAGAGCTTTGGGCTGCAAAATCAGTGTGACCA 60  
 141 GGGAACTTTTGGGAGTGTCTCTGCTTCAGAGCTTTGGGCTGCAAAATCAGTGTGACCA 200  
 61 GTGTGAAGAAATTCAGCTGAACAACAGCTGTCTCTCTCCCGAGTTTCAATTTGTAATTCAC 120  
 201 GTGTGAAGAAATTCAGCTGAACAACAGCTGTCTCTCTCCCGAGTTTCAATTTGTAATTCAC 260  
 121 GGGAACTTTTGGGAGTGTCTCTGCTTCAGAGCTTTGGGCTGCAAAATCAGTGTGACCA 180  
 261 GGGAACTTTTGGGAGTGTCTCTGCTTCAGAGCTTTGGGCTGCAAAATCAGTGTGACCA 320  
 181 CCGAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGGCTCTGCGGGTACCAAGTCTT 240  
 321 CCGAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGGCTCTGCGGGTACCAAGTCTT 380  
 241 CTCTCTCCCGAGGAAATGAACTGAACTGTTGCAATGCTGTGCAACACCTCTTTGTA 300  
 381 CTCTCTCCCGAGGAAATGAACTGAACTGTTGCAATGCTGTGCAACACCTCTTTGTA 440  
 301 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 441 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 500  
 361 CACATCTCTTCTCTCAAAATTTAGCCCTCTCTCTGCGACACATGCTGAAGATG 420  
 501 CACATCTCTTCTCTCAAAATTTAGCCCTCTCTCTGCGACACATGCTGAAGATG 560  
 421 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
 561 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 620  
 481 GATTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 621 GATTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 541 CCGTGTCAAAATTAATGAAGAGCTGCTGAAGAGCTGCTGAATTAATTAATTAATTAAT 600  
 681 CCGTGTCAAAATTAATGAAGAGCTGCTGAAGAGCTGCTGAATTAATTAATTAATTAAT 740  
 601 TTTAGTATGATCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 741 TTTAGTATGATCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 800  
 661 CCGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
 801 CCGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 860  
 721 TTTTGTAAAGGCTTCACTGTCATTCATCCCTGATGGGGCATAGTTTGAAGACTGAGA 780  
 861 TTTTGTAAAGGCTTCACTGTCATTCATCCCTGATGGGGCATAGTTTGAAGACTGAGA 920  
 781 GTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 921 GTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 980  
 841 ACATTTCAAACTTCACTGTCATTCATCCCTGATGGGGCATAGTTTGAAGACTGAGA 900  
 981 ACATTTCAAACTTCACTGTCATTCATCCCTGATGGGGCATAGTTTGAAGACTGAGA 1040  
 901 CTGAGTGGGCTCTAGTACTCGAGACTCAATGACTGGAGCTTGAAGTGGGGCTCGGGCT 960  
 1041 CTGAGTGGGCTCTAGTACTCGAGACTCAATGACTGGAGCTTGAAGTGGGGCTCGGGCT 1100  
 961 CCGCTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
 1101 CCGCTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1160

1021 ACGGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
 1161 ACGGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1220  
 1081 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
 1221 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1280  
 1141 ACGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
 1280 ACGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1360  
 1201 CTGAGTGAAGAAAGCTGTCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
 1340 CTGAGTGAAGAAAGCTGTCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1399  
 1261 CTCTCTCAGT 1370  
 1400 CTCTCTCAGT 1459  
 1321 CAGCATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
 1460 CAGCATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1519  
 1381 AGAGA 1385  
 1520 AGAGA 1524

RESULT 44  
 US-10-218-631-15  
 ; Sequence 15, Application US/10218631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin I.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PIC14  
 ; CURRENT APPLICATION NUMBER: US/10/218,631  
 ; PRIOR FILING DATE: 2002-08-12  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See file wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 15  
 ; LENGTH: 1524



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Db 141 GGCACATTTTTCGGATGTTCTTCTTCAGGCTTTGCGTGAATCCAGTCTTACCA 200
Oy 61 GTGTGAAGATTCACAGTGAACAGACAGTGTCTCTCCCGAGTTCATTTGAATTCAC 120
Db 201 GTGTGAAGATTCACAGTGAACAGACAGTGTCTCTCCCGAGTTCATTTGAATTCAC 260
Oy 121 GGTGAACGTTTCAAGACATGTGTCAAGAAAGATGTATGAGACAAAGTGGCGGATCATGTA 180
Db 261 GGTGAACGTTTCAAGACATGTGTCAAGAAAGATGTATGAGACAAAGTGGCGGATCATGTA 320
Oy 181 CCCGAGTCTGTGCTATCATACAGGCGCTGTCTCATGCGCTGTGCGGGTACAGTCTT 240
Db 321 CCCGAGTCTGTGCTATCATACAGGCGCTGTCTCATGCGCTGTGCGGGTACAGTCTT 380
Oy 241 CTGCTCCCGAGGAAAGTCAAGTCAAGTTCATCAAGTCTGTGCAACACCCCTTTGTAA 300
Db 381 CTGCTCCCGAGGAAAGTCAAGTTCATCAAGTCTGTGCAACACCCCTTTGTAA 440
Oy 301 CGGGCCCAAGGCCCAAGAAAGGGAGTTCGCTCGGCGCTCAGAGGCGTCCGAGC 360
Db 441 CGGGCCCAAGGCCCAAGAAAGGGAGTTCGCTCGGCGCTCAGAGGCGTCCGAGC 500
Oy 361 CACATCTCTTCTCAAAATTAACCTCTTCTCGGACACTGTGAAGTGAAGATG 420
Db 501 CACATCTCTTCTCAAAATTAACCTCTTCTCGGACACTGTGAAGTGAAGATG 560
Oy 421 CCACCCCTCTCTCAATTTTCACAGCCCTGCCCCAACCCCCCACTCCCTCATGTA 480
Db 561 CCACCCCTCTCTCAATTTTCACAGCCCTGCCCCAACCCCCCACTCCCTCATGTA 620
Oy 481 GTTCTCTGCGGTGCTCTTATTTCTGGGAGGAGCGGAGTCTGTTCTTTGTT 540
Db 621 GTTCTCTGCGGTGCTCTTATTTCTGGGAGGAGCGGAGTCTGTTCTTTGTT 680
Oy 541 CCTGTGCAAAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT 600
Db 681 CCTGTGCAAAATTAATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT 740
Oy 601 TTTTGAATGTACTTGAAGAGAGGAGTGAAGTGAAGTCAACCCCATGTCTGTATAC 660
Db 741 TTTTGAATGTACTTGAAGAGAGGAGTGAAGTGAAGTCAACCCCATGTCTGTATAC 800
Oy 661 CGGAGTCAAGGCGCTGAGAGTGTCTTGAAGAGTCAAGTGAAGTGGGCGATCTGCC 720
Db 801 CGGAGTCAAGGCGCTGAGAGTGTCTTGAAGAGTCAAGTGAAGTGGGCGATCTGCC 860
Oy 721 TTTTGAATGTACTTGAAGAGAGTGTCTTGAAGAGTCAAGTGAAGTGGGCGATCTGCC 780
Db 861 TTTTGAATGTACTTGAAGAGAGTGTCTTGAAGAGTCAAGTGAAGTGGGCGATCTGCC 920
Oy 781 GTGAGAGTGAAGTGTCTTGAAGAGGAGGAGTCCACTCAAGAGGCTCCCTGCTTG 840
Db 921 GTGAGAGTGAAGTGTCTTGAAGAGGAGGAGTCCACTCAAGAGGCTCCCTGCTTG 980
Oy 841 ACATTCAAACTTCATGCTCTGAAAGACCATTTCTGTGACGAGAAATGGCTTTGGCGC 900
Db 981 ACATTCAAACTTCATGCTCTGAAAGACCATTTCTGTGACGAGAAATGGCTTTGGCGC 1040
Oy 901 CTGAGTGTGGGCTGTAGTACATGACATGATGATGAGTGGGGCTCGGCGCT 960
Db 1041 CTGAGTGTGGGCTGTAGTACATGACATGATGATGAGTGGGGCTCGGCGCT 1100
Oy 961 CGCTCTGAAGAGTCTTGAAGAAATCTTCTCAAGTTCCTTTCAGAGAGAGTGGCGCGG 1020
Db 1101 CGCTCTGAAGAGTCTTGAAGAAATCTTCTCAAGTTCCTTTCAGAGAGAGTGGCGCGG 1160
Oy 1021 ACGCGAAGAGCAGCGGCGCTGACACAAAGGCGGCGTGTGCGTGTGAGATGGCGATGTA 1080
Db 1161 ACGCGAAGAGCAGCGGCGCTGACACAAAGGCGGCGTGTGCGTGTGAGATGGCGATGTA 1220
Oy 1081 CGCGAGGCGCTTCTGTGTTGGGCTGTGACGAGAGGCGGCGACAGCACTTGC 1140

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Db 1221 CGCGAGGCGCTTCTGTGTTGGGCTGTGCTGACGACGACAGGCGGACAGCACC-TGC 1279
Oy 1141 AGAAGACCCCGCCGAAACTGTGCGAGAGACACGTTATACAGAGCGGGTTGATGACCGAG 1200
Db 1280 AGAAGACCCCGCCGAAACTGTGCGAGAGACACGTTATACAGAGCGGGTTGATGACCGAG 1339
Oy 1201 CTGAGGTGAAGAAAGTCTCCGAGAGGAGGAGATCATGTATGAGCCCGGAATAGAGAC 1260
Db 1340 CTGAGGTGAAGAAAGTCTCCGAGAGGAGGAGATCATGTATGAGCCCGGAATAGAGAC 1399
Oy 1261 CTGCTCAGTGTGCTTGGGTTTGGCCGAGCAGCATGATCTCCAAATCTGGTTGGCATC 1320
Db 1400 CTGCTCAGTGTGCTTGGGTTTGGCCGAGCAGCATGATCTCCAAATCTGGTTGGCATC 1459
Oy 1321 CAGCATACGCGCAATGTCAACATTCAGCCCTGGGCGACAGCAGCAGAGAGAGAC 1380
Db 1460 CAGCATACGCGCAATGTCAACATTCAGCCCTGGGCGACAGCAGCAGAGAGAGAC 1519
Oy 1381 AGAGA 1385
Db 1520 AGAGA 1524

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RESULT 42
US-10-216-168-15
; Sequence 15, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-216-168-15
Query Match 78.1% Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9,6e-234;

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QY 61 GTGTGAAGATTCACAGTACAGACGACGTCCTCCCTCCGAGTTCATTTGAATTCAC 120  
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 Db 201 GTGTGAAGATTCACAGTACAGACGACGTCCTCCCTCCGAGTTCATTTGAATTCAC 260  
 |||||  
 QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGTAGAGCAAGATGCCGGATCATGTA 180  
 |||||  
 Db 261 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGTAGAGCAAGATGCCGGATCATGTA 320  
 |||||  
 QY 181 CCAGATGCTGTGATCATCATCAGCGGCGTCTCATCCCTCTGCCGGGTACAGTCTT 240  
 |||||  
 Db 321 CCAGATGCTGTGATCATCATCAGCGGCGTCTCATCCCTCTGCCGGGTACAGTCTT 380  
 |||||  
 QY 241 CTGCTCCCAAGGAAACTGAACTAGTTGCATCAGCTGCTGAACACCCCTCTTTGAA 300  
 |||||  
 Db 381 CTGCTCCCAAGGAAACTGAACTAGTTGCATCAGCTGCTGAACACCCCTCTTTGAA 440  
 |||||  
 QY 301 CGGGCCCAAGGAAAGGAAAGGAAAGTTCGCTCGGCTCAAGCCAGGGCTCCGAC 360  
 |||||  
 Db 441 CGGGCCCAAGGAAAGGAAAGGAAAGTTCGCTCGGCTCAAGCCAGGGCTCCGAC 500  
 |||||  
 QY 361 CACATTCCTGTTCTCAAAATTCAGCCCTCTCTCGGCAACAGTGGAGCTGAAGAGATG 420  
 |||||  
 Db 501 CACATTCCTGTTCTCAAAATTCAGCCCTCTCTCGGCAACAGTGGAGAGATG 560  
 |||||  
 QY 421 CCACCCCTCTGTCATGTTCTTCCAGCCCTCGCCCAACCCCACTCCCTGAGTGA 480  
 |||||  
 Db 561 CCACCCCTCTGTCATGTTCTTCCAGCCCTCGCCCAACCCCACTCCCTGAGTGA 620  
 |||||  
 QY 481 GTTCTCTCGGGTGTCTTTATTTCTGGGTAGGAGCGGGAGTCCGTTCTTTGTT 540  
 |||||  
 Db 621 GTTCTCTCGGGTGTCTTTATTTCTGGGTAGGAGCGGGAGTCCGTTCTTTGTT 680  
 |||||  
 QY 541 CCTGTGCAAAATATGAAAGAGCTCGGTAAAGCATTCGAAATTAATTCAGCTGAGTAA 600  
 |||||  
 Db 681 CCTGTGCAAAATATGAAAGAGCTCGGTAAAGCATTCGAAATTAATTCAGCTGAGTAA 740  
 |||||  
 QY 601 TTTGAGTATGACTTGAAGAGAGAGAGTGAAGTAAAGTTACCCCATCTGTGTAA 660  
 |||||  
 Db 741 TTTGAGTATGACTTGAAGAGAGAGAGTGAAGTAAAGTTACCCCATCTGTGTAA 800  
 |||||  
 QY 661 CGAGATCAAGGCGCAGGCTGGCAGAGTCAAGTCTTGAAGTCACTGAGTGGGATCGCC 720  
 |||||  
 Db 801 CGAGATCAAGGCGCAGGCTGGCAGAGTCAAGTCTTGAAGTCACTGAGTGGGATCGCC 860  
 |||||  
 QY 721 TTTTGTAAAGCTTCAAGTGTCCATTCCTGATGGGGGATAGTTGAGACTGACA 780  
 |||||  
 Db 861 TTTTGTAAAGCTTCAAGTGTCCATTCCTGATGGGGGATAGTTGAGACTGACA 920  
 |||||  
 QY 781 GTGAGAGTGAAGTCTTGTAGGGCTGGAGGCGCATTCACATCAAGGCTCCCTGCTTG 840  
 |||||  
 Db 921 GTGAGAGTGAAGTCTTGTAGGGCTGGAGGCGCATTCACATCAAGGCTCCCTGCTTG 980  
 |||||  
 QY 841 ACATTCAAACTTCATGCTCTGAAAAACATTCCTGACAGAGAAATGGGTGGTTCGGCC 900  
 |||||  
 Db 981 ACATTCAAACTTCATGCTCTGAAAAACATTCCTGACAGAGAAATGGGTGGTTCGGCC 1040  
 |||||  
 QY 901 CTGAGTGGGCTGATGACTGACACTCAATGACTGGGACTTGAAGTGGGCTGGGCT 960  
 |||||  
 Db 1041 CTGAGTGGGCTGATGACTGACACTCAATGACTGGGACTTGAAGTGGGCTGGGCT 1100  
 |||||  
 QY 961 CGCTCTGAAAAAGTCTTAAGAAAAATCTTCAGTTCCTCTGACAGAGACTGGCCGGG 1020  
 |||||  
 Db 1101 CGCTCTGAAAAAGTCTTAAGAAAAATCTTCAGTTCCTCTGACAGAGACTGGCCGGG 1160  
 |||||  
 QY 1021 ACGCGAAGAGCAACGGGCGGTGACAAAGCGGGCGTGTGCGTGGAGTGGCATGTA 1080  
 |||||  
 Db 1161 ACGCGAAGAGCAACGGGCGGTGACAAAGCGGGCGTGTGCGTGGAGTGGCATGTA 1220  
 |||||  
 QY 1081 CGGCGAGGGCTCTCTGCTGGTGGCTGTGACGAGCAGCGGCGGAGCAGACACCTTGC 1140  
 |||||  
 Db 1221 CGGCGAGGGCTCTCTGCTGGTGGCTGTGACGAGCAGCGGCGGAGCAGACACCTTGC 1279  
 |||||  
 QY 1141 ACGAACAACCGCGAAGAACTGTGCTGAGGAGACCGGTGTACAGAGCGGGTGTATGACGAG 1200  
 |||||

Db 1280 ACGAACAACCGCGAAGAACTGTGCGAGAGACACCGTGTACAGAGAGCGGTTATACCGAG 1339  
 |||||  
 QY 1201 CTGAGGTAGAAAAAGCTCTCCGAGAAAGGAGAGAGATCATGTACGCCGGAATAGAC 1260  
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 Db 1340 CTGAGGTAGAAAAAGCTCTCCGAGAAAGGAGAGAGATCATGTACGCCGGAATAGAC 1399  
 |||||  
 QY 1261 CTGCTCAAGTGTGCTGGGTTGGCCGACCATGATCTCCGAATCTGGTGGCATC 1320  
 |||||  
 Db 1400 CTGCTCAAGTGTGCTGGGTTGGCCGACCATGATCTCCGAATCTGGTGGCATC 1459  
 |||||  
 QY 1321 CAGCATACGCGCAATGTCAACAATTCAGCCCTGGGCAAGACAGAGAGAGAGAGAC 1380  
 |||||  
 Db 1460 CAGCATACGCGCAATGTCAACAATTCAGCCCTGGGCAAGACAGAGAGAGAGAGAC 1519  
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 QY 1381 AGAGA 1385  
 |||||  
 Db 1520 AGAGA 1524

RESULT 41  
 US-10-216-167-15  
 ; Sequence 15, Application US/10216167  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530P1CA  
 ; CURRENT APPLICATION NUMBER: US/10/216,167  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 15  
 ; LENGTH: 1524  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-216-167-15

Query Match 78.1%; Score 1264; DB 42; Length 1524;  
 Best Local Similarity 99.9%; Pred. No. 9.6e-234;  
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Caps 1;  
 QY 1 GGCACCTTTTGGCGATGTCTCTGCTTCCAGGCTTTGCGGCTGCAAAATCCAGTGTACCA 60

121 GGTGAAGCTTCAAGACATGTGTCAGAAAGATGATGAGGACAAAGTGGCGGATCATGTA 180  
122 GGTGAAGCTTCAAGACATGTGTCAGAAAGATGATGAGGACAAAGTGGCGGATCATGTA 180  
261 GGTGAAGCTTCAAGACATGTGTCAGAAAGATGATGAGGACAAAGTGGCGGATCATGTA 320  
181 CGGCAAGTCTGTGATCATGAGCGGCTGTCTCATCGCTCTGCGGGATACAGTCTT 240  
182 CGGCAAGTCTGTGATCATGAGCGGCTGTCTCATCGCTCTGCGGGATACAGTCTT 240  
321 CGGCAAGTCTGTGATCATGAGCGGCTGTCTCATCGCTCTGCGGGATACAGTCTT 380  
241 CTGCTCCCCAGGAAAGTCACTGATTTGATGATGATGATGATGATGATGATGATGAT 300  
381 CTGCTCCCCAGGAAAGTCACTGATTTGATGATGATGATGATGATGATGATGATGAT 440  
301 CGGCAAGTCTGTGATCATGAGCGGCTGTCTCATCGCTCTGCGGGATACAGTCTT 360  
441 CGGCAAGTCTGTGATCATGAGCGGCTGTCTCATCGCTCTGCGGGATACAGTCTT 500  
361 CACCATCTGTCTCTCAATTAATGAGCTTCTGCGGACACTGCTGAAGCTGAAGAGATG 420  
501 CACCATCTGTCTCTCAATTAATGAGCTTCTGCGGACACTGCTGAAGCTGAAGAGATG 560  
421 CACCCCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
561 CACCCCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 620  
481 GTTCTCTGAGGCTCTCTTCTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
621 GTTCTCTGAGGCTCTCTTCTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 680  
541 CCTGTGCAATTAATGAAGAGCTGCTGAAGAGCTGCTGAAGAGCTGCTGAAGAGAT 600  
681 CCTGTGCAATTAATGAAGAGCTGCTGAAGAGCTGCTGAAGAGCTGCTGAAGAGAT 740  
601 TTTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
741 TTTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800  
661 CGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
801 CGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 860  
721 TTTTGTAAAGCTCTCAAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 780  
861 TTTTGTAAAGCTCTCAAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 920  
781 GTGAGAGTACGTTTCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
921 GTGAGAGTACGTTTCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 980  
841 ACATTCAAATTCATGCTCTGTAAGAGCTGCTGTAAGAGCTGCTGTAAGAGCTGCTGTA 900  
981 ACATTCAAATTCATGCTCTGTAAGAGCTGCTGTAAGAGCTGCTGTAAGAGCTGCTGTA 1040  
901 CTGAGTGTGGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
1041 CTGAGTGTGGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1100  
961 CGCTGTGAAGAGCTTGAAGAAATCTTCTGATGATGATGATGATGATGATGATGATGAT 1020  
1101 CGCTGTGAAGAGCTTGAAGAAATCTTCTGATGATGATGATGATGATGATGATGATGAT 1160  
1021 ACAGCAAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
1161 ACAGCAAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1220  
1081 CGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
1221 CGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1279  
1141 ACAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
1280 ACAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1339

1201 CTGAGTGTGAAGAAAGCTCTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
1340 CTGAGTGTGAAGAAAGCTCTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1399  
1261 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
1400 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459  
1321 CAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
1460 CAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1519  
1381 AGAGA 1385  
1520 AGAGA 1524  
RESULT 40  
US-10-216-166-15  
Sequence 15, Application US/10216166  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerilsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C9  
CURRENT APPLICATION NUMBER: US/10/216,166  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See file Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-216-166-15  
Query March 78.1% Score 1264; DB 42; Length 1524;  
Best Local Similarity 99.9%; Pred. No. 9.6e-234;  
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
1 GGCACCTTTTGGCGGATGTTCTTCTTCCAGGCTTTCGCGTTCGAATTCAGTGTCTACCA 60  
141 GGCACCTTTTGGCGGATGTTCTTCTTCCAGGCTTTCGCGTTCGAATTCAGTGTCTACCA 200



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Db 321 CCGCAGATCTGTGCATATAGAGCGGCTGTCTCATCGCCTCGCGGGTACCACTCTT 380
Qy 241 CTGCTCCCGGAGAACTGAATCTAGTTGATCAGCTGCTGCAACACCCCTTTGTA 300
Db 381 CTGCTCCCGGAGAACTGAATCTAGTTGATCAGCTGCTGCAACACCCCTTTGTA 440
Qy 301 CGGCGCAAGGCGGCAAGAAAGGGAGTTGCTCGGCGCCCTCAGGCGCAGGCGCTCCGAC 360
Db 441 CGGCGCAAGGCGGCAAGAAAGGGAGTTGCTCGGCGCCCTCAGGCGCAGGCGCTCCGAC 500
Qy 361 CACCATCTGTCTCTCAATTAAGCCCTCTCTCGGCAACACCTGCTGAGCTGAAGAGATG 420
Db 501 CACCATCTGTCTCTCAATTAAGCCCTCTCTCGGCAACACCTGCTGAGCTGAAGAGATG 560
Qy 421 CCACCCCTCTCTGATTTCTTCCAGCCCTCGCCCAACCCCTCAGCTGAGAGGA 480
Db 561 CCACCCCTCTCTGATTTCTTCCAGCCCTCGCCCAACCCCTCAGCTGAGAGGA 620
Qy 481 GTTCTCTGCGGTGTCTTTTATTTCTGGGTAGGAGCGGAGTCCGTCTCTTTGTT 540
Db 621 GTTCTCTGCGGTGTCTTTTATTTCTGGGTAGGAGCGGAGTCCGTCTCTTTGTT 680
Qy 541 CCTGTGCAATATATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAT 600
Db 681 CCTGTGCAATATATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAT 740
Qy 601 TTTTCTGATGTCTTGAAGAGAGAGTGAAGTGAAGTTCACCCCTGCTGTGTATAC 660
Db 741 TTTTCTGATGTCTTGAAGAGAGAGTGAAGTGAAGTTCACCCCTGCTGTGTATAC 800
Qy 661 CGGAGTCAAGGCGGAGCTGGCAGAGTCACTTCTTGAAGTCACTGAGTGGGCTCTCC 720
Db 801 CGGAGTCAAGGCGGAGCTGGCAGAGTCACTTCTTGAAGTCACTGAGTGGGCTCTCC 860
Qy 721 TTTTCTGAAGCCTCCAGTGTCCATTCCTGATGGGGCATAGTTTGAGACTGCGAGA 780
Db 861 TTTTCTGAAGCCTCCAGTGTCCATTCCTGATGGGGCATAGTTTGAGACTGCGAGA 920
Qy 781 GTGAGAGTACGTTTTCTTAGGGCTGAGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 840
Db 921 GTGAGAGTACGTTTTCTTAGGGCTGAGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 980
Qy 841 ACATTCAAACTTCATGCTCTGAAAAACCAATTCCTGACAGCAATTTGGCTGGTTCGGGC 900
Db 981 ACATTCAAACTTCATGCTCTGAAAAACCAATTCCTGACAGCAATTTGGCTGGTTCGGGC 1040
Qy 901 CTGAGTTGGGCTCTAGTACTGAGACATCATGACTGGGACTTAGACTGGGGCTCGGCTT 960
Db 1041 CTGAGTTGGGCTCTAGTACTGAGACATCATGACTGGGACTTAGACTGGGGCTCGGCTT 1100
Qy 961 CGCTGTGAAGAGTGTGAAGAAATCTTCTCAGTTCTCTCTTGCAGAGAGACTGGGCGCGG 1020
Db 1101 CGCTGTGAAGAGTGTGAAGAAATCTTCTCAGTTCTCTCTTGCAGAGAGACTGGGCGCGG 1160
Qy 1021 ACGCGAAGAGCAAGCGGCGCTGCACAAAGCGGCGCTGCGGTGGTGAAGTGGCGCATGTA 1080
Db 1161 ACGCGAAGAGCAAGCGGCGCTGCACAAAGCGGCGCTGCGGTGGTGAAGTGGCGCATGTA 1220
Qy 1081 CGCGGAGCGGCTCTCTGCTTGGGCTGCTGAGAGCAGAGGCGGCGAGCAGACCTTGC 1140
Db 1221 CGCGGAGCGGCTCTCTGCTTGGGCTGCTGAGAGCAGAGGCGGCGAGCAGACCTTGC 1279
Qy 1141 ACGAAGACCCGCGGAAAGTGTGCGAGGACACGCTGACAGAGCGGCTGATGACCGAG 1200
Db 1280 ACGAAGACCCGCGGAAAGTGTGCGAGGACACGCTGACAGAGCGGCTGATGACCGAG 1339
Qy 1201 CTGAGGTAGAAAAAGTCTCCGAGAAAGGAGAGGATCATGTACGCCGGAAGTAGGAC 1260
Db 1340 CTGAGGTAGAAAAAGTCTCCGAGAAAGGAGAGGATCATGTACGCCGGAAGTAGGAC 1399
Qy 1261 CTCGTCCAGTCTGTGCTTGGGCTTGGCCGAGCATGATCTCCGAATCTGTTGGGCAATC 1320

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Db 1400 CTGCTCCAGTCTGCTTGGGCTTGGCCGAGCCCATGATCTCCGAATCTGTGGGCATC 1459
Qy 1321 CAGCATAGGCGCAATGTCAACAAATCAGCCCTGGGCGAGACAGCAGAGGAGAGAC 1380
Db 1460 CAGCATAGGCGCAATGTCAACAAATCAGCCCTGGGCGAGACAGCAGAGGAGAGAC 1519
Qy 1381 AGAGA 1385
Db 1520 AGAGA 1524

RESULT 38
US-10-216-164-15
; Sequence 15, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P105
; CURRENT APPLICATION NUMBER: US/10/216, 164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119, 480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-164-15

Query Match 78.18; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9, 6e-234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```



Qy	241	CTGCTCCCCAGGAAACGAACCTAGTTTGATCAGCTGCTGCAACACCCTTTTGTAA	300
Db	381	CTGCTCTCCCAAGGAAACGAACCTAGTTTGATCAGCTGCTGCAACACCCTTTTGTAA	440
Qy	301	CGGGCCAAGGGCCCAAGAAAAGGGAGATTTGCGCTCGGCGCTTAGGGCCAGAGGCTCCGCAC	360
Db	441	CGGGCCAAGGGCCCAAGAAAAGGGAGATTTGCGCTCGGCGCTTAGGGCCAGAGGCTCCGCAC	500
Qy	361	CACCAATCCTGTTTCTCTCAAAATTAGCCCTCTTCTGCGCACACTGCTGAAGCTGAAGAGATG	420
Db	501	CACCAATCCTGTTTCTCTCAAAATTAGCCCTCTTCTGCGCACACTGCTGAAGCTGAAGAGATG	560
Qy	421	CCACCCTCCCGCATTTGTCTTCACGCGCGCGCCCAACCCCCCAACCTCCCTAGATGA	480
Db	561	CCACCCTCCCTCGCATTTGTCTTCACGCGCGCGCCCAACCCCCCAACCTCCCTAGATGA	620
Qy	481	CTTTCTTCTGGGTGTCTTTTATTTCTGGGTAGGGAGCGGAGTCCGCTGTTCTTTTGT	540
Db	621	CTTTCTTCTGGGTGTCTTTTATTTCTGGGTAGGGAGCGGAGTCCGCTGTTCTTTTGT	680
Qy	541	CCTGTGCAAAATPATGAAGAAGCTCGTAAAGCATTTCTGAATAAATTCAGCCGTAGCTAAT	600
Db	681	CCTGTGCAAAATPATGAAGAAGCTCGTAAAGCATTTCTGAATAAATTCAGCCGTAGCTAAT	740
Qy	601	TTTTCAATGTACTTTGAAGAGAGAGAGGTGGAGAGTGAAGATTACACCCCATGTCTGTATAC	660
Db	741	TTTTCAATGTACTTTGAAGAGAGAGAGGTGGAGAGTGAAGATTACACCCCATGTCTGTATAC	800
Qy	661	CGGAGTCAAGGCCCAAGGCTGGCAGAGTATAGTCTTTAGAAGTCACTGTAGGTGGGCACTGGCC	720
Db	801	CGGAGTCAAGGCCCAAGGCTGGCAGAGTATAGTCTTTAGAAGTCACTGTAGGTGGGCACTGGCC	860
Qy	721	TTTTTAAAGCCTCCAGTGTCCATTTCATCCCTGATGGGGCACTAGTTTGAGACTGCAGA	780
Db	861	TTTTTAAAGCCTCCAGTGTCCATTTCATCCCTGATGGGGCACTAGTTTGAGACTGCAGA	920
Qy	781	GGAGAGTACGATTTCTTAAAGGTGGAGGGGCCAGTTCCCACTCAAGGCTCCCTGCTTG	840
Db	921	GGAGAGTACGATTTCTTAAAGGTGGAGGGGCCAGTTCCCACTCAAGGCTCCCTGCTTG	980
Qy	841	ACATTCAAACTTCATGCTGCTCGAAGAACATTTCTCTGACAGAGAAATGGGCTGGTTTCGGGC	900
Db	981	ACATTCAAACTTCATGCTGCTCGAAGAACATTTCTCTGACAGAGAAATGGGCTGGTTTCGGGC	1040
Qy	901	CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGGCACTTAGACTGGGGCTCGGCT	960
Db	1041	CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGGCACTTAGACTGGGGCTCGGCT	1100
Qy	961	CGCTCTGAAAAGTCTTAAAGAAATCTTCTCAATTTCTCTTGACAGAGCATGGCGCGGG	1020
Db	1101	CGCTCTGAAAAGTCTTAAAGAAATCTTCTCAATTTCTCTTGACAGAGCATGGCGCGGG	1160
Qy	1021	ACGCGAAGAGCAAGGGCGCGTGCACAAAGGGGGCGGTGCGGGGTGGAGTGGCGGATGA	1080
Db	1161	ACGCGAAGAGCAAGGGCGCGTGCACAAAGGGGGCGGTGCGGGGTGGAGTGGCGGATGA	1220
Qy	1081	CGCGAGGCGCTTCTCGTGTGTGGCGTGTGACAGCAGAGGGGGCAGCAGACACTTTGC	1140
Db	1221	CGCGAGGCGCTTCTCGTGTGTGGCGTGTGACAGCAGAGGGGGCAGCAGACACTTTGC	1279
Qy	1141	ACGAACACCCGCCCAAACTGCTGCGAGAGACACCGTGTACAGAGCGGGTTGATGACCGAG	1200
Db	1280	ACGAACACCCGCCCAAACTGCTGCGAGAGACACCGTGTACAGAGCGGGTTGATGACCGAG	1339
Qy	1201	CTGAGGTGTAAGAAAACGCTCCGAGAAAGGGAGAGGATCATGTACGCCCGCGGAAGTAGAC	1266
Db	1340	CTGAGGTGTAAGAAAACGCTCCGAGAAAGGGAGAGGATCATGTACGCCCGCGGAAGTAGAC	1399
Qy	1261	CTCGTCCAGTGTGCTTTGGGTTTGGCCGACAGCCATATCTCCGAATCTGTTGGGCATTC	1320
Db	1400	CTCGTCCAGTGTGCTTTGGGTTTGGCCGACAGCCATATCTCCGAATCTGTTGGGCATTC	1455
Qy	1321	CAGCATACGGCCAAATGTCCACACATTCAGCCCTTGCGCAGACACGAGAGGAGAGAC	1380

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Db      1460 CAGCATACGCGCAATGTCAACAACAACTACGCCCTGGGCGACACAGCAGAGGAGAGAC 1519
QY      1381 AGAGA 1385
Db      1520 AGAGA 1524

RESULT 37
US-10-216-163-15
; Sequence 15, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-15

Query Match      78.1%; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9,6e+234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 GGCACATTTTGGCGGATTTCTTCTTCAGGCTTTGGCGTGCACAAATTCAGTGTACCA 60
Db      141 GGCACATTTTTCGGGATTTCTTCTTCAGGCTTTGGCGTGCACAAATTCAGTGTACCA 200
QY      61 GTGTAAAGATTCACGCTGCACACACGACTGCTCTCCGCCCGGATTCATTTGTAAATTCAC 120
Db      201 GTGTAAAGATTCACGCTGCACACACGACTGCTCTCCGCCCGGATTCATTTGTAAATTCAC 260
QY      121 GGTGAACGTTCAAGACATGTGTCAAGAAAGTGAATGAGGACAAAGTGGCGGATCATGTA 180
Db      261 GGTGAACGTTCAAGACATGTGTCAAGAAAGTGAATGAGGACAAAGTGGCGGATCATGTA 320
QY      181 CCGCAAGTCGTGTGCATCATCAGCGCGCTGTCTCATCGCCTTGTGCCGGGTACACATCTTT 240

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Db 141 GGCACATTTTGGCGGATTGTTCTTCCAGAGGCTTTGCGCTGCMAATCCAGTGTACCA 200
QY 61 GTGTAAATAATTCAGCTGAACAAAGACTGCTCCCTCCCGCAGTTCAATTTGAATTCAC 120
Db 201 GTGTAAATAATTCAGCTGAACAAAGACTGCTCCCTCCCGCAGTTCAATTTGAATTCAC 260
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
Db 261 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 320
QY 181 CCGCAAGTCTGTGATCATCATAGCGGCTGTCTCATGCTCTGTCCGGGTACAGTCTT 240
Db 321 CCGCAAGTCTGTGATCATCATAGCGGCTGTCTCATGCTCTGTCCGGGTACAGTCTT 380
QY 241 CTGCTCCCGAGGAAAGTGAATCATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 381 CTGCTCCCGAGGAAAGTGAATCATGATGATGATGATGATGATGATGATGATGATGAT 440
QY 301 CCGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTCGGCGCTCAGCGCCAGGCGTCCGAC 360
Db 441 CCGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTCGGCGCTCAGCGCCAGGCGTCCGAC 500
QY 361 CACCAATCCTGTCTCAAAATTTAGCCCTCTCTCGGCAACATGCTGAAGTGAATG 420
Db 501 CACCAATCCTGTCTCAAAATTTAGCCCTCTCTCGGCAACATGCTGAAGTGAATG 560
QY 421 CACACCCCTCTGTCAATTTGTTTCCAGGCGCTCGGCGCCAGCCCTCCTCTGATGA 480
Db 561 CACACCCCTCTGTCAATTTGTTTCCAGGCGCTCGGCGCCAGCCCTCCTCTGATGA 620
QY 481 GTTCTCTGCGGTCTCTTTTATTTCTGCGTGAAGAGCGGAGTCCGTTCTCTTTTGT 540
Db 621 GTTCTCTGCGGTCTCTTTTATTTCTGCGTGAAGAGCGGAGTCCGTTCTCTTTTGT 680
QY 541 CCTGTGCAAAATTAAGAGAGTGGTAAAGATCTCTGAATTAATTCAGCTGACTGAT 600
Db 681 CCTGTGCAAAATTAAGAGAGTGGTAAAGATCTCTGAATTAATTCAGCTGACTGAT 740
QY 601 TTTCAATATGATCTGAAGAGAGTGGTAAAGATCTCTGAATTAATTCAGCTGACTGAT 660
Db 741 TTTCAATATGATCTGAAGAGAGTGGTAAAGATCTCTGAATTAATTCAGCTGACTGAT 800
QY 661 CCGAGTCAAGGCGCAGAGTGCAGAGTCAAGTCTTGAAGTCAAGTGGGATCTGCTCC 720
Db 801 CCGAGTCAAGGCGCAGAGTGCAGAGTCAAGTCTTGAAGTCAAGTGGGATCTGCTCC 860
QY 721 TTTTGAAGGCTCCAGTGTCCATCCATCCCTGATGGGGGATGTTTGAAGTGCAGA 780
Db 861 TTTTGAAGGCTCCAGTGTCCATCCATCCCTGATGGGGGATGTTTGAAGTGCAGA 920
QY 781 GTGAGAGTGCATTTTCTTGAAGGCTGAGAGGCGCAATTCCTCAAGGCTCCCTGCTTG 840
Db 921 GTGAGAGTGCATTTTCTTGAAGGCTGAGAGGCGCAATTCCTCAAGGCTCCCTGCTTG 980
QY 841 ACATTTCAAACTTCATGCTCTGAAAAACATTTCTCTGACAGCAAGATTTGGCTTTCGCGC 900
Db 981 ACATTTCAAACTTCATGCTCTGAAAAACATTTCTCTGACAGCAAGATTTGGCTTTCGCGC 1040
QY 901 CTGAGTGGGCTCTAGTACCTGAGACATCAATGATGGGACTTGAAGTGGGCTGGGCT 960
Db 1041 CTGAGTGGGCTCTAGTACCTGAGACATCAATGATGGGACTTGAAGTGGGCTGGGCT 1100
QY 961 CCGTCTGAAGAAATGCTTAAGAAATCTTCTCAGTTCTCTTTCAGAGAGACTGGGCGG 1020
Db 1101 CCGTCTGAAGAAATGCTTAAGAAATCTTCTCAGTTCTCTTTCAGAGAGACTGGGCGG 1160
QY 1021 ACGGCAAGAGCAAGGCGGCTGCACAAAGCGGCGCTGTCCGTGGTGAAGTCCGATGTA 1080
Db 1161 ACGGCAAGAGCAAGGCGGCTGCACAAAGCGGCGCTGTCCGTGGTGAAGTCCGATGTA 1220
QY 1081 CCGGCAAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1221 CCGGCAAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279

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QY 1141 ACGAAGACCCCGGAAACCTGTGAGAGACACCGTGTACAGAGGAGGTTGATGACCGAG 1200
Db 1280 ACGAAGACCCCGGAAACCTGTGAGAGACACCGTGTACAGAGGAGGTTGATGACCGAG 1339
QY 1201 CTGAGGTAGAAAAACGTTCTCCGAAAGGAGAGAGATCATGTAAGCCCGGAAGTAGAG 1260
Db 1340 CTGAGGTAGAAAAACGTTCTCCGAAAGGAGAGAGATCATGTAAGCCCGGAAGTAGAG 1399
QY 1261 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1400 CTGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459
QY 1321 CAGCATAGGCGCAATGTCAACAATATGAGCCCTGAGGAGAGACAGAGAGGAGAGAG 1380
Db 1460 CAGCATAGGCGCAATGTCAACAATATGAGCCCTGAGGAGAGAGAGAGAGAGAGAG 1519
QY 1381 AGAGA 1385
Db 1520 AGAGA 1524

```

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RESULT 35
US-10-216-160-15
; Sequence 15, Application us/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geriltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Malanbe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-216-160-15

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Query Match 78.1%; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9, 6e-234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGCACATTTTGGCGGATTGTTCTTCCAGAGGCTTTGCGCTGCMAATCCAGTGTACCA 60
Db 141 GGCACATTTTGGCGGATTGTTCTTCCAGAGGCTTTGCGCTGCMAATCCAGTGTACCA 200
QY 61 GTGTGAAGATTCAGAGTGAACAACGACTGCTCTCCCGGATTTCAATTTGAATTCAC 120
Db 201 GTGTGAAGATTCAGAGTGAACAACGACTGCTCTCCCGGATTTCAATTTGAATTCAC 260
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
Db 261 GGTGAACGTTCAAGACATGTGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 320
QY 181 CCGCAAGTCTGTGATCATCATAGCGGCTGTCTCATGCTCTGTCCGGGTACAGTCTT 240
Db 321 CCGCAAGTCTGTGATCATCATAGCGGCTGTCTCATGCTCTGTCCGGGTACAGTCTT 380
QY 241 CTGCTCCCGAGGAAAGTGAATCATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 381 CTGCTCCCGAGGAAAGTGAATCATGATGATGATGATGATGATGATGATGATGATGAT 440

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|||||
Db 201 GTGTGAAGATTCAGACGTGACACAGACGCTCCCTCCCGAGTTCATTGTGAATTCAC 260
Oy 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGCAAAATGCGCGGATATGTA 180
Db 261 GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGCAAAATGCGCGGATATGTA 320
Oy 181 CGCAAGTCTGTGATCATCATCAGCGCCGTGTCTCATCCGCTTGGCGGGATACAGTCTT 240
Db 321 CGCAAGTCTGTGATCATCATCAGCGCCGTGTCTCATCCGCTTGGCGGGATACAGTCTT 380
Oy 241 CTGTCTCCAGGGAATGACTGATGTTGATCATGCTGTGCAACACCCCTCTTTGTA 300
Db 381 CTGTCTCCAGGGAATGACTGATGTTGATCATGCTGTGCAACACCCCTCTTTGTA 440
Oy 301 CGGGCCAAAGGCGCAAGAAAGGGAAGTTCTGCGCGCCCTCAGGCGCAGGCTCCGAC 360
Db 441 CGGGCCAAAGGCGCAAGAAAGGGAAGTTCTGCGCGCCCTCAGGCGCAGGCTCCGAC 500
Oy 361 CACATCTCTGTTCTCAATTAATTAAGCCCTCTTCTGCGCACACTGTGAGCTGAGAGATG 420
Db 501 CACATCTCTGTTCTCTCAATTAATTAAGCCCTCTTCTGCGCACACTGTGAGCTGAGAGATG 560
Oy 421 CCACCCCTCTGATGTTGTTCTTCCAGCCCTGCCCCAACCCCCACCTCCCTGATGA 480
Db 561 CCACCCCTCTGATGTTGTTCTTCCAGCCCTGCCCCAACCCCCACCTCCCTGATGA 620
Oy 481 GTTCTCTGCGGTGTCCTTTTATCTGGGTAGGAGCGGAGATCCGTGTCTCTTTGTT 540
Db 621 GTTCTCTGCGGTGTCCTTTTATCTGGGTAGGAGCGGAGATCCGTGTCTCTTTGTT 680
Oy 541 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTCGATTAATTAATTCAGCTGATGAT 600
Db 681 CCTGTGCAATTAATGAAGAGCTCGTAAAGCATTCGATTAATTAATTCAGCTGATGAT 740
Oy 601 TTTTCACTATGTTCTTGAAGAGAGAGGTGAGTGAAGTTCAACCCCATGTCTGTGAAC 660
Db 741 TTTTCACTATGTTCTTGAAGAGAGAGGTGAGTGAAGTTCAACCCCATGTCTGTGAAC 800
Oy 661 CGAGAGTCAAGGCGAGGCTGGCAGAGTCACTCTTGAAGTCACTGAGGTGGGCACTCTCC 720
Db 801 CGAGAGTCAAGGCGAGGCTGGCAGAGTCACTCTTGAAGTCACTGAGGTGGGCACTCTCC 860
Oy 721 TTTTGTAAAGCCTCCAGTGTCCATTCATCCCTGATGGGGCATGTTGAGATGACAGA 780
Db 861 TTTTGTAAAGCCTCCAGTGTCCATTCATCCCTGATGGGGCATGTTGAGATGACAGA 920
Oy 781 GTGAGAGTACCTTTTCTTGAAGGCTGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 840
Db 921 GTGAGAGTACCTTTTCTTGAAGGCTGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 980
Oy 841 ACATTCAAACTTCATGCTCTGAAAAACATTCCTGTGACAGCAATTTGGTGTGGGCG 900
Db 981 ACATTCAAACTTCATGCTCTGAAAAACATTCCTGTGACAGCAATTTGGTGTGGGCG 1040
Oy 901 CTGAGTTGGGCTCTGATGACTCTGAGACTCAATGAGTGGGACTTGAAGTGGGGCTG 960
Db 1041 CTGAGTTGGGCTCTGATGACTCTGAGACTCAATGAGTGGGACTTGAAGTGGGGCTG 1100
Oy 961 CGCTCTGAAAATGCTTGAAGAAATCTTCTCAGTTCTCTTCAAGAGACTGTGGCCGG 1020
Db 1101 CGCTCTGAAAATGCTTGAAGAAATCTTCTCAGTTCTCTTCAAGAGACTGTGGCCGG 1160
Oy 1021 ACAGCAAGAGCAAGGCGCTGACAAAGCGGCGCTGCGGTGGTGGATGCGCATGTA 1080
Db 1161 ACAGCAAGAGCAAGGCGCTGACAAAGCGGCGCTGCGGTGGTGGATGCGCATGTA 1220
Oy 1081 CGGCAAGGCGCTTCTGTGTTGGCGTGTGACGACAGGCGGAGAGACACAGCACTTGC 1140
Db 1221 CGGCAAGGCGCTTCTGTGTTGGCGTGTGACGACAGGCGGAGAGACACAGCACTTGC 1200
Oy 1141 AGGAACACCGCGCAAACTGCTGCGAGGACACCGTGTACAGAGGCGGTGATGACGAG 1200
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Db 1280 AGGAACACCGCGCAAACTGCTGAGAGACACCGTGTACAGAGCGGTTGATGACCGAG 1339
Oy 1201 CTGAGTAGAAGAAACGTCCTCCGAGAGGAGAGATCATGTACCCCGAGTAGAGAC 1260
Db 1340 CTGAGTAGAAGAAACGTCCTCCGAGAGGAGAGATCATGTACCCCGAGTAGAGAC 1399
Oy 1261 CTGCTCAGTCTGCTTGGGTTGGGCGCGCAGCCATGATCTCCGAAATCTGTGGGCATC 1320
Db 1400 CTGCTCAGTCTGCTTGGGTTGGGCGCGCAGCCATGATCTCCGAAATCTGTGGGCATC 1459
Oy 1321 CAGCATACGGCCAAATGTCACAAACATCAGCCCTGTGGCAGACAGAGAGAGAGAC 1380
Db 1460 CAGCATACGGCCAAATGTCACAAACATCAGCCCTGTGGCAGACAGAGAGAGAGAC 1519
Oy 1381 AGAGA 1385
Db 1520 AGAGA 1524

```

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RESULT 34
US-10-216-159A-15
; Sequence 15, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-159A-15

Query Match 78.1%; Score 1264; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 9,6e-234;
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Oy 1 GCGCACTTTTGGCGATGTTGTTCTTCCAGGCTTGGCCTGCAAAATCCAGTGTACCA 60
|||||

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Query Match 80.2%; Score 1299; DB 31; Length 1917;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-240;  
 Matches 1519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 79 GAACAACGACTGCTCCCTCCCGAGTTCATTTGTAATTCACGCGTGAACGTTCAAGACAT 138
    |||
Db 373 GAACAACGACTGCTCCCTCCCGAGTTCATTTGTAATTCACGCGTGAACGTTCAAGACAT 432
QY 139 GTGTGAGAAGAAGTGAAGAGCAAAAGTCCGGGATCATATGCCAGTCTCTGTCATC 198
    |||
Db 433 GTGTGAGAAGAAGTGAAGAGCAAAAGTCCGGGATCATATGCCAGTCTCTGTCATC 492
QY 199 ATCAGGCGGCTGTCTCATGCGCTGCGGGATCAGTCTCTCTCCCGAGGAAACT 258
    |||
Db 493 ATCAGGCGGCTGTCTCATGCGCTGCGGGATCAGTCTCTCTCCCGAGGAAACT 552
QY 259 GAATCTAGTTTCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCAAAGGCCAAGAA 318
    |||
Db 553 GAATCTAGTTTCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCAAAGGCCAAGAA 612
QY 319 AAGGGGAATTCGCTGCGCTGCGGCTCAGGGCCAGGCTCCGACACCATCTCTTCTGAA 378
    |||
Db 613 AAGGGGAATTCGCTGCGCTGCGGCTCAGGGCCAGGCTCCGACACCATCTCTTCTGAA 672
QY 379 ATTAGCCCTCTCTCTGCGACACTGCTGAAGCTGAAGAGATCCACCCCTCTCTGATTC 438
    |||
Db 673 ATTAGCCCTCTCTCTGCGACACTGCTGAAGCTGAAGAGATCCACCCCTCTCTGATTC 732
QY 439 TTCTTCACGCTCGCCGCCCAACCCGCCACCTCCCTGAGTGAATTTCTTGGGTGCTCT 498
    |||
Db 733 TTCTTCACGCTCGCCGCCCAACCCGCCACCTCCCTGAGTGAATTTCTTGGGTGCTCT 792
QY 499 TTTATTTCTGGTGAAGGAGGCGGAGTCCGTTCTCTTTGTCCGTCGCAAAATATGAAA 558
    |||
Db 793 TTTATTTCTGGTGAAGGAGGCGGAGTCCGTTCTCTTTGTCCGTCGCAAAATATGAAA 852
QY 559 GAGCTCGTGAAGCATTTCTGAATTAATTCAGCTGATGAATTTCACTATGACTTAA 618
    |||
Db 853 GAGCTCGTGAAGCATTTCTGAATTAATTCAGCTGATGAATTTCACTATGACTTAA 912
QY 619 GGAAGAGGTGAGTGAAGATTCACCCCATGCTGTGTAAACGGAGTCAAGGGCAGGCT 678
    |||
Db 913 GGAAGAGGTGAGTGAAGATTCACCCCATGCTGTGTAAACGGAGTCAAGGGCAGGCT 972
QY 679 GGCAGAGTCACTCTTAAGAGTCACTAGAGTGGGATCTGCTTTTGTAAAGCCCTCCAGT 738
    |||
Db 973 GGCAGAGTCACTCTTAAGAGTCACTAGAGTGGGATCTGCTTTTGTAAAGCCCTCCAGT 1032
QY 739 GTTCATTCATCCCTGATGAGGGGATAGTTTGAAGTCACTGAGAGTGAAGTGGTTTCT 798
    |||
Db 1033 GTTCATTCATCCCTGATGAGGGGATAGTTTGAAGTCACTGAGAGTGAAGTGGTTTCT 1092
QY 799 TAGGGCTGAGGGGAGTCCCATCTCAAGGCTCCCTGCTTGAACATTCATGCT 858
    |||
Db 1093 TAGGGCTGAGGGGAGTCCCATCTCAAGGCTCCCTGCTTGAACATTCATGCT 1152
QY 859 CCTGAAACCATCTCTCTGAGAGAAATTTGGCTTTGGCGCTGAGTTGGGCTTATGTG 918
    |||
Db 1153 CCTGAAACCATCTCTCTGAGAGAAATTTGGCTTTGGCGCTGAGTTGGGCTTATGTG 1212
QY 919 ACTGAGACTCAATGACTGAGACTAGACTGGGGCTCGGCTCGCTGAAAGTGCCTTA 978
    |||
Db 1213 ACTGAGACTCAATGACTGAGACTAGACTGGGGCTCGGCTCGCTGAAAGTGCCTTA 1272
QY 979 AGAAATATCTTCTCAAGTTCTCTTGCAGAGAGATGCGCGGAGCCGGAAGCAAGCGGC 1038
    |||
Db 1273 AGAAATATCTTCTCAAGTTCTCTTGCAGAGAGATGCGCGGAGCCGGAAGCAAGCGGC 1332
QY 1039 GCTGCACAAAGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1098
    |||
Db 1333 GCTGCACAAAGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1392

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QY 1099 GGTGGCGTGTCTGACGAGACAGGCGGACAGACACTTTCAGCAAGAACCCGCGAAG 1158
    |||
Db 1393 GGTGGCGTGTCTGACGAGACAGGCGGACAGACACTTTCAGCAAGAACCCGCGAAG 1451
QY 1159 TGTTCGAGAGACACCGTGTACAGAGCGGGGTGATGACCAAGCTGAGGTGAAAAACGTC 1218
    |||
Db 1452 TGTTCGAGAGACACCGTGTACAGAGCGGGGTGATGACCAAGCTGAGGTGAAAAACGTC 1511
QY 1219 TCCGAGAAGGGGAGAGGATCATGTACGCGCGGAAGTAGGACCTCGTCAGTGGCTTG 1278
    |||
Db 1512 TCCGAGAAGGGGAGAGGATCATGTACGCGCGGAAGTAGGACCTCGTCAGTGGCTTG 1571
QY 1279 GGTGGCGCGGACGATGATCTCCGAATCTGTTGGGATTCAGCATACGAGCAATGTC 1338
    |||
Db 1572 GGTGGCGCGGACGATGATCTCCGAATCTGTTGGGATTCAGCATACGAGCAATGTC 1631
QY 1339 ACAACATCAGCCCTGGGACACGACAGCAGAGGAGAGACAGAGAAAAAGAAACACA 1398
    |||
Db 1632 ACAACATCAGCCCTGGGACACGACAGCAGAGGAGAGACAGAGAAAAAGAAACACA 1691
QY 1399 GCATGAGAACACAGTAATGATTAACATTAATTAATTAATTAATTAATTAATTAAT 1458
    |||
Db 1692 GCATGAGAACACAGTAATGATTAACATTAATTAATTAATTAATTAATTAATTAAT 1751
QY 1459 ACTGGCCAGGAATGTATCAATTTTCAAGTGTGACTTGACAGCTTCTTTGCGACAA 1518
    |||
Db 1752 ACTGGCCAGGAATGTATCAATTTTCAAGTGTGACTTGACAGCTTCTTTGCGACAA 1811
QY 1519 GCAAGAGAGATTTAAACAGTGTTCAAACCCGGGAGGTTGCTGTGTAAAGAGACC 1578
    |||
Db 1812 GCAAGAGAGATTTAAACAGTGTTCAAACCCGGGAGGTTGCTGTGTAAAGAGACC 1871
QY 1579 ATTAATGCTTTAGACAGTGA 1600
    |||
Db 1872 ATTAATGCTTTAGACAGTGA 1893

```

## RESULT 33

US-10-119-480-15

Sequence 15, Application US/10119480

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3530P1C1

CURRENT APPLICATION NUMBER: US/10/119,480

CURRENT FILING DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 246

Prior Application removed - See file wrapper or Palm

SEQ ID NO 15

LENGTH: 1524

TYPE: DNA

ORGANISM: Homo Sapien

US-10-119-480-15

Query Match 78.1%; Score 1264; DB 40; Length 1524;

Best Local Similarity 99.9%; Pred. No. 9.6e-234;

Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 GGCACATTTTGGCGGATTTGTTTCTTCCAGCGTTTGGCTGCAATCCAGTGTACCA 60
    |||
Db 141 GGCACATTTTGGCGGATTTGTTTCTTCCAGCGTTTGGCTGCAATCCAGTGTACCA 200
QY 61 GTGTGAAGAATTCAGCTGAACAACGACTCTCTCCCGGAGTTCAATGTGCAATGCAAC 120

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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1170-001
; CURRENT APPLICATION NUMBER: US/09/652.917
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151.422
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2477
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-652-917-2477

Query Match      80.2%  Score 1299; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 1,76-240;
Matches 1519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 79 GAACAAAGCAGTCTCTCCCGGAGTTCATTTGTGATTCAGCAGGTGAACGTTCAAGACAT 138
DB 373 GAAACAAAGCAGTCTCTCCCGGAGTTCATTTGTGATTCAGCAGGTGAACGTTCAAGACAT 432
QY 139 GTGTGAGAAAGAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCGTGTGATC 198
DB 433 GTGTGAGAAAGAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCGTGTGATC 492
QY 199 ATCAGCGGCTCTCTATCCCTCTCTCCGGGATCAGGATCCTTCTCTCCCGAAGGAAACT 258
DB 493 ATCAGCGGCTCTCTATCCCTCTCTCCGGGATCAGGATCCTTCTCTCCCGAAGGAAACT 552
QY 259 GAACATCAGTTTGCATCAGTCTGCTGCAACACCCCTTTTGTACGGGCGCAAGGCCCAAGAA 318
DB 553 GAACATCAGTTTGCATCAGTCTGCTGCAACACCCCTTTTGTACGGGCGCAAGGCCCAAGAA 612
QY 319 AAGGGAGATTTCTGCTCGCCGCTCAGGCGAGGCTCCGACACCCATCTCTTCTCTCAA 378
DB 613 AAGGGAGATTTCTGCTCGCCGCTCAGGCGAGGCTCCGACACCCATCTCTTCTCTCAA 672
QY 379 ATTAGCCCTCTCTGCGGACACGCTGAGAGCAAGAGAGATCCACCCCTCTCTGATTTG 438
DB 673 ATTAGCCCTCTCTGCGGACACGCTGAGAGCAAGAGAGATCCACCCCTCTCTGATTTG 732
QY 439 TTCTTTCACGCTCTGCGCCCAACCCCAACCCCTCTCTGATGAGTTCTTCTGCTGCTCT 498
DB 733 TTCTTTCACGCTCTGCGCCCAACCCCAACCCCTCTCTGATGAGTTCTTCTGCTGCTCT 792
QY 499 TTTATTTCTGGGATGAGGAGCGGAGTCCGTCTCTTTTGTCTCTGCTGCAAAATTAAGAA 558
DB 793 TTTATTTCTGGGATGAGGAGCGGAGTCCGTCTCTTTTGTCTCTGCTGCAAAATTAAGAA 852
QY 559 GAGCTCGGTAAGGCAATTCGAATTAATTCAGCTGACTGAATTTTCAGTATGACTTGA 618
DB 853 GAGCTCGGTAAGGCAATTCGAATTAATTCAGCTGACTGAATTTTCAGTATGACTTGA 912
QY 619 GGAAGAGGTGAGAGTGAAGTTTCAACCCCATGCTGTGTACCCGAGATCAAGGCCAGGCT 678
DB 913 GGAAGAGGTGAGAGTGAAGTTTCAACCCCATGCTGTGTACCCGAGATCAAGGCCAGGCT 972
QY 679 GGCAGAGTCACTCTTGAAGTACTGAGGTGGGCAATCTGCTTTTGTAAAGCTTCACT 738
DB 973 GGCAGAGTCACTCTTGAAGTACTGAGGTGGGCAATCTGCTTTTGTAAAGCTTCACT 1032
QY 739 GTCCATTTCCATCCCTANTGGGGGAGTATGTTTGTAGCTGAGAGTGAAGTGAAGTCTTCT 798
DB 1033 GTCCATTTCCATCCCTANTGGGGGAGTATGTTTGTAGCTGAGAGTGAAGTGAAGTCTTCT 1092
QY 799 TAGGGCTGAGGGGCGAGTTCCACTCAAGGCTCCCTGCTTGAATTCAAACTTCACTGCT 858
DB 1093 TAGGGCTGAGGGGCGAGTTCCACTCAAGGCTCCCTGCTTGAATTCAAACTTCACTGCT 1152
QY 859 CCGTGAATTCATTTCTGCGAGCAGAAATTTGGCTGTTTCCGGCTGAGTTGGGCTCTAGTG 918
DB 1153 CCGTGAATTCATTTCTGCGAGCAGAAATTTGGCTGTTTCCGGCTGAGTTGGGCTCTAGTG 1212

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QY 919 ACTGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCTCTGCTGAAAGTGTCTTA 978
DB 1213 ACTGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCTCTGCTGAAAGTGTCTTA 1272
QY 979 AGAAATCTTCTCAGTCTCTCTTTCAGAGAGACTGCGCGGAGCGGAGAGCAACGGGCT 1038
DB 1273 AGAAATCTTCTCAGTCTCTCTTTCAGAGAGACTGCGCGGAGCGGAGAGCAACGGGCT 1332
QY 1039 GCTGACAAAGCGGGGCTGTGCTGTGAGAGTCCCATGTACCGGAGGCGCTTCTGCT 1098
DB 1333 GCTGACAAAGCGGGGCTGTGCTGTGAGAGTCCCATGTACCGGAGGCGCTTCTGCT 1392
QY 1099 GGTGGGCTGCTGAGGAGCAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1158
DB 1393 GGTGGGCTGCTGAGGAGCAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1451
QY 1159 TGCTGCGAGGACACCGTGTACAGAGGCGGTTGATGACCGAGCTGAGTGAAGAAACGTC 1218
DB 1452 TGCTGCGAGGACACCGTGTACAGAGGCGGTTGATGACCGAGCTGAGTGAAGAAACGTC 1511
QY 1219 TCCGAGAAAGGAGAGAGATCATGTACGCCGGAAGTAGAGCTCGTCCAGTCTGCTTG 1278
DB 1512 TCCGAGAAAGGAGAGAGATCATGTACGCCGGAAGTAGAGCTCGTCCAGTCTGCTTG 1571
QY 1279 GGTGGGCGGAGCAGTATCTCCGAAATCTGGTGGGCAATCCAGATACGCCCAATGTC 1338
DB 1572 GGTGGGCGGAGCAGTATCTCCGAAATCTGGTGGGCAATCCAGATACGCCCAATGTC 1631
QY 1339 ACANCAATCAGCCCTGGGAGACAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1398
DB 1632 ACANCAATCAGCCCTGGGAGACAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1691
QY 1399 GCATGAGACACAGTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1458
DB 1692 GCATGAGACACAGTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1751
QY 1459 ACTGGCCAGGAAATGTAACCAATTTTTCAGTGTGACCTTGTGACCTTCTTTTGCACAA 1518
DB 1752 ACTGGCCAGGAAATGTAACCAATTTTTCAGTGTGACCTTGTGACCTTCTTTTGCACAA 1811
QY 1519 GCAAGAGAGATTTTAACACTTCTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGAC 1578
DB 1812 GCAAGAGAGATTTTAACACTTCTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGAC 1871
QY 1579 AFTAATGCTTTAGACAGTGTGA 1600
DB 1872 AFTAATGCTTTAGACAGTGTGA 1893

RESULT 32
US-09-801-833-7188
; Sequence 7188, Application us/09801833
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, M. Alexandra
; TITLE OF INVENTION: NOCUTIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600.1037-005
; CURRENT APPLICATION NUMBER: US/09/801.833
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 09/371,168
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/095,907
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/103,145
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 8285
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7188
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-833-7188

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QY	79	GAACACGACTGCTCTCTCCCGGAGTCACTTGTAATTCACGGTGAACGTTCAAGACAT	13
Db	373	GAACACGACTGCTCTCTCCCGGAGTCACTTGTAATTCACGGTGAACGTTCAAGACAT	43
QY	139	GTTCTGAAAAGAGTGATGAGACAAAGTCCCGGATCATGTACCCCAAGTCTTGATC	191
Db	433	GTTCTGAAAAGAGTGATGAGACAAAGTCCCGGATCATGTACCCCAAGTCTTGATC	493
QY	199	ATCAGGGGCTGTCTCATTCGCTCTGCGGGGTACCAAGTCTTTCGCTCCCAAGGAAACT	251
Db	493	ATCAGGGGCTGTCTCATTCGCTCTGCGGGGTACCAAGTCTTTCGCTCCCAAGGAAACT	551
QY	259	GAACTCAGTTTGCATCAGCTGCTGCAACACCCTTTTGTAACGGGGCCAAAGCCACAGAA	311
Db	553	GAACTCAGTTTGCATCAGCTGCTGCAACACCCTTTTGTAACGGGGCCAAAGCCACAGAA	611
QY	319	AAGGGGAAGTTCGCTCGGCCCTCAGGCCAAGGGCTCCGACACACATCTGTTCTTCA	371
Db	613	AAGGGGAAGTTCGCTCGGCCCTCAGGCCAAGGGCTCCGACACACATCTGTTCTTCA	671
QY	379	ATTACCCCTCTCTCGGACACACTGCTGAAGCTGAAAGAGATGCCAACCCCTCTCGCATTG	431
Db	673	ATTACCCCTCTCTCGGACACACTGCTGAAGCTGAAAGAGATGCCAACCCCTCTCGCATTG	731
QY	439	TTCCTTCAGACCCTCCGCCCAACCCGCCACCTCCCTGATGAGTTCTTTCGGGGTTCCT	491
Db	733	TTCCTTCAGACCCTCCGCCCAACCCGCCACCTCCCTGATGAGTTCTTTCGGGGTTCCT	791
QY	499	TTTATTCTGGGTAGGGACGGGAGTCCGTGTTCTTTTGTCTCTGTCCAATTAATGAA	551
Db	793	TTTATTCTGGGTAGGGACGGGAGTCCGTGTTCTTTTGTCTCTGTCCAATTAATGAA	851
QY	559	GAGCTCGGTAAAGCATTTCTGAATAATTACAGCTGACTGAATTTTCAGATGTACTTGAA	611
Db	853	GAGCTCGGTAAAGCATTTCTGAATAATTACAGCTGACTGAATTTTCAGATGTACTTGAA	911
QY	619	GGAAGAGAGTGGAGGAAAGTTCAACCCCATGCTGTGTAAACGGAGATCAAGGGCAGGCT	671
Db	913	GGAAGAGAGTGGAGGAAAGTTCAACCCCATGCTGTGTAAACGGAGATCAAGGGCAGGCT	971

QY	679	GGCAGAGTCACCTCCTTGAAGTACACAGATGGGGGACACCTGCTTTGTAAACCTCCAGT	738
Db	973	GGCAGAGTCACCTCCTTGAAGTACACAGATGGGGGACACCTGCTTTGTAAACCTCCAGT	1032
QY	739	GTCATTCATCCCTGATGGGGGACATAGTTTGAAGCTGCAGATGAGATGACGTGTTTCT	798
Db	1033	GTCATTCATCCCTGATGGGGGACATAGTTTGAAGCTGCAGATGAGATGACGTGTTTCT	1092
QY	799	TAGGGCTGGAGGGCCAGTTCCTCACCTCAAGGCTCCCTGCTTACATTCMAACTTCATGCT	858
Db	1093	TAGGGCTGGAGGGCCAGTTCCTCACCTCAAGGCTCCCTGCTTACATTCMAACTTCATGCT	1152
QY	859	CCTGAAAAACATTCCTGACAGAGAAATTTGGGCTGTTCCGGCTCAGATTGGGCTTACTG	918
Db	1153	CCTGAAAAACATTCCTGACAGAGAAATTTGGGCTGTTCCGGCTCAGATTGGGCTTACTG	1212
QY	919	ACTGAGACTCAATGACTGGGACTTATGACTGGGGGCTCGGCTCGCTGTAAGAGTGCCTTA	978
Db	1213	ACTGAGACTCAATGACTGGGACTTATGACTGGGGGCTCGGCTCGCTGTAAGAGTGCCTTA	1272
QY	979	AGAAAATCTTCTCAGTTCCTCTTGACAGAGACTGGCGCGGGAGCGCAAGAGACAGGGC	1038
Db	1273	AGAAAATCTTCTCAGTTCCTCTTGACAGAGAGACTGGCGCGGGAGCGCAAGAGACAGGGC	1332
QY	1039	GCTGCACAAAAGCGGGGCGCTGCTGCTGGATGGGATGGCGCATATACGGCAGCGCTTCTGT	1098
Db	1333	GCTGCACAAAAGCGGGGCGCTGCTGCTGGATGGGATGGCGCATATACGGCAGCGCTTCTGT	1392
QY	1099	GGTGTGGCTGCTCAGCAGACAGAGCGCGCACACAGACACTTGCACGACAAACCGCGCGAAC	1158
Db	1393	GGTGTGGCTGCTCAGCAGACAGAGCGCGCACACAGACACTTGCACGACAAACCGCGCGAAC	1451
QY	1159	TGCTGCGAGGACACCGTGTACAGAGCGGGTGTATACCGAGCTGAGGTAGAAAAAGCTC	1218
Db	1452	TGCTGCGAGGACACCGTGTACAGAGCGGGTGTATACCGAGCTGAGGTAGAAAAAGCTC	1511
QY	1219	TCCGAGAAAGGGGAGAGGAAATGATAGCGCCGGAAATGAGACCTGCTCCACTGCTGTG	1278
Db	1512	TCCGAGAAAGGGGAGAGGAAATGATAGCGCCGGAAATGAGACCTGCTCCACTGCTGTG	1571
QY	1279	GGTTTGGCCGACCCATGATCCCTCGCAATCTGTTGGGCAATCCAGCATACGGCCAAATGTC	1338
Db	1572	GGTTTGGCCGACCCATGATCCCTCGCAATCTGTTGGGCAATCCAGCATACGGCCAAATGTC	1631
QY	1339	ACAAACAATCAGCCCTGGGCAACAGAGCAGAGGAGGAGAGACAGAGAAAAAGAAAAACA	1398
Db	1632	ACAAACAATCAGCCCTGGGCAACAGAGCAGAGGAGGAGAGAGAGAGAAAAAGAAAAACA	1691
QY	1399	GCATGGAACACAGTAAATGAATAAACCAATTAATATTGAGCCCTGCTGTGCTGCTT	1458
Db	1692	GCATGGAACACAGTAAATGAATAAACCAATTAATATTGAGCCCTGCTGTGCTGCTT	1751
QY	1459	ACTGGCCAGGAAATGGTACCAATTTTTCAGTGTGAGCTTACAGACTTCTTTTCCACAA	1518
Db	1752	ACTGGCCAGGAAATGGTACCAATTTTTCAGTGTGAGCTTACAGACTTCTTTTCCACAA	1811
QY	1519	GCAAGAGAGAAATTTAACTGTTTAAACCCGGGGGAGTGGCTGTGTAAAGAAAGACC	1578
Db	1812	GCAAGAGAGAAATTTAACTGTTTAAACCCGGGGGAGTGGCTGTGTAAAGAAAGACC	1871
QY	1579	ATTAAATGCTTTAGACAGTGTGA	1600
Db	1872	ATTAAATGCTTTAGACAGTGTGA	1893

RESULT 31  
US-09-652-917-2477  
Sequence 2477, Application US/09652917  
: GENERAL INFORMATION:  
: APPLICANT: Shyjan, Andrew W.  
: APPLICANT: Holtzman, Douglas A.  
: APPLICANT: Distefano, Peter  
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES





Qy	1039	GCCTGCACCAAGCGGCGCTGTGCGGTGGTAGTGCGCATGTACGCGCAGCGCTTCTCGT	1098
Db	1333	GCTGCACCAAGCGGCGCGCTGTGCGGTGGTAGTGCGCATGTACGCGCAGCGCTTCTCGT	1392
Qy	1099	GGTTGGCGGTGCTGCAGGAGACAGAGGGGGGACACACACACTTGGACGAACCCCGCGAAAC	1158
Db	1393	GGTTGGCGGTGCTGCAGGAGACAGAGGGGGGACACACACACTTGGACGAACCCCGCGAAAC	1451
Qy	1159	TGCTGCGAGGACACCGTGTACAGGAGCGGGGTGATGACCGAGGTGAGTAGAAAAAGTC	1218
Db	1452	TGCTGCGAGGAGACACCGTGTACAGGAGCGGGGTGATGACCGAGGTGAGTAGAAAAAGTC	1511
Qy	1219	TCCGAGAAAGGGAGGAGAGCATCTGTACGCGCGGAAAGTAGAGACCTGCTCCAGTCTGCTTG	1278
Db	1512	TCCGAGAAAGGGAGGAGAGCATCTGTACGCGCGGAAAGTAGAGACCTGCTCCAGTCTGCTTG	1571
Qy	1279	GGTTTGGCCGCGAGGCATGATCTTCGGAATCTGGTTGGCATCCAGCATACGGCCATGTC	1338
Db	1572	GGTTTGGCCGCGAGGCATGATCTTCGGAATCTGGTTGGCATCCAGCATACGGCCATGTC	1631
Qy	1339	ACMACATCAGCCCTTGGGCGACACGACGAGGAGGAGACAGAGAAAAAGAAAAACA	1398
Db	1632	ACMACATCAGCCCTTGGGCGACACGACGAGGAGGAGACAGAGAAAAAGAAAAACA	1691
Qy	1399	GCATGAGAACACACTAATTAATGAATPAAACATAAATATTATTAGCCCTCTGTTCTGTCTT	1458
Db	1692	GCATGAGAACACACTAATTAATGAATPAAACATAAATATTATTAGCCCTCTGTTCTGTCTT	1751
Qy	1459	ACTGGCCGAGAAATGATPAAACATTTTTCAGGTGTGGACTGTGACACCTTCTTTGCCACAA	1518
Db	1752	ACTGGCCGAGAAATGATPAAACATTTTTCAGGTGTGGACTGTGACACCTTCTTTGCCACAA	1811
Qy	1519	GCAAGAGAGAAATTTTAACACTGTTTCAAAACCCGCGGAGTGTGGCTGTGTTAAGAAAGCC	1578
Db	1812	GCAAGAGAGAAATTTTAACACTGTTTCAAAACCCGCGGAGTGTGGCTGTGTTAAGAAAGCC	1871
Qy	1579	ATTAAATGCTTTAGACAGGTGA 1600	
Db	1872	ATTAAATGCTTTAGACAGGTGA 1893	

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RESULT 28
US-09-652-128-7518
; Sequence 7518, Application US/09652128
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1171-001
; CURRENT APPLICATION NUMBER: US/09/652,128
; PRIOR APPLICATION NUMBER: 2000-08-30
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 10265
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 7518
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-652-128-7518

```

	Query Match	80.2%	Score 1299;	DB 25;	Length 1917;
	Best Local Similarity	99.8%	Pred. No. 1.76-240;		
	Matches 1519;	Conservative	0;	Mismatches 2;	Indels 1; Gaps 1
QY	79	GAACACGACTGCTCTCCCGAGATTCATTGTGATTCAGCAGGTGAACGTTAAAGCAT	138		
Db	373	GAACAAAGCATGCTCTCCCGAGATTCATTGTGATTCAGCAGGTGAACGTTAAAGCAT	432		
QY	139	GTCACAAAGATGATGAGCAAAAGTCCGGATCATGTACCGCAAGTCTGTGCATTC	198		

Dp	433	CGTCAGAAABAATGATGATGAGCAAAAGTCCGGGATCATGTACCGCAAGCTCTGTGCATC	492
Qy	199	ATCAGCGCCTGTCTCATCAGCCTCTGCGGGGTACAGAGTCTCTTGCTGCCAGGAAACT	258
Dp	493	ATCAGCGCCTGTCTCATCAGCCTCTGCGGGGTACAGAGTCTCTTGCTGCCAGGAAACT	553
Qy	259	GAACCTACATTTGCTACAGTGTGTGCAACAACCCCTCTTTGTAAACGGGCCAAGGCCAAGAA	318
Dp	553	GAACCTACATTTGCTACAGTGTGTGCAACAACCCCTCTTTGTAAACGGGCCAAGGCCAAGAA	612
Qy	319	AAGGGGAAGTTTCTGCCCTCGGCCCTCAGCGCAGGGGTCCGCACACATCTGTGTCTCAAA	378
Dp	613	AAGGGGAAGTTTCTGCCCTCGGCCCTCAGCGCAGGGGTCCGCACACATCTGTGTCTCAAA	672
Qy	379	ATTAGCCCTCTCTCGGCAACACTGCTGAAGCTGAAGAGATGCCAACCCCTCTGTCAATG	438
Dp	673	ATTAGCCCTCTCTCGGCAACACTGCTGAAGCTGAAGAGATGCCAACCCCTCTGTCAATG	732
Qy	439	TTCTTCCAGCCCTCGGCCCAACCCCCACCTCCCTGAGTATTTCTTCTGGGTGTCCT	498
Dp	733	TTCTTCCAGCCCTCGGCCCAACCCCCACCTCCCTGAGTATTTCTTCTGGGTGTCCT	792
Qy	499	TTTATTTGGGTTGGGAGGGGGAGTCCGTCTCTTTTGTCTGTGCAATATATGAAA	558
Dp	793	TTTATTTGGGTTGGGAGGGGGAGTCCGTCTCTTTTGTCTGTGCAATATATGAAA	852
Qy	559	GAGCTCGGTAAAGCATCTTGAATTAATTCACGCTGACATTTTTCAGTATGTACTGAA	618
Dp	853	GAGCTCGGTAAAGCATCTTGAATTAATTCACGCTGACATTTTTCAGTATGTACTGAA	912
Qy	619	GGAGGAGGGGAGGAGGAAAGTTCCACCCCATGTCTGTGTAAACGGAGTCAAGGCCAGCT	678
Dp	913	GGAGGAGGGGAGGAGGAAAGTTCCACCCCATGTCTGTGTAAACGGAGTCAAGGCCAGCT	972
Qy	679	GCGAGAGTCAAGTCTTAGAAGTCACTAGAGTGGGCACTCTGCTTTTGAAGCTCCACT	738
Dp	973	GCGAGAGTCAAGTCTTAGAAGTCACTAGAGTGGGCACTCTGCTTTTGAAGCTCCACT	1032
Qy	739	GTCATTTCCATCCCTGATGTGGGGCATAGTTTGAGACTGCAAGTGAAGTGAAGCTTTTCT	798
Dp	1033	GTCATTTCCATCCCTGATGTGGGGCATAGTTTGAGACTGCAAGTGAAGTGAAGCTTTTCT	1092
Qy	799	TAGGCTGAGAGGGGCAGTTTCCACATCAAGGCTCCCTGCTGTGACATTCATCACTCATGCT	858
Dp	1093	TAGGCTGAGAGGGGCAGTTTCCACATCAAGGCTCCCTGCTGTGACATTCATCACTCATGCT	1152
Qy	859	CCTGAAACCATTTCTCTGACAGCAAAATTTGGCTGGTTTGGCGCTGTGATTTGGGCTCTAGTG	918
Dp	1153	CCTGAAACCATTTCTCTGACAGCAAAATTTGGCTGGTTTGGCGCTGTGATTTGGGCTCTAGTG	1212
Qy	919	ACTCGAGACTCAATGACTGGGACTTAAGTGGGGCTTCGGCTCTGCTGTAAAGTGTCTTA	978
Dp	1213	ACTCGAGACTCAATGACTGGGACTTAAGTGGGGCTTCGGCTCTGCTGTAAAGTGTCTTA	1272
Qy	979	AGAAAATCTTCTCAGTTCTTCTTTCAGAGGACTTGGCGCCGGGACCGAAGACCAACGGGC	1038
Dp	1273	AGAAAATCTTCTCAGTTCTTCTTTCAGAGGACTTGGCGCCGGGACCGAAGACCAACGGGC	1332
Qy	1039	GCTGCAACAACCGGGCCCTGTCCGTGTGAGTGGCCCAATGTACGGGCAAGGGCTTTCGT	1098
Dp	1333	GCTGCAACAACCGGGCCCTGTCCGTGTGAGTGGCCCAATGTACGGGCAAGGGCTTTCGT	1392
Qy	1099	GGTGTGCGTCTGACGAGCAGAGCGGCGAGACAGCACTTGTGACGAACAAACCGCGGAAC	1158
Dp	1393	GGTGTGCGTCTGACGAGCAGAGCGGCGAGACAGCACTTGTGACGAACAAACCGCGGAAC	1452
Qy	1159	TGCTGCAAGACACCGTGTCTCAGAGACGGGTTGATGACCAAGCTGAGTTAGAAAACGTC	1218
Dp	1452	TGCTGCAAGACACCGTGTCTCAGAGACGGGTTGATGACCAAGCTGAGTTAGAAAACGTC	1512
Qy	1219	TCCGAGAAAGGGAGAGATCATGTACGGCCGGAAGTGAAGACCTGTCCACTCTGCTTG	1278
Dp	1512	TCCGAGAAAGGGAGAGATCATGTACGGCCGGAAGTGAAGACCTGTCCACTCTGCTTG	1572



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Db 1033 GTCCATTCATCCCTGATGGGGGCACTAGTTGAGACTGCAAGATGAGAGTACGATTTCT 1092
Oy 799 TAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTGCTTGACATTTCAAACTTCATGCT 858
Db 1093 TAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTGCTTGACATTTCAAACTTCATGCT 1152
Oy 859 CCTGAAACCATTTCTCTGACAGCAGAAATGGCTGGTTTGGCCCTGAGTTGGGCTCTAGTG 918
Db 1153 CCTGAAACCATTTCTCTGACAGCAGAAATGGCTGGTTTGGCCCTGAGTTGGGCTCTAGTG 1212
Oy 919 ACTCGAGCTCAATGACTGAGGAGCTTAGACTGGGGCTGCGCTCGCTCGAAGATGCTTA 978
Db 1213 ACTCGAGCTCAATGACTGAGGAGCTTAGACTGGGGCTGCGCTCGCTCGAAGATGCTTA 1272
Oy 979 AGAAATCTTCTCAGTTCTCTGAGAGAGACTGGCGCGGAGCGGAGAGCAAGCGGC 1038
Db 1273 AGAAATCTTCTCAGTTCTCTGAGAGAGACTGGCGCGGAGCGGAGAGCAAGCGGC 1332
Oy 1039 GCTGCAAAAGGGGGGGGCTGGTGGTGGAGTGGGAGTGGAGCGGAGGAGGAGGCTCTGCT 1098
Db 1333 GCTGCAAAAGGGGGGGGCTGGTGGTGGAGTGGGAGTGGGAGCGGAGGAGGAGGCTCTGCT 1392
Oy 1099 GATTGGCTGCTGCAAGCAGAGAGCGGCGAGCAGCAGCCTTGACAGCAACCGCGGAAAC 1158
Db 1393 GATTGGCTGCTGCAAGCAGAGAGCGGCGAGCAGCAGCCTTGACAGCAACCGCGGAAAC 1451
Oy 1159 TGGTGGAGAGACCGCTGTACAGAGAGCGGCTTGATGACCGAGCTAGGTAAAGAAAGCTC 1218
Db 1452 TGGTGGAGAGACCGCTGTACAGAGAGCGGCTTGATGACCGAGCTAGGTAAAGAAAGCTC 1511
Oy 1219 TCCGAGAGGGGAGAGAGATCATGTACGGCCGGAAGTAGAGCCTGCTCAGTCTGCTTG 1278
Db 1512 TCCGAGAGGGGAGAGAGATCATGTACGGCCGGAAGTAGAGCCTGCTCAGTCTGCTTG 1571
Oy 1279 GATTGGCCCGCAGCATGATCTCTCCAGATCTGCTGGCATCCAGCATCGGCCATGTC 1338
Db 1572 GATTGGCCCGCAGCATGATCTCTCCAGATCTGCTGGCATCCAGCATCGGCCATGTC 1631
Oy 1339 ACAACATACGCGCTGGGCGAGACAGCAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1398
Db 1632 ACAACATACGCGCTGGGCGAGACAGCAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1691
Oy 1399 GCATGAGACAGATTAATGAATTAACATTAATTAATTAATTAATTAATTAATTAATTAAT 1458
Db 1692 GCATGAGACAGATTAATGAATTAACATTAATTAATTAATTAATTAATTAATTAATTAAT 1751
Oy 1459 ACTGGCCAGAGAAATGTTACCAATTTTTCATGTTGGACTTGACAGCTTCTTTTGGCACA 1518
Db 1752 ACTGGCCAGAGAAATGTTACCAATTTTTCATGTTGGACTTGACAGCTTCTTTTGGCACA 1811
Oy 1519 GCAGAGAGATTTACAGCTGTTCAAAACCGGGGAGTGGCTGTGTAAAGAAAGAGCC 1578
Db 1812 GCAGAGAGATTTACAGCTGTTCAAAACCGGGGAGTGGCTGTGTAAAGAAAGAGCC 1871
Oy 1579 ATTAATGCTTTAGACAGTGA 1600
Db 1872 ATTAATGCTTTAGACAGTGA 1893

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; SEQ ID NO 6191
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-121-6191
Query Match 80.2%; Score 1299; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 1,7e-240;
Matches 1519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 79 GAACAACGACTCTCTCTCCCGAGTTCATTGTGATTTGACAGGTGAACCTTCAAGACAT 138
Db 373 GAACAACGACTCTCTCTCCCGAGTTCATTGTGATTTGACAGGTGAACCTTCAAGACAT 432
Oy 139 GGTGCAAGAAAGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
Db 433 GGTGCAAGAAAGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
Oy 199 ATCAGCGGCTGTCTCATGCTCTGCGGGTACCAAGTCTTCTGCTCCAGGGAACCT 258
Db 493 ATCAGCGGCTGTCTCATGCTCTGCGGGTACCAAGTCTTCTGCTCCAGGGAACCT 552
Oy 259 GAACCTAGTTGATCAGCTGCTGCAACACCCCTTTGTAACGGGAGCCAAAGCCAAAGAA 318
Db 553 GAACCTAGTTGATCAGCTGCTGCAACACCCCTTTGTAACGGGAGCCAAAGCCAAAGAA 612
Oy 319 AAGGGAAGTTGCTGCTCGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAG 378
Db 613 AAGGGAAGTTGCTGCTCGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAG 672
Oy 379 ATTAGCCCTCTTCTGCGCACTGCTGAAGCTGAAGAGAGATGCCACCCCTTCGTCATG 438
Db 673 ATTAGCCCTCTTCTGCGCACTGCTGAAGCTGAAGAGAGATGCCACCCCTTCGTCATG 732
Oy 439 TTCTTCAGGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 498
Db 733 TTCTTCAGGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 792
Oy 499 TTTATTCGTGGTAGGAGAGCGGAGTCCGTCTCTTTTGTCTGCTGCTGAATTAATGA 558
Db 793 TTTATTCGTGGTAGGAGAGCGGAGTCCGTCTCTTTTGTCTGCTGCTGAATTAATGA 852
Oy 559 GAGTCGCTTAACCATCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 618
Db 853 GAGTCGCTTAACCATCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 912
Oy 619 GGAAGAGGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 678
Db 913 GGAAGAGGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 972
Oy 679 GGCAGAGTCACTGCTTAAGAGTCACTGAGTGGGCACTTCTCTTTTGTAAAGCTTCAGT 738
Db 973 GGCAGAGTCACTGCTTAAGAGTCACTGAGTGGGCACTTCTCTTTTGTAAAGCTTCAGT 1032
Oy 739 GTCCATTCATCCCTGATGAGGGGAGATGTTGAGAGCTGCAAGATGAGATGAGATGAGTTC 798
Db 1033 GTCCATTCATCCCTGATGAGGGGAGATGTTGAGAGCTGCAAGATGAGATGAGATGAGTTC 1092
Oy 799 TAGGGCTGAGAGGCGAGTCCCACTCAAGGCTCCCTGCTTACATTTCAAACTTCATGCT 858
Db 1093 TAGGGCTGAGAGGCGAGTCCCACTCAAGGCTCCCTGCTTACATTTCAAACTTCATGCT 1152
Oy 859 CCTGAAACCATTTCTCTGACAGCAGAAATGGCTGGTTTGGCCCTGAGTTGGGCTCTAGTG 918
Db 1153 CCTGAAACCATTTCTCTGACAGCAGAAATGGCTGGTTTGGCCCTGAGTTGGGCTCTAGTG 1212
Oy 919 ACTGAGACTCAATGACTGGGAGCTTAGACTGGGCTGCGCTGCTGTAAGAGTGCCTTA 978
Db 1213 ACTGAGACTCAATGACTGGGAGCTTAGACTGGGCTGCGCTGCTGTAAGAGTGCCTTA 1272
Oy 979 AGAAATCTTCTCAGTTCTCTTCAAGAGACTGGCGCGGAGCGGAGAGAGAGAGAGAGAG 1038
Db 1273 AGAAATCTTCTCAGTTCTCTTCAAGAGAGACTGGCGCGGAGCGGAGAGAGAGAGAGAG 1332

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RESULT 27
US-09-652-121-6191
; Sequence 6191, Application US/09652121
; GENERAL INFORMATION:
; APPLICANT: Dislefono, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1188-001
; CURRENT APPLICATION NUMBER: US/09/652.121
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151.129
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 7615
; SOFTWARE: FastSeq for Windows Version 4.0

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Db 553 GAACCTGATGTTGCTAGCTGCTGCAACACCCCTTTGTAGAGGGCCAAAGCCCAAGAA 612  
OY 319 AAGGGGAAGTTTGTGCTGGCCCTGAGGCCAGGGCTCCGACACACATCTGTTCTCAA 378  
Db 613 AAGGGGAAGTTTGTGCTGGCCCTGAGGCCAGGGCTCCGACACACATCTGTTCTCAA 672  
OY 379 ATTAGCCCTCTTCTGGGCACTGCTGAAGCTGAAGAGATGCCACCCCTCTCATATG 438  
Db 673 ATTAGCCCTCTTCTGGGCACTGCTGAAGCTGAAGAGATGCCACCCCTCTCATATG 732  
OY 439 TTCTTCCACCCCTCGCCCCAACCCCTCCCTGAGTGAAGTTTCTTGGGTGCT 498  
Db 733 TTCTTCCACCCCTCGCCCCAACCCCTCCCTGAGTGAAGTTTCTTGGGTGCT 792  
OY 499 TTATATCTGGGTAGGAGGGGAGTCCGTTCTCTTTTGTCTCTGTGCAATTAATGAA 558  
Db 793 TTATATCTGGGTAGGAGGGGAGTCCGTTCTCTTTTGTCTCTGTGCAATTAATGAA 852  
OY 559 GAGCTCGGTAAAGCATTTCTGAATTAATTCAGCCTGACTGAATTTTCAATATGCTGAA 618  
Db 853 GAGCTCGGTAAAGCATTTCTGAATTAATTCAGCCTGACTGAATTTTCAATATGCTGAA 912  
OY 619 GGAAGAGGTGAGAGTAAAGTTTCAACCCCTATCTGTGTAAACCGAGTCAAGCCAGCT 678  
Db 913 GGAAGAGGTGAGAGTAAAGTTTCAACCCCTATCTGTGTAAACCGAGTCAAGCCAGCT 972  
OY 679 GGCAGAGTATGCTCTTGAAGTCACTGAGTGGGATCGCTTTTGTAAAGCTCCAGT 738  
Db 973 GGCAGAGTATGCTCTTGAAGTCACTGAGTGGGATCGCTTTTGTAAAGCTCCAGT 1032  
OY 739 GTCCATTTCCATCCCTGATGGGGGATGTTTGAAGTCACTGAGTGAAGTGAAGTTCCT 798  
Db 1033 GTCCATTTCCATCCCTGATGGGGGATGTTTGAAGTCACTGAGTGAAGTGAAGTTCCT 1092  
OY 799 TAGGGCTGAGGGGATGTTTCCACTCAAGGCTCCCTGCTTACATTCAAATTTATGCT 858  
Db 1093 TAGGGCTGAGGGGATGTTTCCACTCAAGGCTCCCTGCTTACATTCAAATTTATGCT 1152  
OY 859 CCTGAAGACATTTCTGTCAGAGAGAAATTTGGTGTTCGCGCTGAGTGGGCTCTAGT 918  
Db 1153 CCTGAAGACATTTCTGTCAGAGAGAAATTTGGTGTTCGCGCTGAGTGGGCTCTAGT 1212  
OY 919 ACTCGAGCTCAATGACTGGGACTTAGACTGGGCTCGGCTCGCTGTGAAAAGTCTTA 978  
Db 1213 ACTCGAGCTCAATGACTGGGACTTAGACTGGGCTCGGCTCGCTGTGAAAAGTCTTA 1272  
OY 979 AGAAATCTTCTCAGTTCTCTTGCAGAGAGTGGGCTGGGAGCGGAAGACCAAGGCT 1038  
Db 1273 AGAAATCTTCTCAGTTCTCTTGCAGAGAGTGGGCTGGGAGCGGAAGACCAAGGCT 1332  
OY 1039 GCTGCAGAAAGCGGGCTGTGCTGTGTGAGTGGCATGTACGGGAGGCTCTCTGCT 1098  
Db 1333 GCTGCAGAAAGCGGGCTGTGCTGTGTGAGTGGCATGTACGGGAGGCTCTCTGCT 1392  
OY 1099 GGTGGCTGCTGTCAGACGACGAGCGGCTGACGACCTTGCAGCAACACCCCGGAAAC 1158  
Db 1393 GGTGGCTGCTGTCAGACGACGAGCGGCTGACGACCTTGCAGCAACACCCCGGAAAC 1452  
OY 1159 TGTGTGAGAGACCGCTGTACAGAGAGCGGTTGATGACCGACTGAGTGAAGAAACGTC 1218  
Db 1452 TGTGTGAGAGACCGCTGTACAGAGAGCGGTTGATGACCGACTGAGTGAAGAAACGTC 1512  
OY 1219 TCCGAGAAAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1278  
Db 1512 TCCGAGAAAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1572  
OY 1279 GGTGGCTGCTGTCAGACGACGAGCGGCTGACGACCTTGCAGCAACACCCCGGAAAC 1338  
Db 1572 GGTGGCTGCTGTCAGACGACGAGCGGCTGACGACCTTGCAGCAACACCCCGGAAAC 1632  
OY 1339 ACACCAATGAGCCCTGAG 1398  
|||||

Db 1632 ACACCAATGAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1691  
OY 1399 GCATGAGAACACAGTAAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1458  
Db 1692 GCATGAGAACACAGTAAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1751  
OY 1459 ACTGGCCAGGAATGATGAACCAATTTTTCAGTGTGTGACTGTGACAGCTCTTTTGCACAA 1518  
Db 1752 ACTGGCCAGGAATGATGAACCAATTTTTCAGTGTGTGACTGTGACAGCTCTTTTGCACAA 1811  
OY 1519 GCAGAGAGAGATTTAACAATTTTTCAGTGTGTGACTGTGACAGCTCTTTTGCACAA 1578  
Db 1812 GCAAGAGAGAGATTTAACAATTTTTCAGTGTGTGACTGTGACAGCTCTTTTGCACAA 1871  
OY 1579 ATTAATGCTTTAGACAGTGA 1600  
Db 1872 ATTAATGCTTTAGACAGTGA 1893

RESULT 25  
US-09-644-873-9077  
: Sequence 9077, Application US/09644873  
: GENERAL INFORMATION:  
: APPLICANT: SIOS-Santiago, Immaculada  
: APPLICANT: Holtzman, Douglas A.  
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
: FILE REFERENCE: 1600.1169-001  
: CURRENT FILING DATE: 2000-08-28  
: PRIOR FILING DATE: 1999-08-27  
: NUMBER OF SEQ ID NOS: 11286  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 9077  
: LENGTH: 1917  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
US-09-644-873-9077

Query Match 80.2%; Score 1299; DB 25; Length 1917;  
Best Local Similarity 99.8%; Pred. No. 1.7e-240;  
Matches 1519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
OY 79 GAACAGAGCTGCTCTCCCGGAGTTCATTTGATGACAGGAGTGAAGCTTCAAGCAT 138  
Db 373 GAACAGAGCTGCTCTCCCGGAGTTCATTTGATGACAGGAGTGAAGCTTCAAGCAT 432  
OY 139 GTGTGAGAAAGTATGATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATC 198  
Db 433 GTGTGAGAAAGTATGATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATC 492  
OY 199 ATCAGGGGCTGTCTCATGCTGCTGCGGGTATACATCTTCTGCTCCGAGGAAACT 258  
Db 493 ATCAGGGGCTGTCTCATGCTGCTGCGGGTATACATCTTCTGCTCCGAGGAAACT 552  
OY 259 GAACATGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCAAGGCCAAGAA 318  
Db 553 GAACATGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCAAGGCCAAGAA 612  
OY 319 AAGGGAAGTTTCTGCTGCGCTGAGGCGGCTGCGGAGTCCGACACCATCTCTCTCAA 378  
Db 613 AAGGGAAGTTTCTGCTGCGCTGAGGCGGCTGCGGAGTCCGACACCATCTCTCTCAA 672  
OY 379 ATTAGCCCTCTTCTGGGCACTGCTGAAGCTGAAGAGATGCCACCCCTCTCATATG 438  
Db 673 ATTAGCCCTCTTCTGGGCACTGCTGAAGCTGAAGAGATGCCACCCCTCTCATATG 732  
OY 439 TTCTTCCACCCCTCGCCCCAACCCCTCCCTGAGTGAAGTTTCTTGGGTGCT 498  
Db 733 TTCTTCCACCCCTCGCCCCAACCCCTCCCTGAGTGAAGTTTCTTGGGTGCT 792  
OY 499 TTATATCTGGGTAGGAGGGGAGTCCGTTCTCTTTTGTCTCTGTGCAATTAATGAA 558  
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Db 1627 GCGAACCTTTTGGCGATGTTCTTCCAGGCTTTGGCGTGAATTCAGTCTACCA 1568
Qy 61 GTGTGAAGAAATTCAGCTGACAGACAGCTGCTCCCGGAGTCAATGTAATGAC 120
Db 1567 GTGTGAAGAAATTCAGCTGACAGACAGCTGCTCCCGGAGTCAATGTAATGAC 1508
Qy 121 GGTGAAGCTTCAAGACATGTCAGAAAGATGATGAGAAAGTGGCGGATCATGTA 180
Db 1507 GGTGAAGCTTCAAGACATGTCAGAAAGATGATGAGAAAGTGGCGGATCATGTA 1448
Qy 181 CCGCAAGTCTCTGTGATCATACAGCGGCTGTCTATCGCTTCCCGGATACAGTCTT 240
Db 1447 CCGCAAGTCTCTGTGATCATACAGCGGCTGTCTATCGCTTCCCGGATACAGTCTT 1388
Qy 241 CTGCTCTCCAGGAAACCTAATCTAGTTGATCATAGCTGCTGCAACACCCCTTTGTA 300
Db 1387 CTGCTCTCCAGGAAACCTAATCTAGTTGATCATAGCTGCTGCAACACCCCTTTGTA 1328
Qy 301 CCGGCGCAAGGCGCCAAAGAAAGGAAAGTCTGCTCGGCTCAGGCGCAGGCTCCGAC 360
Db 1327 CCGGCGCAAGGCGCCAAAGAAAGGAAAGTCTGCTCGGCTCAGGCGCAGGCTCCGAC 1268
Qy 361 CACCATCTGTTCTCTCAAAATAGCCCTCTTCTGCGACACTGCTAAGCTAAGAGATG 420
Db 1267 CACCATCTGTTCTCTCAAAATAGCCCTCTTCTGCGACACTGCTAAGCTAAGAGATG 1208
Qy 421 CCACCCCTCTCTGATGTTCTTCCAGGCTCTGCGCCCAACCCCTACCTCCCTAGTA 480
Db 1207 CCACCCCTCTCTGATGTTCTTCCAGGCTCTGCGCCCAACCCCTACCTCCCTAGTA 1148
Qy 481 GTTCTTCTGCGGTCCTTCTTATTCGAGGAGCGGAGTCCGTTCTCTTTGT 540
Db 1147 GTTCTTCTGCGGTCCTTCTTATTCGAGGAGCGGAGTCCGTTCTCTTTGT 1088
Qy 541 CCTGTGCAAAATATGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT 600
Db 1087 CCTGTGCAAAATATGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAAT 1028
Qy 601 TTTTCAGTATGATCTGAAGAGAGAGTGAAGTGAAGTCAACCCCAATGCTGTGTAC 660
Db 1027 TTTTCAGTATGATCTGAAGAGAGAGTGAAGTGAAGTCAACCCCAATGCTGTGTAC 968
Qy 661 CCGAGTCAAGGCGCAGGCTGCGAGAGTCACTCTTGAAGTCACTGAGGTGGGCACTCTCC 720
Db 967 CCGAGTCAAGGCGCAGGCTGCGAGAGTCACTCTTGAAGTCACTGAGGTGGGCACTCTCC 908
Qy 721 TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGGGATGTTGAGACTGACGA 780
Db 907 TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGGGATGTTGAGACTGACGA 848
Qy 781 GTGAGAGTACGCTTTTCTTAAAGGCTGAGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 840
Db 847 GTGAGAGTACGCTTTTCTTAAAGGCTGAGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 788
Qy 841 ACATTCAAACCTTCATGCTCTGAAAAACATTTCTGACAGCAGAAATTTGCTGTGGCGC 900
Db 787 ACATTCAAACCTTCATGCTCTGAAAAACATTTCTGACAGCAGAAATTTGCTGTGGCGC 728
Qy 901 CTGAGTGTGGGCTCTAGTACTGAGACATCAATGACTGGGACTTGAAGTGGGCTCGGCT 960
Db 727 CTGAGTGTGGGCTCTAGTACTGAGACATCAATGACTGGGACTTGAAGTGGGCTCGGCT 668
Qy 961 GCGCTGAAAGAGTGTAAAGAAATCTTCTGATCTCTCTTGCAGAGAGACAGCGGCGG 1020
Db 667 GCGCTGAAAGAGTGTAAAGAAATCTTCTGATCTCTCTTGCAGAGAGACAGCGGCGG 608
Qy 1021 ACGCGAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCTGCTGTGAGAGTGCAGATTA 1080
Db 607 ACGCGAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCTGCTGTGAGAGTGCAGATTA 548
Qy 1081 CCGCGAGCGGCTTCTGTGTGTGTGCGGTCTGACGACAGCGGCGGAGCAGACACCTTGC 1140
Db 547 CCGCGAGCGGCTTCTGTGTGTGTGCGGTCTGACGACAGCGGCGGAGCAGACACCTTGC 489

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Qy 1141 ACGAACACCGCGCAAACTGCTGCGAGACACCGTGAACAGAGCGGGTGTATACCCAG 1200
Db 488 ACGAACACCGCGCAAACTGCTGCGAGACACCGTGAACAGAGCGGGTGTATACCCAG 429
Qy 1201 CTGAGGTGAAAAAGCTCTCGAGAAAGGAGAGATGATGTAACGCCCGGAAGTAGAC 1260
Db 428 CTGAGGTGAAAAAGCTCTCGAGAAAGGAGAGATGATGTAACGCCCGGAAGTAGAC 369
Qy 1261 CTGCTCCAGTGTGCTGTTGGTTGGCCGACCATGATCTCTCCGAATCTGTGGGATC 1320
Db 368 CTGCTCCAGTGTGCTGTTGGTTGGCCGACCATGATCTCTCCGAATCTGTGGGATC 309
Qy 1321 CAGCATACGGCAATGTCACAAATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1380
Db 308 CAGCATACGGCAATGTCACAAATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 249
Qy 1381 AGAGAAAAAGAAAAACAGACATGAGAACACAGTAATGAATAAAAACATTAATTTAG 1440
Db 248 AGAGAAAAAGAAAAACAGACATGAGAACACAGTAATGAATAAAAACATTAATTTAG 189
Qy 1441 CCCCTGTCTGTGCTTACTGCGCAGGAAATGTTACCAATTTTCACTGTGGACTTGA 1500
Db 188 CCCCTGTCTGTGCTTACTGCGCAGGAAATGTTACCAATTTTCACTGTGGACTTGA 129
Qy 1501 CAGCTCTTTTGCACAAAGAGAGAGATTTAACAAGTTTCAACCCGCGGGAGTTGG 1560
Db 128 CAGCTCTTTTGCACAAAGAGAGAGATTTAACAAGTTTCAACCCGCGGGAGTTGG 69
Qy 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGA 1600
Db 68 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGA 29

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RESULT 24
US-09-371-168-7188
; Sequence 7188, Application US/093711168
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, M. Alexandra
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE OF INVENTION: HUMAN BRAIN LIBRARY
; FILE REFERENCE: MLN98-37PA
; CURRENT APPLICATION NUMBER: US/09/371,168
; EARLIER FILING DATE: 1999-08-10
; EARLIER APPLICATION NUMBER: 60/095,907
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/103,145
; NUMBER OF SEQ ID NOS: 8285
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7188
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-168-7188

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Query Match 80.2%; Score 1299; DB 17; Length 1917;
Best Local Similarity 99.8%; Pred. No. 1,7e-240;
Matches 1519; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 79 GAACAAGACAGCTGCTCCCGAGTTCATTTGTAATTTGACAGGTGAACGTTGAACAT 138
Db 373 GAACAAGACAGCTGCTCCCGAGTTCATTTGTAATTTGACAGGTGAACGTTGAACAT 432
Qy 139 GTGTCAAGAAAGAGTGTGAGCAAAAGTGCAGGATCATGTACCGCAAGTCTGTGCATC 198
Db 433 GTGTCAAGAAAGAGTGTGAGCAAAAGTGCAGGATCATGTACCGCAAGTCTGTGCATC 492
Qy 199 ATCAGCGGCTGTGTATGCTGCTTGCAGGAGTACAGTCTTCTGCTCCCGAGGAACT 258
Db 493 ATCAGCGGCTGTGTATGCTGCTTGCAGGAGTACAGTCTTCTGCTCCCGAGGAACT 552
Qy 259 GAATCAAGTTTGAATCAAGTGTGCAACACCCCTTTTGAAGGGGCAAGGCCAAGAA 318

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; SEQ ID NO 4458
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-710-281-4458

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Query Match	85.18;	Score 1377;	DB 28;	Length 1925;
Best Local Similarity	99.88;	Pred. NO. 1.9e-255;		
Matches 1597; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1.

Oy	1	GGCAACATTTTGGGGATTGTTCTTTCGCTTCACAGGCTTTGGCGTGCACAAATCAGTGGCTACCA	60
Db	1627	GGCAACATTTTGGGGATTGTTCTTTCGCTTCACAGGCTTTGGCGTGCACAAATCAGTGGCTACCA	1568
Oy	61	GTTGTAAGAATTCACAGCTGAACAACAAGCTGCTCTCCCCGAGTTTCATTGTGTAATTCAC	120
Db	1567	GTTGTAAGAATTCACAGCTGAACAACAAGCTGCTCTCTCCCCGAGTTTCATTGTGTAATTCAC	1508
Oy	121	GGTAAGGTTTCAACATGTGTGTCAGAAAGAAGTGAAGAGCAAGAGCGCGGGATCATCTA	180
Db	1507	GGTAAGGTTTCAACATGTGTGTCAGAAAGAAGTGAAGAGCAAGAGTCCCGGGATCATCTA	1448
Oy	181	CCGCAAGTCCGTGTGTCATCATCAGCGGCTGTCTCATCGGCTCTGGCGGGTACACAGTCTT	240
Db	1447	CCGCAAGTCCGTGTGTCATCATCAGCGGCTGTCTCATCGGCTCTGGCGGGTACACAGTCTT	1388
Oy	241	CTGCTCCCCAGGAACTGAATCTAGTTTGTCATCAGCTGCTGCAMACCCCTCTTTGTAA	300
Db	1387	CTGCTCCCCAGGAACTGAATCTAGTTTGTCATCAGCTGCTGCAMACCCCTCTTTGTAA	1328
Oy	301	CGGGCAAGGGCCCAAGAAAAGGGGAATGTCGTGGCGGCTCAGGGCCAGGGGCTCCGAC	360
Db	1327	CGGGCAAGGGCCCAAGAAAAGGGGAATGTCGTGGCGGCTCAGGGCCAGGGGCTCCGAC	1268
Oy	361	CACCATCTGTTCTCTCAAAATTAAGCCCTCTCTGGGACACTGCTGAAGCTGAAGAGATG	420
Db	1267	CACCATCTGTTCTCTCAAAATTAAGCCCTCTCTGGGACACTGCTGAAGCTGAAGAGATG	1208
Oy	421	CCACCCCTCTCTGCATGTTCTTCACGCCCTCGCCCCAACCCCCCACTCCCTGATGTA	480
Db	1207	CCACCCCTCTCTGCATGTTCTTCACGCCCTCGCCCCAACCCCCCACTCCCTGATGTA	1148
Oy	481	GTTTCTTCTGGGTGTCCTTTATCTCTGGAAGGAGGAGCGGAGTCCGTCTCTTTGTT	540
Db	1147	GTTTCTTCTGGGTGTCCTTTATCTCTGGAAGGAGGAGCGGAGTCCGTCTCTTTGTT	1088
Oy	541	CCTGTGCAAAATTAATGAAGAGCTCGGTAAAGCAATTCGAATAATTCACACTGAGTCAAT	600
Db	1087	CCTGTGCAAAATTAATGAAGAGCTCGGTAAAGCAATTCGAATAATTCACACTGAGTCAAT	1028
Oy	601	TTTTAGTATGTACTTGAAGAGAGGAGTGAAGTAAGTTCACCCCATGCTGTGTAAAC	660
Db	1027	TTTTAGTATGTACTTGAAGAGAGGAGTGAAGTAAGTTCACCCCATGCTGTGTAAAC	968
Oy	661	CGGAGTCAAGGCCAGAGCTGGCAGAGTCAAGTCTTAAAGTCACTGAAGGTGGCATCTGCC	720
Db	967	CGGAGTCAAGGCCAGAGCTGGCAGAGTCAAGTCTTAAAGTCACTGAAGGTGGCATCTGCC	908
Oy	721	TTTTGAAGGCTCCAGTGTCAATTCATCCGTGATGAGGGGCAATGATTGAGACGTGCACA	780
Db	907	TTTTGAAGGCTCCAGTGTCAATTCATCCGTGATGAGGGGCAATGATTGAGACGTGCACA	848
Oy	781	GTTGAGAGTACGATTTCTTTAGAGGCTGAAGGGCCAGTTCCACACTCAAGGGCTCCCTGCTTG	840
Db	847	GTTGAGAGTACGATTTCTTTAGAGGCTGAAGGGCCAGTTCCACACTCAAGGGCTCCCTGCTTG	788
Oy	841	ACAATTCAAACTTCATGCTCTTGAAAAACCATTTCTCTGCACAGAAATGGCTGTTTCGGCG	900
Db	787	ACAATTCAAACTTCATGCTCTTGAAAAACCATTTCTCTGCACAGAAATGGCTGTTTCGGCG	728
Oy	901	CTGAGTGGGCTCTGTGATCTCGAGACTCAATGATGATGGGACTTAAGATGGGGCTGGGCT	960
Db	727	CTGAGTGGGCTCTGTGATCTCGAGACTCAATGATGATGGGACTTAAGATGGGGCTGGGCT	668

Qy	961	CGCTCGAAAGGCGCTTAGAAATATCTCTCACTTCTCTCGAGAGACATGCGCGGG	1020
Dy	667	CGCTCTGAAGAAGCTTAAAGAAATATTTCTCAAGTTCTCTTGACAGAGACTGCGCGGG	608
Qy	1021	ACCGGAAGACACACGGGCGCTGCACAAACGGGCGCTCGTGGTGTGAGTGGCCATGTA	1080
Dy	607	ACCGGAAGACACACGGGCGGTGACAAACGGGCGCTCGGTGGTGTGAGTGGCCATGTA	548
Qy	1081	CGCGCAGCGCCTTCTCGTGGTTGCGTCTGCACGACACGCGCGCACACACCTTGC	1140
Dy	547	CGCGCAGCGCCTTCTCGTGGTTGCGTCTGCACGACACGCGCGCACACACCTTGC	489
Qy	1141	ACGAACACCGCGCGAAACTCTCTCGAGGACACCGTGTACAGAGCGGGTTATACCGAG	1200
Dy	488	ACGAACACCGCGCGAAACTCTCTCGAGGACACCGTGTACAGAGCGGGTTATACCGAG	429
Qy	1201	CTGAGTAGAAGAAACGTCTCCGAGAAAGGAGAGGATCTATACGCCCGAATAGAGAC	1260
Dy	428	CTGAGTAGAAGAAACGTCTCCGAGAAAGGAGAGGATCTATACGCCCGAAGTAGAC	369
Qy	1261	CTGCTCAGTGTGCTGGTGGTTGGCGGACGATGATCTCCGAATCTGGTGGGCAATC	1320
Dy	368	CTGCTCAGTGTGCTGGTGGTTGGCGGACGATGATCTCTCGAATCTGTTGGGCAATC	309
Qy	1321	CAGCATACGGCCATGTCAACAAATCAGCCCTGGGCAGACACGAGCAGAGAGGAGAC	1380
Dy	308	CAGCATACGGCCATGTCAACAAATCAGCCCTGGGCAGACACGAGCAGAGAGGAGAC	249
Qy	1381	AGAGAAAGAAAGACACAGCATGAGAAACACAGTAATGAATGAATGAATGAATGAATGA	1440
Dy	248	AGAGAAAGAAAGAAACACAGCATGAGAAACACAGTAATGAATGAATGAATGAATGAATGA	189
Qy	1441	CCCCCTGTTCTGTGCTTACTGTGCCAGAGAAATGTATACAAATTTTTCAGTGTGACTGA	1500
Dy	188	CCCCCTGTTCTGTGCTTACTGTGCCAGAGAAATGTATACAAATTTTTCAGTGTGACTGA	129
Qy	1501	CAGCTTCTTTTGCACACAGCAGAGAGAAATTTAACACTGTTCAAACCCGGGGAGTTGG	1560
Dy	128	CAGCTTCTTTTGCACACAGCAGAGAGAAATTTAACACTGTTCAAACCCGGGGAGTTGG	69
Qy	1561	CTGTGTTAAGAAAGACCATTAATGCTTTAGACACTGTA 1600	
Dy	68	CTGTGTTAAGAAAGACCATTAATGCTTTAGACACTGTA 29	

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RESULT 23
US-09-726-805-1608/C
: Sequence 1608, Application US/09726805
: GENERAL INFORMATION:
: APPLICANT: Geating, David P.
: APPLICANT: Holzman, Douglas A.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600, 2017-001
: CURRENT APPLICATION NUMBER: US/09/726, 805
: CURRENT FILING DATE: 2000-11-30
: PRIOR APPLICATION NUMBER: 60/168,140
: PRIOR FILING DATE: 1999-11-30
: NUMBER OF SEQ ID NOS: 2158
: SOFTWARE: PastSeq for Windows Version 4.0
: SEQ ID NO 1608
: LENGTH: 1925
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-726-805-1608

```

Query Match	85.1%	Score 1377	DB 29	length 1925
Best Local Similarity	99.8%	Pred. No. 1.9e-255		
Matches 1597; Conservative	0	Mismatches 2	Indels 1	Gaps 1
<p>QY 1 GGCACCTTTTGGGCAATTCCTTCCTCCAGGCTTGGCGCAAAATCAGTCACCA 60</p> <p>     </p>				

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: APPLICANT: Silos-Santiago, Inmaculada
: APPLICANT: Disiefano, Peter
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600.2020-001
: CURRENT APPLICATION NUMBER: US/09/659,997
: CURRENT FILING DATE: 2000-10-30
: PRIOR APPLICATION NUMBER: 60/162,359
: PRIOR FILING DATE: 1999-10-29
: NUMBER OF SEQ ID NOS: 12714
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 11085
:
: LENGTH: 1925
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
US-09-659-997-11085

```

Query Match	85.1%	Score 1377;	DB 27	Length 1925;
Best Local Similarity	99.8%	Pred. No. 1.9e-255;		
Matches 1597;	Conservative 0;	Mismatches 2;		
			Indels 1;	Gaps 1;

QY	1	GGCACTTTTGGCGATTGTTCTTCTTCACAGCTTTGGCGTGCAAATCACTGGTACCA	60
Dp	1627	GGCACTTTTGGCGATTGTTCTTCTTCACAGCTTTGGCGTGCAAATCACTGGTACCA	1568
QY	61	GTTGTAAGAATTCACGTGAAACACGACTGCTCTCCCGATTCATTGTGAATTTGCAC	120
Dp	1567	GTTGTAAGAATTCACGTGAAACACGACTGCTCTCCCGATTCATTGTGAATTTGCAC	1508
QY	121	GGTGAAGCTTCAAGCATGTGTCAAAAGAAATGTGAGCAAAAGTCCGGATCATGTA	180
Dp	1507	GGTGAAGCTTCAAGCATGTGTCAAAAGAAATGTGAGCAAAAGTCCGGATCATGTA	1448
QY	181	CCGCAAGTCTGTGATCATCAGCGGCTGTGTCTATCGCTCTGTGCGGGATCACAGTCC	240
Dp	1447	CCGCAAGTCTGTGATCATCAGCGGCTGTGTCTATCGCTCTGTGCGGGATCACAGTCC	1388
QY	241	CTGCTCCCCAGGAAACTGAACTCAGTTTGATCATCGTGTGCAACACCCCTCTTTGTA	300
Dp	1387	CTGCTCCCCAGGAAACTGAACTCAGTTTGATCATCGTGTGCAACACCCCTCTTTGTA	1328
QY	301	CGGGCCAAAGGCCCAAGAAAAGGGAAAGTTCTGCTCCGGCCCTCAAGGCCAGGGCTCCGAC	360
Dp	1327	CGGGCCAAAGGCCCAAGAAAAGGGAAAGTTCTGCTCCGGCCCTCAAGGCCAGGGCTCCGAC	1268
QY	361	CACCATCTGTTCTGTCAAATTAAGCCCTTTCTCGGCACACTGCTGAAGTGAAGAGATG	420
Dp	1267	CACCATCTGTTCTGTCAAATTAAGCCCTTTCTCGGCACACTGCTGAAGTGAAGAGATG	1208
QY	421	CCACCCCTCTCTGCATYTTTCTTCAGACGCCCTGCGCCCCAACCCCCACCTCCCTGAATGA	480
Dp	1207	CCACCCCTCTCTGCATYTTTCTTCAGACGCCCTGCGCCCCAACCCCCACCTCCCTGAATGA	1148
QY	481	GTTTCTTCTGGGTGCTCTTATCTGGGTGAAGGAGCGGGAGTCCGTCTCTTTTGT	540
Dp	1147	GTTTCTTCTGGGTGCTCTTATCTGGGTGAAGGAGCGGGAGTCCGTCTCTTTTGT	1088
QY	541	CCGTGCAAAATTAATGAAGAAGCTCGTTAAACATTCTGAATAAATTCAGCTGACTGAAT	600
Dp	1087	CCGTGCAAAATTAATGAAGAAGCTCGTTAAACATTCTGAATAAATTCAGCTGACTGAAT	1028
QY	601	TTTTCAGTATGTACTTGAAGAGAGAGGTGAGTGAAGATTCACCCCATGTCTGTGAAC	660
Dp	1027	TTTTCAGTATGTACTTGAAGAGAGAGGTGAGTGAAGATTCACCCCATGTCTGTGAAC	968
QY	661	CGGAGCTAAAGGCCAAGGCTGGCAGAGTCAAGTCTTAAGAAGTCACTGAGTGGGCATCTGCC	720
Dp	967	CGGAGCTAAAGGCCAAGGCTGGCAGAGTCAAGTCTTAAGAAGTCACTGAGTGGGCATCTGCC	908
QY	721	TTTTTGTAAAGCTCTCACTGTCATTTCCATCCCTGATGGGGCATAGTTTGAAGACTGCGAGA	780
Dp	907	TTTTTGTAAAGCTCTCACTGTCATTTCCATCCCTGATGGGGCATAGTTTGAAGACTGCGAGA	848

Qy	781	GTGAGAGTACGCTTTTCTTTAGGCGTGGAGGGCCAGTTCCACACCAAGGCGCTCCGCTTG	840
Db	847	GTGAGAGTACGCTTTTCTTTAGGCGTGGAGGGCCAGTTCCACACCAAGGCGCTCCGCTTG	788
Qy	841	ACATTCAACTTCATGCTCTCTGAAAAACCATTTCTGCGACGAAATTGCGTGGTTTCGCGC	900
Db	787	ACATTCAAACTTCATGCTCTCTGAAAAACCATTTCTGCGACGAAATTGCGTGGTTTCGCGC	728
Qy	901	CTGAGTTGGGCTCTAGTACGTCGAGCATCAATACAGTGGAGCTTAAGCTGCGGCT	960
Db	727	CTGAGTTGGGCTCTAGTACGTCGAGCATCAATACAGTGGAGCTTAAGCTGCGGCT	668
Qy	961	CGCTCTGAAAAGTCTTAAGAAAATCTTCTCAGTTCTCCTTGGCAGAGCACTGGCCCGG	1020
Db	667	CGCTCTGAAAAGTCTTAAGAAAATCTTCTCAGTTCTCCTTGGCAGAGCACTGGCCCGG	608
Qy	1021	ACGCGAAGACGACAGGGCGCTGACCAAGCGGCGCTGTGCGTGTTGAGTCCGCACTGA	1080
Db	607	ACGCGAAGACGACAGGGCGCTGACCAAGCGGCGCTGTGCGTGTTGAGTCCGCACTGA	548
Qy	1081	CGCGAGGCGCTTCTCGTGGTTGGCCGTCGTGACGACAGCGGGGCGACACACCTTCG	1140
Db	547	CGCGAGGCGCTTCTCGTGGTTGGCCGTCGTGACGACAGCGGGGCGACACACCTTCG	489
Qy	1141	ACGAAACACCGCGCAAACTGCTGCGAGACACCGTGTACAGAGCGCGGTTGATGACCGAG	1200
Db	488	ACGAAACACCGCGCAAACTGCTGCGAGACACCGTGTACAGAGCGCGGTTGATGACCGAG	429
Qy	1201	CTGAGGTGAAAACGTCCTCCGGAAGGGAGAGAGATCATGTAGCCCGGAAAGTAGAAC	1260
Db	428	CTGAGGTGAAAACGTCCTCCGGAAGGGAGAGAGATCATGTAGCCCGGAAAGTAGAAC	369
Qy	1261	CTCGTCACGTGCTGCTGGGTTTGGCCGCGACGCATGATCCTCCGAACTGTGTTGGGCATC	1320
Db	368	CTCGTCACGTGCTGCTGGGTTTGGCCGCGACGCATGATCCTCCGAACTGTGTTGGGCATC	309
Qy	1321	CAGCATACGGCCATGTCCACAACAATTCAGCCCTGGGCAACACAGACGAGGAGGAGAAC	1380
Db	308	CAGCATACGGCCATGTCCACAACAATTCAGCCCTGGGCAACACAGACGAGGAGGAGAAC	249
Qy	1381	AGAGAAAAGAAAACACACGAGTGAAGAACACAGTAATTAATAAACCATAAATTTTAG	1440
Db	248	AGAGAAAAGAAAACACACGAGTGAAGAACACAGTAATTAATAAACCATAAATTTTAG	189
Qy	1441	CCCCCTGTGTTCTGTGCTTACTGCGCCACGAAATGTGTCACATTTTTCAGTGTTCCTGGA	1500
Db	188	CCCCCTGTGTTCTGTGCTTACTGCGCCACGAAATGTGTCACATTTTTCAGTGTTCCTGGA	129
Qy	1501	CAGCTCTTTTGGCCACAGCAGACAGAGAATTTAACACTCTTTCAAAACCGGGGAGCTGG	1560
Db	128	CAGCTCTTTTGGCCACAGCAGACAGAGAATTTAACACTCTTTCAAAACCGGGGAGCTGG	69
Qy	1561	CTGTGTTAAAGAAAGACCATTAATCTCTTTAGACAGTGA 1600	
Db	68	CTGTGTTAAAGAAAGACCATTAATCTCTTTAGACAGTGA 29	
RESULT 22			
US-09-710-281-4458/c			
; Sequence 4458, Application US/09710281			
; GENERAL INFORMATION:			
; APPLICANT: Hunter, John J.			
; APPLICANT: Shyjan, Andrew W.			
; APPLICANT: Subdel, Nide			
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES			
; TITLE OF INVENTION: THEREFOR			
; FILE REFERENCE: 1600.2036-001			
; CURRENT APPLICATION NUMBER: US/09/710.281			
; PRIOR FILING DATE: 2000-11-10			
; PRIOR FILING DATE: 1999-11-09			
; NUMBER OF SEQ ID NOS: 5803			
; SOFTWARE: FastSeq for Windows Version 4.0			





OY 1381 AGAGAAAAAGAAAAACACAGATGAGAGACAGTAAATGAATAAACATTAATATTAG 1440  
 Db 248 AGAGAAAAAGAAAAACACAGATGAGAGACAGTAAATGAATAAACATTAATATTAG 189  
 OY 1441 CCCCTCTGTTCTGCTTACTGCGCAGAAATGGTACCAATTTTTCAGTGTGACCTGA 1500  
 Db 188 CCCCTCTGTTCTGCTTACTGCGCAGAAATGGTACCAATTTTTCAGTGTGACCTGA 129  
 OY 1501 CAGCTTCTTTTGCACACAGAGAGAAATTAACACGTTTTCACACCCCGGGAGTTGG 1560  
 Db 128 CAGCTTCTTTTGCACACAGAGAGAAATTAACACGTTTTCACACCCCGGGAGTTGG 69  
 OY 1561 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 1600  
 Db 68 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 29

RESULT 19  
 US-09-652-128-9375/c  
 : Sequence 9375, Application US/09652128  
 : GENERAL INFORMATION:  
 : APPLICANT: Shyjan, Andrew W.  
 : APPLICANT: Holtzman, Douglas A.  
 : TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
 : FILE REFERENCE: 1600.1171-001  
 : CURRENT APPLICATION NUMBER: US/09/652.128  
 : PRIOR FILING DATE: 2000-08-30  
 : PRIOR APPLICATION NUMBER: 60/151.133  
 : NUMBER OF SEQ ID NOS: 10265  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 9375  
 : LENGTH: 1925  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : US-09-652-128-9375

Query Match 85.18; Score 1377; DB 25; Length 1925;  
 Best Local Similarly 99.8%; Pred. No. 1.9e-255;  
 Matches 1597; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 GGCACACTTTTGGGATGTTCTTCTCCAGGCTTTGGCGTCAATCAAGTCTACCA 60  
 Db 1627 GGCACACTTTTGGGATGTTCTTCTCCAGGCTTTGGCGTCAATCAAGTCTACCA 1568  
 OY 61 GTGTGAAGAAATTCAGCTGAACAAGACTGCTCTCCCGAGTTTCAATGTGAATTGGAC 120  
 Db 1567 GTGTGAAGAAATTCAGCTGAACAAGACTGCTCTCCCGAGTTTCAATGTGAATTGGAC 1508  
 OY 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180  
 Db 1507 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 1448  
 OY 181 CCGCAAGTCTCTGTCATCATCAAGCGCTGTCTCATCGCTGCGCGGATACCAATCTT 240  
 Db 1447 CCGCAAGTCTCTGTCATCATCAAGCGCTGTCTCATCGCTGCGCGGATACCAATCTT 1388  
 OY 241 CTGCTCTCCCAAGGAAATCAAGTCAAGTGTGATCAAGTGTGCAACACCCCTCTTTGTA 300  
 Db 1387 CTGCTCTCCCAAGGAAATCAAGTGTGATCAAGTGTGCAACACCCCTCTTTGTA 1328  
 OY 301 CCGGGCCAGAGCCCAAGAAAAAGGGAAGTTCTGCTCCGCGCTCAGGCGCAGGCTCCGAC 360  
 Db 1327 CCGGGCCAGAGCCCAAGAAAAAGGGAAGTTCTGCTCCGCGCTCAGGCGCAGGCTCCGAC 1268  
 OY 361 CACCATCTCTGTTCTCAAAATAGCCCTCTTCTGCGCACTGCTGAAGCTGAAGAGATG 420  
 Db 1267 CACCATCTCTGTTCTCAAAATAGCCCTCTTCTGCGCACTGCTGAAGCTGAAGAGATG 1208  
 OY 421 CCACCCCTCTGCAATGTGTCTTCAAGCCCTGCGCCCAACCCCAACCTCTCTGAGTGA 480

Db 1207 CCACCCCTCTCTGATGTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 1148  
 OY 481 GTTCTTCTGGGATGCTCTTCTTATTCGCTGAGGAGCGGGAGTCCGTCTCTTTGTT 540  
 Db 1147 GTTCTTCTGGGATGCTCTTCTTATTCGCTGAGGAGCGGGAGTCCGTCTCTTTGTT 1088  
 OY 541 CCTGTCAAAATTAATGAAGAGCTCGGTAAAGCATCTGTAATTAATTCAGCTGACTAAT 600  
 Db 1087 CCTGTCAAAATTAATGAAGAGCTCGGTAAAGCATCTGTAATTAATTCAGCTGACTAAT 1028  
 OY 601 TTTTCAATATGTTCTGAAGAGAGGAGTGAATGAATTAATTAATTAATTAATTAATTAAT 660  
 Db 1027 TTTTCAATATGTTCTGAAGAGAGGAGTGAATGAATTAATTAATTAATTAATTAATTAAT 968  
 OY 661 CCGAGTCAAGGCGCAGGCTGCGAGAGTCAAGTCTTGAAGATCACTGAGTGGGATCTGGC 720  
 Db 967 CCGAGTCAAGGCGCAGGCTGCGAGAGTCAAGTCTTGAAGATCACTGAGTGGGATCTGGC 908  
 OY 721 TTTTGTAAAGCTCCAGTGTCCATTTCCATCCCTGATGGGGCATATTGAGACTGAGA 780  
 Db 907 TTTTGTAAAGCTCCAGTGTCCATTTCCATCCCTGATGGGGCATATTGAGACTGAGA 848  
 OY 781 GTGAGAGTGAAGTCTTCTTGAAGGCGGAGGCGGAGTCCCACTCAAGGCTCCCTGCTG 840  
 Db 847 GTGAGAGTGAAGTCTTCTTGAAGGCGGAGGCGGAGTCCCACTCAAGGCTCCCTGCTG 788  
 OY 841 ACATTCAAATCTCATGCTCTCTGAAACCATTTCTGACAGCAGAAATGGCTGGTGGCG 900  
 Db 787 ACATTCAAATCTCATGCTCTCTGAAACCATTTCTGACAGCAGAAATGGCTGGTGGCG 728  
 OY 901 CTGAGTGGGCTCTAGTGAAGTCAAGTCAATGACTGAGCTTGAAGTGGGCTGGGCT 960  
 Db 727 CTGAGTGGGCTCTAGTGAAGTCAAGTCAATGACTGAGCTTGAAGTGGGCTGGGCT 668  
 OY 961 GCTCTGAAAAGTCTTGAAGAAATCTTCTCAATCTCTCTGACAGAGAGTGGGCGCGG 1020  
 Db 667 GCTCTGAAAAGTCTTGAAGAAATCTTCTCAATCTCTCTGACAGAGAGTGGGCGCGG 608  
 OY 1021 ACGGGAAGAGCAACGGGCGCTGCAAAAGCGGCGCTGTCGGTGTGAGTCCGATGTA 1080  
 Db 607 ACGGGAAGAGCAACGGGCGCTGCAAAAGCGGCGCTGTCGGTGTGAGTCCGATGTA 548  
 OY 1081 CGGCGAGGCGCTCTCTGCTGTTGGGTTGGCGTGCAGCAGCGGCGGAGCACACACCTTGC 1140  
 Db 547 CGGCGAGGCGCTCTCTGCTGTTGGGTTGGCGTGCAGCAGCGGCGGAGCACACACCTTGC 489  
 OY 1141 ACGAACACCCCGGAAACTGCTCGAGGACACCGTGTACAGAGCGGGTGTGATGACCGAG 1200  
 Db 488 ACGAACACCCCGGAAACTGCTCGAGGACACCGTGTACAGAGCGGGTGTGATGACCGAG 429  
 OY 1201 CTGAGGTAGAAGAAAGCTCTCCGAGAGGAGGAGGATCATGTACGCCCGGAATAGGAC 1260  
 Db 428 CTGAGGTAGAAGAAAGCTCTCCGAGAGGAGGAGGATCATGTACGCCCGGAATAGGAC 369  
 OY 1261 CTGCTCAGTCTGCTTGGGTTGGCGCAGCATGATCCCGAATCTGTTGGGCAATC 1320  
 Db 368 CTGCTCAGTCTGCTTGGGTTGGCGCAGCATGATCCCGAATCTGTTGGGCAATC 309  
 OY 1321 CAGCATACGGCCCAATGTCAACAATCAAGCCTGGGCAAGCAGCAGAGGAGGAGAGAC 1380  
 Db 308 CAGCATACGGCCCAATGTCAACAATCAAGCCTGGGCAAGCAGCAGAGGAGGAGAGAC 249  
 OY 1381 AGAGAAAAAGAAAAACACACATGAGAGACAGTAAATGAATTAATTAATTAATTAATTAAT 1440  
 Db 248 AGAGAAAAAGAAAAACACACATGAGAGACAGTAAATGAATTAATTAATTAATTAATTAAT 189  
 OY 1441 CCCCTCTGTTCTGCTTACTGCGCAGAAATGTACCAATTTTTCAGTGTGACTTGA 1500  
 Db 188 CCCCTCTGTTCTGCTTACTGCGCAGAAATGTACCAATTTTTCAGTGTGACTTGA 129  
 OY 1501 CAGCTTCTTTTGCACACAGAGAGAGAAATTAACATCTGTTCAAAACCGGGGAGTTGG 1560  
 Db 128 CAGCTTCTTTTGCACACAGAGAGAGAAATTAACATCTGTTCAAAACCGGGGAGTTGG 69



Db 1435 ACGAACACCCCGCCAACTGCTGCGAGACACCGTGTACAGAGCGGGTTGATGACCGAG 1494  
Qy 1201 CTGAGGTGAAAAAGCTCTCCGAGAGGGAGAGATCATGTACGCCCGAAGTAGAGAC 1260  
Db 1495 CTGAGGTGAAAAAGCTCTCCGAGAGGGAGAGATCATGTACGCCCGAAGTAGAGAC 1554  
Qy 1261 CTGCTCAGTGTGCTGGGTTTGGCCGACGACCATGATCTCCGAAATCTGTTGGGCATC 1320  
Db 1555 CTGCTCAGTGTGCTGGGTTTGGCCGACGACCATGATCTCCGAAATCTGTTGGGCATC 1614  
Qy 1321 CAGCATACGCCCATGTATCAACAATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1380  
Db 1615 CAGCATACGCCCATGTATCAACAATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1674  
Qy 1381 AAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGATTAATTAATTAATTTAG 1440  
Db 1675 AAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGATTAATTAATTAATTTAG 1734  
Qy 1441 CCCCTCTGTTCTGTCTTACTGACGACGAGAAATGATACCAATTTTTCAGTGTGACTGA 1500  
Db 1735 CCCCTCTGTTCTGTCTTACTGACGACGAGAAATGATACCAATTTTTCAGTGTGACTGA 1794  
Qy 1501 CAGCTTCTTTTGCACAGCAAGAGAGATTAACACTGTTCACAAACCCGGGGAGTTGG 1560  
Db 1795 CAGCTTCTTTTGCACAGCAAGAGAGATTAACACTGTTCACAAACCCGGGGAGTTGG 1854  
Qy 1561 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAAA 1607  
Db 1855 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAAA 1901

RESULT 18  
US-09-652-121-7293/c  
; Sequence 7293, Application US/09652121  
; GENERAL INFORMATION:  
; APPLICANT: Disefano, Peter  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.1188-001  
; CURRENT APPLICATION NUMBER: US/09/652,121  
; CURRENT FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/151,129  
; PRIOR FILING DATE: 1999-08-30  
; NUMBER OF SEQ ID NOS: 7615  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7293  
; LENGTH: 1925  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-652-121-7293

Query Match 85.1%; Score 1377; DB 25; Length 1925;  
Best Local Similarity 99.8%; Pred. No. 1.9e-253;  
Matches 1597; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 GGCACATTTTGGGATTTGTTCTTCTCCAGGCTTGGCGTGAACATCAGTGTACCA 60  
Db 1627 GGCACATTTTGGGATTTGTTCTTCTCCAGGCTTGGCGTGAACATCAGTGTACCA 1568  
Qy 61 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCTCCCGAGTTATTGTGAATTGCAC 120  
Db 1567 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCTCCCGAGTTATTGTGAATTGCAC 1508  
Qy 121 GGTGAAGCTTCAAGACATGTGTGCAAGAAAGATGAGAGCAAGTGGCGGATCATGTA 180  
Db 1507 GGTGAAGCTTCAAGACATGTGTGCAAGAAAGATGAGAGCAAGTGGCGGATCATGTA 1448  
Qy 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTATCGCCTGCGGGATACCAATCTCTT 240  
Db 1447 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTATCGCCTGCGGGATACCAATCTCTT 1388  
Qy 241 CTGCTCCCGAGGAACTGAAGTGTGATCAGTGTGTGAACACCCCTCTTTGTA 300

Db 1387 CTGCTCCCGAGGAAACTGAACCTAGTTTGCATCAGTGTGCAACACCCCTTTGTA 1328  
Qy 301 CGGGCCAAAGGCCCAAGAAAAAGGAGATTCTGCTCGGCCCTTAGGCCAGGGCTCCGCCAC 360  
Db 1327 CGGGCCAAAGGCCCAAGAAAAAGGAGATTCTGCTCGGCCCTTAGGCCAGGGCTCCGCCAC 1268  
Qy 361 CACCATCTGTGCTCAAAATTTAGCCCTCTCTCGGCACTGTGTGAAGCTGAAGAGATG 420  
Db 1267 CACCATCTGTGCTCAAAATTTAGCCCTCTCTCGGCACTGTGTGAAGCTGAAGAGATG 1208  
Qy 421 CCACCCCTCTCTGCAATGTTCTTCCAGCCCTCGGCCCAACCCCCCACTCTCTGAGTGA 480  
Db 1207 CCACCCCTCTCTGCAATGTTCTTCCAGCCCTCGGCCCAACCCCCCACTCTCTGAGTGA 1148  
Qy 481 GTTCTTCTGGGTCTCTTTATTTCTGGGTGAGAGGGAGGCCGTCTCTTTGTT 540  
Db 1147 GTTCTTCTGGGTCTCTTTATTTCTGGGTGAGAGGGAGGCCGTCTCTTTGTT 1088  
Qy 541 CCTGTCAAAATTAAGAAAGAGCTGCTGAACATTTCTGAATTAATTAATTAATTAAT 600  
Db 1087 CCTGTCAAAATTAAGAAAGAGCTGCTGAACATTTCTGAATTAATTAATTAATTAAT 1028  
Qy 601 TTTTCAGTATGTAATTGAAGAAAGAGTGAAGTGAAGTTACCCCATGCTGTGTAAAC 660  
Db 1027 TTTTCAGTATGTAATTGAAGAAAGAGTGAAGTGAAGTTACCCCATGCTGTGTAAAC 968  
Qy 661 CGGAGTCAAGGCGCAGGCTGGGACAGTCACTTGAAGTCACTGAGTGGGATCTGCC 720  
Db 967 CGGAGTCAAGGCGCAGGCTGGGACAGTCACTTGAAGTCACTGAGTGGGATCTGCC 908  
Qy 721 TTTTGAAGCCCTCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 780  
Db 907 TTTTGAAGCCCTCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 848  
Qy 781 GTGAGAGTACGTTTCTTAAGGCGTGGAGGGCCAGTCCCACTCAAGGCTCCCTGCC 840  
Db 847 GTGAGAGTACGTTTCTTAAGGCGTGGAGGGCCAGTCCCACTCAAGGCTCCCTGCC 788  
Qy 841 ACATTCAAACTTCATGCTCTGAAAAACATTTCTGACAGCAAAATTTGGCTGTTCCGCC 900  
Db 787 ACATTCAAACTTCATGCTCTGAAAAACATTTCTGACAGCAAAATTTGGCTGTTCCGCC 728  
Qy 901 CTGAGTTGGGCTCTAGTACTGACCTGAGACTCATGACTGGGACTTGAAGTGGGCTGCC 960  
Db 727 CTGAGTTGGGCTCTAGTACTGACCTGAGACTCATGACTGGGACTTGAAGTGGGCTGCC 668  
Qy 961 CGCTCTGAAGAAAGTCTTAAGAAATTTCTCAAGTCTCTCTGACAGAGACTGGGCGCGG 1020  
Db 667 CGCTCTGAAGAAAGTCTTAAGAAATTTCTCAAGTCTCTCTGACAGAGACTGGGCGCGG 608  
Qy 1021 ACGGGAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGGGTGGAGTGGCCATGTA 1080  
Db 607 ACGGGAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGGGTGGAGTGGCCATGTA 548  
Qy 1081 CGGCGAGGCTCTGTGTGTGGTGGCTGCTGACAGCAAGGGGGAGAGCAAGCACTTGC 1140  
Db 547 CGGCGAGGCTCTGTGTGTGGTGGCTGCTGACAGCAAGGGGGAGAGCAAGCACTTGC 489  
Qy 1141 ACGAACACCCCGGAAACTCTGCGAGACACCGTGTACAGAGAGCGGGTTGATGACGAG 1200  
Db 488 ACGAACACCCCGGAAACTCTGCGAGACACCGTGTACAGAGAGCGGGTTGATGACGAG 429  
Qy 1201 CTGAGGTGAAAAAGCTGTCCGAGAAAGGGAGAGATCATGTAGCCCGGAAAGTAGAG 1260  
Db 428 CTGAGGTGAAAAAGCTGTCCGAGAAAGGGAGAGATCATGTAGCCCGGAAAGTAGAG 369  
Qy 1261 CTGCTCAGTGTGCTGGGTTTGGCCGACGACCATATCTCCGAATCTGTGTGGGATC 1320  
Db 368 CTGCTCAGTGTGCTGGGTTTGGCCGACGACCATATCTCCGAATCTGTGTGGGATC 309  
Qy 1321 CAGCATACGGCCAAATGTACAAACATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1380  
Db 308 CAGCATACGGCCAAATGTACAAACATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 249

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Oy 1141 ACGAACCCCGCCGAAATGCTGCGAGACACCGTGTACAGAGCGGGTGTGACCGGAG 1200
    |||
Db 1435 ACGAACACCCCGCGAAATGCTGCGAGACACCGTGTACAGAGCGGGTGTGACCGGAG 1494
Oy 1201 CTGAGGTAGAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAATGAGAC 1260
    |||
Db 1495 CTGAGGTAGAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAATGAGAC 1554
Oy 1261 CTCGTCACATGCTGCTGGGTTGGCCGAGCATGATCTCCGAATCGTTGGGGCATC 1320
    |||
Db 1555 CTCGTCACATGCTGCTGGGTTGGCCGAGCATGATCTCCGAATCTGGTTGGGGCATC 1614
Oy 1321 CAGCATAGCGCCCAATGTCAACAATCAAGCCCTGGGACAGACGAGAGAGAGAGAC 1380
    |||
Db 1615 CAGCATAGCGCCCAATGTCAACAATCAAGCCCTGGGACAGACGAGAGAGAGAGAC 1674
Oy 1381 AGAGAAAAGAAAACACAGCATGAGACACAGTAATGAATAAACCATTAATATTTAG 1440
    |||
Db 1675 AGAGAAAAGAAAACACAGCATGAGACACAGTAATGAATAAACCATTAATATTTAG 1734
Oy 1441 CCCCTCTTCTGCTGCTTACTGGCCAGGAAATGGTACCATTCTTTCAGTGTGGACTTGA 1500
    |||
Db 1735 CCCCTCTTCTGCTGCTTACTGGCCAGGAAATGGTACCATTCTTTCAGTGTGGACTTGA 1794
Oy 1501 CAGCTTCTTTGGCAACAAGACAGAGAAATTTAACTCTTTCAACCCGGGGAGTTGG 1560
    |||
Db 1795 CAGCTTCTTTGGCAACAAGACAGAGAAATTTAACTCTTTCAACCCGGGGAGTTGG 1854
Oy 1561 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAA 1607
    |||
Db 1855 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAA 1901

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RESULT 17
US-09-808-383-4454
; Sequence 4454, Application US/09808383
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600.1046-002
; CURRENT APPLICATION NUMBER: US/09/808,383
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 09/397,022
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: US 60/100,465
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: US 60/106,443
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 60/107,257
; PRIOR FILING DATE: 1998-11-15
; PRIOR APPLICATION NUMBER: US 60/126,906
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/132,099
; NUMBER OF SEQ ID NOS: 5775
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4454
; LENGTH: 1918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-808-383-4454

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Query Match      85.5%; Score 1384; DB 31; Length 1918;
Best Local Similarity 99.8%; Pred. No. 8.8e-257;
Matches 1604; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Oy 1 GGCACATTTTTCGAGATGCTCTGCTGCTCAGGCTTGGCGCAAAATCCAGTCTACCA 60
    |||
Db 296 GGCACATTTTTCGAGATGCTCTGCTGCTCAGGCTTGGCGCAAAATCCAGTCTACCA 355
Oy 61 GTGTGAAGATTCAGCTGAAACAGACATGCTCTCCCGAGTTCATTGTGAATTTGCAC 120

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Db 356 GTGTGAAGATTCAGCTGAAACAGACATGCTCTCCCGAGTTCATTGTGAATTTGCAC 415
Oy 121 GGTGAAGATTCAGACATGCTGCAAGAAAGATGATGAGCAAAATGCCGGATTCATGTA 180
    |||
Db 416 GGTGAAGATTCAGACATGCTGCAAGAAAGATGATGAGCAAAATGCCGGATTCATGTA 475
Oy 181 CCGCAAGTCTGTGATCATCATGAGGCGCTGTCTCATGCGCTTGGCGGGTATCAAGTCTT 240
    |||
Db 476 CCGCAAGTCTGTGATCATCATGAGGCGCTGTCTCATGCGCTTGGCGGGTATCAAGTCTT 535
Oy 241 CTGCTCCCGAGGAAATGAACTGAACTGATTTGCAATCAGTGTGCAAAACCCCTTTGTAA 300
    |||
Db 536 CTGCTCCCGAGGAAATGAACTGAACTGATTTGCAATCAGTGTGCAAAACCCCTTTGTAA 595
Oy 301 CGGGCCAAAGGCCCAAGAAAAGGGAAATTTGCTGCTGCGCCCTCAGGCCAAGGGCTCCGAC 360
    |||
Db 596 CGGGCCAAAGGCCCAAGAAAAGGGAAATTTGCTGCTGCGCCCTCAGGCCAAGGGCTCCGAC 655
Oy 361 CACCATCTGTTTCTCAATTTACCCCTCTTCTGCGACACACTGCTGAAGCTGAAGAGATG 420
    |||
Db 656 CACCATCTGTTTCTCAATTTACCCCTCTTCTGCGACACACTGCTGAAGCTGAAGAGATG 715
Oy 421 CCAACCCCTCTGATTTGTTCTTCCAGCCCTGCGCCCAACCCCTCCCTGATGTA 480
    |||
Db 716 CCAACCCCTCTGATTTGTTCTTCCAGCCCTGCGCCCAACCCCTCCCTGATGTA 775
Oy 481 GTTCTCTTGGGGTCTCTTTTATTTGAGGAGAGGAGAGGAGTCTGTTCTTTTGT 540
    |||
Db 776 GTTCTCTTGGGGTCTCTTTTATTTGAGGAGAGGAGAGTCTGTTCTTTTGT 835
Oy 541 CCTGTCAATATATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTTACGCTGAT 600
    |||
Db 836 CCTGTCAATATATGAAGAGCTCGGTAAAGCATTTCTGAATTAATTTACGCTGAT 895
Oy 601 TTTCAATATGTTGAAAGAGAGGAGTGAAGTGAAGTTCACCCCATGTTGTTGATC 660
    |||
Db 896 TTTCAATATGTTGAAAGAGAGGAGTGAAGTGAAGTTCACCCCATGTTGTTGATC 955
Oy 661 CGGAGTCAAGGCGGAGCTGTGAGAGTCACTTCTTGAAGTCACTGAGTGGGATCTGCC 720
    |||
Db 956 CGGAGTCAAGGCGGAGCTGTGAGAGTCACTTCTTGAAGTCACTGAGTGGGATCTGCC 1015
Oy 721 TTTTGAAGAGCTCCAGAGTCCATTCATCCCTGATGGGGGATGTTGAGATGCA 780
    |||
Db 1016 TTTTGAAGAGCTCCAGAGTCCATTCATCCCTGATGGGGGATGTTGAGATGCA 1075
Oy 781 GTGAGAGTACGTTTCTTGAAGGCTGAGGCGCACTTCCATCAAGGCTCCCTGCTTG 840
    |||
Db 1076 GTGAGAGTACGTTTCTTGAAGGCTGAGGCGCACTTCCATCAAGGCTCCCTGCTTG 1135
Oy 841 ACATTCAACTCATGCTGCTGAAACCAATCTCTGACGACGAATTTGCTGTTTCCGC 900
    |||
Db 1136 ACATTCAACTCATGCTGCTGAAACCAATCTCTGACGACGAATTTGCTGTTTCCGC 1195
Oy 901 CTGAGTGGGCTGATGACTGAGACTCAATGACTGGAGCTTGAAGCTGGGGCTCGGCT 960
    |||
Db 1196 CTGAGTGGGCTGATGACTGAGACTCAATGACTGGAGCTTGAAGCTGGGGCTCGGCT 1255
Oy 961 CGCTCTGAAAAGTGTCTTAAGAAATCTTCTCAGTCTCTTTCAGAGAGACTGGCGCGG 1020
    |||
Db 1256 CGCTCTGAAAAGTGTCTTAAGAAATCTTCTCAGTCTCTTTCAGAGAGACTGGCGCGG 1315
Oy 1021 ACGGAAGAGCAAGGGGCGTGCACAAAGGGGGCGTGGCTGTGAGTGGCATGTA 1080
    |||
Db 1316 ACGGAAGAGCAAGGGGCGTGCACAAAGGGGGCGTGGCTGTGAGTGGCATGTA 1375
Oy 1081 CGCGAGGCGCTTCTGTTGTTGGCTGTGACAGCAGAGGGCGCACAGCAACCTTGC 1140
    |||
Db 1376 CGCGAGGCGCTTCTGTTGTTGGCTGTGACAGCAGAGGGCGCACAGCAACCTTGC 1434
Oy 1141 ACGAACACCGCCGAAACTGCTGAGAGACACGTTGACAGAGCGGTTGATGACGAG 1200
    |||

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QY 1441 CCCCTGTTCTGTTGCTTACTGAGCAAAATGTCACAAATTTTTCAGTGTGGAATTGA 1500  
 |||||  
 Db 1719 CCCCTGTTCTGTTGCTTACTGAGCAAAATGTCACAAATTTTTCAGTGTGGAATTGA 1778  
 QY 1501 CAGCTTCTTTGGCAGACAGAGAGAAATTTTAACTGTTTCAAAACCCGGGGAGTTGG 1560  
 |||||  
 Db 1779 CAGCTTCTTTGGCAGACAGAGAGAAATTTTAACTGTTTCAAAACCCGGGGAGTTGG 1838  
 QY 1561 CTGTGTTAAAGAAAGACATTAAATGCTTTAGACAGTGTAAAAA  
 |||||  
 Db 1839 CTGTGTTAAAGAAAGACATTAAATGCTTTAGACAGTGTAAAAA  
 |||||

RESULT 15  
 PCT-US02-29964-16  
 ; Sequence 16, Application PC/TUS0229964  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Ren, Feiyan  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Zhao, Qing A.  
 ; APPLICANT: Wang, Jian-Rui  
 ; APPLICANT: Xue, Aibong J.  
 ; APPLICANT: Wang, Duntui  
 ; APPLICANT: Ghosh, Maladika  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Mehrman, Tom  
 ; APPLICANT: Zhou, Ping  
 ; APPLICANT: Goodrich, Ryle W.  
 ; APPLICANT: Haley, Vicente, Dana  
 ; APPLICANT: Dimanac, Radoje T  
 ; TITLE OF INVENTION: Novel Nucleic Acids and  
 ; FILE REFERENCE: 809ACIP PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US02/29964  
 ; CURRENT FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/323,739  
 ; PRIOR FILING DATE: 2001-09-19  
 ; PRIOR APPLICATION NUMBER: US 09/488,725  
 ; PRIOR FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US 09/552,317  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: US 09/491,404  
 ; PRIOR FILING DATE: 2000-01-25  
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623  
 ; PRIOR FILING DATE: 2001-01-25  
 ; PRIOR APPLICATION NUMBER: US 09/496,914  
 ; PRIOR FILING DATE: 2000-02-03  
 ; PRIOR APPLICATION NUMBER: US 09/560,875  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/03800  
 ; PRIOR FILING DATE: 2001-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/515,126  
 ; PRIOR FILING DATE: 2000-02-28  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 992  
 ; SOFTWARE: PC\_FL\_genes Version 6.0  
 ; SEQ ID NO 16  
 ; LENGTH: 1967  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (338)..(763)  
 ; PCT-US02-29964-16  
 Query Match 85.7%; Score 1388; DB 1: Length 1967;  
 Best Local Similarity 99.8%; Pred. No. 1.5e-257;  
 Matches 1608; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGAACCTTTTGGCGATTTGTTCTTCCAGGCTTTGCCGTGCAATCCAGTGTACCA 60  
 |||||  
 Db 358 GGAACCTTTTGGCGATTTGTTCTTCCAGGCTTTGCCGTGCAATCCAGTGTACCA 417  
 QY 61 GTGTGAATATCCAGCTGAGCAACAGAGCTCTCCGCCAGTTTCATTTGAAATTCAC 120  
 |||||  
 Db 418 GTGTGAATATCCAGCTGAGCAACAGAGCTCTCCGCCAGTTTCATTTGAAATTCAC 477  
 QY 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGTGAGAGCAAGTCCGGGATCATGTA 180  
 |||||  
 Db 478 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGTGAGAGCAAGTCCGGGATCATGTA 537  
 QY 181 CCGCAAGTCTGTGATCATGAGGCGCTGTCTCATCCCTCTCGCGGGTACAGTCTT 240  
 |||||  
 Db 538 CCGCAAGTCTGTGATCATGAGGCGCTGTCTCATCCCTCTCGCGGGTACAGTCTT 597  
 QY 241 CTGCTCCCGAGGAAAGTGAATCTAGTTGCATCAGCTGTGCAACACCCCTTTTGTAA 300  
 |||||  
 Db 598 CTGCTCCCGAGGAAAGTGAATCTAGTTGCATCAGCTGTGCAACACCCCTTTTGTAA 657  
 QY 301 CGGCGCAAGGCCCAAGAAAGGGGAAGTTCTGCCCTCGGCGCCAGGCGTCCGAC 360  
 |||||  
 Db 658 CGGCGCAAGGCCCAAGAAAGGGGAAGTTCTGCCCTCGGCGCCAGGCGTCCGAC 717  
 QY 361 CACCATCTGTCTCAATTAATTAAGCCCTCTCTCGGACACTGCTGAAGCTGAAGAGATG 420  
 |||||  
 Db 718 CACCATCTGTCTCAATTAATTAAGCCCTCTCTCGGACACTGCTGAAGAGATG 777  
 QY 421 CCAGCCCTCTGTCATTTGTTTCCAGCCCTCGGCCCCCAACCCCGACCTCCGTAGAGA 480  
 |||||  
 Db 778 CCAGCCCTCTGTCATTTGTTTCCAGCCCTCGGCCCCCAACCCCGACCTCCGTAGAGA 837  
 QY 481 GTTCTTCTGGGATGCTCTTTATTTCTGGGTAGGAGCGGAGTCCGTGTTCTTTGTT 540  
 |||||  
 Db 838 GTTCTTCTGGGATGCTCTTTATTTCTGGGTAGGAGCGGAGTCCGTGTTCTTTGTT 897  
 QY 541 CCTGTCAATAATGAAGAGAGCTCGGTAAAGATTTCTGAATTAATTCAGCTGATGAT 600  
 |||||  
 Db 898 CCTGTCAATAATGAAGAGAGCTCGGTAAAGATTTCTGAATTAATTCAGCTGATGAT 957  
 QY 601 TTTCATTAATGTTTGAAGAGAGAGTGAAGTGAAGTCAACCCCACTGCTGTATAC 660  
 |||||  
 Db 958 TTTCATTAATGTTTGAAGAGAGTGAAGTGAAGTCAACCCCACTGCTGTGTATAC 1017  
 QY 661 CGAGTCAAGGCGCAGGCTGACAGTCACTCTTGAAGTCACTGAGTGGGCATCTGCC 720  
 |||||  
 Db 1018 CGAGTCAAGGCGCAGGCTGACAGTCACTCTTGAAGTCACTGAGTGGGCATCTGCC 1077  
 QY 721 TTTTGTAAAGCTTCCAGTGTCCATTCCATTCCTGATGGGGCATTAATTGAGACTGCAGA 780  
 |||||  
 Db 1078 TTTTGTAAAGCTTCCAGTGTCCATTCCATTCCTGATGGGGCATTAATTGAGACTGCAGA 1137  
 QY 781 GTGAGAGTACGTTTCTTTAGGGCTGAGGGCCAGTTCACACTCAAGAGCTCCCTCTTG 840  
 |||||  
 Db 1138 GTGAGAGTACGTTTCTTTAGGGCTGAGGGCCAGTTCACACTCAAGAGCTCCCTCTTG 1197  
 QY 841 ACATTCAAACTCATGCTCTGAAACCATTTCTGACAGCAAGATTGCTGTTTGGCCG 900  
 |||||  
 Db 1198 ACATTCAAACTCATGCTCTGAAACCATTTCTGACAGCAAGATTGCTGTTTGGCCG 1257  
 QY 901 CTGAGTTGGGCTCTAGAGACTCGAGACTCAATAGCTGGGCTTGAAGTGGGCTCGGCT 960  
 |||||  
 Db 1258 CTGAGTTGGGCTCTAGAGACTCGAGACTCAATAGCTGGGCTTGAAGTGGGCTCGGCT 1317  
 QY 961 CGCTCTGAAGAGCTTAAAGAAATCTTCTCAGTTCTCTTTCAGAGAGACTGGCGCGGG 1020  
 |||||  
 Db 1318 CGCTCTGAAGAGCTTAAAGAAATCTTCTCAGTTCTCTTTCAGAGAGACTGGCGCGGG 1377  
 QY 1021 ACAGGAAGAGCAACGCGCTGCAACAAGCGGCGCTGTGCTGGTGTGGATGGGCAATGA 1080  
 |||||  
 Db 1378 ACAGGAAGAGCAACGCGCTGCAACAAGCGGCGCTGTGCTGGTGTGGATGGGCAATGA 1437



QY 1081 CGCGAGGCGCTTCTGCTGTTGGCTGCTGAGGAGGCGGCGAGCAGACCTTGC 1140  
 |||||  
 Db 1360 CGCGAGGCGCTTCTGCTGTTGGCTGCTGAGGAGGCGGCGAGCAGACCTTGC 1418  
 QY 1141 ACGAACACCCGCCGAATCTGCTGAGGAGCAGCCTGTACAGAGCGGTTGATACCGGAG 1200  
 |||||  
 Db 1419 ACGAACACCCGCCGAATCTGCTGAGGAGCAGCCTGTACAGAGCGGTTGATACCGGAG 1478  
 QY 1201 CTGAGGTAGAAAAAGCTCTCCGAGAGGAGGAGATCATGTACGCCCGAAGTAGAGC 1260  
 |||||  
 Db 1479 CTGAGGTAGAAAAAGCTCTCCGAGAGGAGGAGATCATGTACGCCCGAAGTAGAGC 1538  
 QY 1261 CTGCTCAGTCTGCTGTTGGCTTGGCGGAGCCATGATCTCCGATCTGTTGGCTTC 1320  
 |||||  
 Db 1539 CTGCTCAGTCTGCTGTTGGCTTGGCGGAGCCATGATCTCCGATCTGTTGGCTTC 1598  
 QY 1321 CAGCATAGGCGCAATGTCACAAATCAGCCCTGGGAGAGCAGAGAGAGAGAGC 1380  
 |||||  
 Db 1599 CAGCATAGGCGCAATGTCACAAATCAGCCCTGGGAGAGCAGAGAGAGAGAGC 1658  
 QY 1381 AGAGAAAAAGAAAAACAGCATGAGAACAGTAATGAATAAAAACCATAAATATTTAG 1440  
 |||||  
 Db 1659 AGAGAAAAAGAAAAACAGCATGAGAACAGTAATGAATAAAAACCATAAATATTTAG 1718  
 QY 1441 CCCCTCTGCTGCTGCTTACTGCGCAGAGAAATGTCATTTTTCAGTGTGAGCTTGA 1500  
 |||||  
 Db 1719 CCCCTCTGCTGCTGCTTACTGCGCAGAGAAATGTCATTTTTCAGTGTGAGCTTGA 1778  
 QY 1501 CAGCTTCTTTTGGCAGAGAGAGAGAAATTAACCTTTTCAAAACCCGGGAGATTGG 1560  
 |||||  
 Db 1779 CAGCTTCTTTTGGCAGAGAGAGAGAAATTAACCTTTTCAAAACCCGGGAGATTGG 1838  
 QY 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTT 1619  
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 Db 1839 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTT 1897

# RESULT 13

US-09-970-966-214  
 ; Sequence 214, Application US/09970966  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Molesh, David Alan  
 ; APPLICANT: Filing, Steven P.  
 ; APPLICANT: Xu, Jianshun  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.4846  
 ; CURRENT APPLICATION NUMBER: US/09/970.966  
 ; CURRENT FILING DATE: 2001-10-02  
 ; NUMBER OF SEQ ID NOS: 215  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 214  
 ; LENGTH: 1897  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-970-966-214

Query Match 86.2% Score 1396: DB 36: Length 1897:  
 Best Local Similarity 99.8% Pred. No. 4.4e-259:  
 Matches 1616: Conservative 0: Mismatches 2: Indels 1: Gaps 1:

QY 1 GCGAATCTTTTGGGATGTTCTTCTCAGAGCTTTGCGCTGCAAAATCCAGTCTACCA 60  
 |||||  
 Db 280 GCGAATCTTTTGGGATGTTCTTCTCAGAGCTTTGCGCTGCAAAATCCAGTCTACCA 339  
 QY 61 GTGTGAAGATTCAGCTGACACAGACTGCTCTCCGCCAGTTTCATTTGATTTGAC 120  
 |||||  
 Db 340 GTGTGAAGATTCAGCTGACACAGACTGCTCTCCGCCAGTTTCATTTGATTTGAC 399  
 QY 121 GGTGAAGCTTCAAGACATGTCTCAGAAAGAGTGTGAGGAGAAATGCCGGATCATGTA 180  
 |||||  
 Db 400 GGTGAAGCTTCAAGACATGTCTCAGAAAGAGTGTGAGGAGAAATGCCGGATCATGTA 459

QY 181 CGCGAAGTCTCTGTGATCATCAGGCGCTGTCTCATCGCCTTGCAGGATACAGTCTT 240  
 |||||  
 Db 460 CGCGAAGTCTCTGTGATCATCAGGCGCTGTCTCATCGCCTTGCAGGATACAGTCTT 519  
 QY 241 CTGCTCCCGAGGAAATCTGAATCTAGTTGATCATCTGCTGCAACACCCCTCTTTTAA 300  
 |||||  
 Db 520 CTGCTCCCGAGGAAATCTGAATCTAGTTGATCATCTGCTGCAACACCCCTCTTTTAA 579  
 QY 301 CCGGCGCAAGGCCCAAGAAAGGGGAAAGTTCTGCGCTCGGCGCTCAGGCGAGGCTCCGAC 360  
 |||||  
 Db 580 CCGGCGCAAGGCCCAAGAAAGGGGAAAGTTCTGCGCTCGGCGCTCAGGCGAGGCTCCGAC 639  
 QY 361 CACCATCTGTTCTCTCAATTAATGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
 |||||  
 Db 640 CACCATCTGTTCTCTCAATTAATGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 699  
 QY 421 CCAACCCCT 480  
 |||||  
 Db 700 CCAACCCCT 759  
 QY 481 GTTCT 540  
 |||||  
 Db 760 GTTCT 819  
 QY 541 CCTGTGCAAAATTAATGAAGAGCTCGTAAAGCATTTGATTAATTAATTAATTAATTA 600  
 |||||  
 Db 820 CCTGTGCAAAATTAATGAAGAGCTCGTAAAGCATTTGATTAATTAATTAATTAATTA 879  
 QY 601 TTTTCAGTATGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
 |||||  
 Db 880 TTTTCAGTATGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939  
 QY 661 CGAGTCAAGAGCGCAGGCTGCGAGAGTCACTCTTGAAGTCACTGAGTGGCATCTGCG 720  
 |||||  
 Db 940 CGAGTCAAGAGCGCAGGCTGCGAGAGTCACTCTTGAAGTCACTGAGTGGCATCTGCG 999  
 QY 721 TTTTGTAAAGCTTCAATGCTTCAATCCCTGATGGGGGCAATGTTGAGACTGACAGA 780  
 |||||  
 Db 1000 TTTTGTAAAGCTTCAATGCTTCAATCCCTGATGGGGGCAATGTTGAGACTGACAGA 1059  
 QY 781 GTGAGAGTGAAGCTTTCTTGAAGGCTGAGAGGCGAGTTCCTCACTCAAGAGCTTCC 840  
 |||||  
 Db 1060 GTGAGAGTGAAGCTTTCTTGAAGGCTGAGAGGCGAGTTCCTCACTCAAGAGCTTCC 1119  
 QY 841 ACATTCAAATCTCATGCTCTCTGAAACCATTTCTCTGAGAGAAATGGCTGTTGCGGC 900  
 |||||  
 Db 1120 ACATTCAAATCTCATGCTCTCTGAAACCATTTCTCTGAGAGAAATGGCTGTTGCGGC 1179  
 QY 901 CTGAGTTGGGCTTGAAGTCTGAGTCTGAGTCAATGACTGGACTTGAAGTGGGCTCGGCT 960  
 |||||  
 Db 1180 CTGAGTTGGGCTTGAAGTCTGAGTCTGAGTCAATGACTGGACTTGAAGTGGGCTCGGCT 1239  
 QY 961 CGCTGTGAAGAGTCTTGAAGAAATCTTCTCAGTTCTCTTGCAGAGAGTGGCGCGGG 1020  
 |||||  
 Db 1240 CGCTGTGAAGAGTCTTGAAGAAATCTTCTCAGTTCTCTTGCAGAGAGTGGCGCGGG 1299  
 QY 1021 ACGGAGAGAGCAGCGGCGCTGACACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 |||||  
 Db 1300 ACGGAGAGAGCAGCGGCGCTGACACAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCT 1359  
 QY 1081 CGCGAGGCGCTTCTGCTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 |||||  
 Db 1360 CGCGAGGCGCTTCTGCTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1418  
 QY 1141 ACGAACACCCGCCGAATCTGCTGAGGAGCAGCCTGTACAGAGCGGTTGATACCGGAG 1200  
 |||||  
 Db 1419 ACGAACACCCGCCGAATCTGCTGAGGAGCAGCCTGTACAGAGCGGTTGATACCGGAG 1478  
 QY 1201 CTGAGGTAGAAAAAGCTCTCCGAGAGGAGGAGATCATGTACGCCCGAAGTAGAGC 1260  
 |||||  
 Db 1479 CTGAGGTAGAAAAAGCTCTCCGAGAGGAGGAGATCATGTACGCCCGAAGTAGAGC 1538

QY	1	GGCACTTTTGGGATGTTCTTGCTCCAGGCTTTGGGCTGCAAATCCAGTCTACCA	60
Db	280	GGCACTTTTGGGATGTTCTTGCTCCAGGCTTTGGGCTGCAAATCCAGTCTACCA	33
QY	61	GTGTGAATAATTCAGCTGAACACGACTCTCTCCCGGATTCATTGTGAATTCAC	12
Db	340	GTGTGAATAATTCAGCTGAACACGACTCTCTCCCGGATTCATTGTGAATTCAC	39
QY	121	GGTGAAGTTTAAACATGTGTGAGAAAGATGTAGGACCAATGCGGGATCATGTA	18
Db	400	GGTGAAGTTTAAACATGTGTGAGAAAGATGTAGGACCAATGCGGGATCATGTA	45
QY	181	CCGGAAGTCTGTGTGATCATCAGCGGCTGTCTCATCGCTGTGCGGGATCAGTCTT	24
Db	460	CCGGAAGTCTGTGTGATCATCAGCGGCTGTCTCATCGCTGTGCGGGATCAGTCTT	51
QY	241	CTGTCTCCCAAGGGAATCTGAATCACTTTTGACATCAGCTCTGCAACACCCTTTGTAA	30
Db	520	CTGTCTCCCAAGGGAATCTGAATCACTTTTGACATCAGCTCTGCAACACCCTTTGTAA	57
QY	301	CGGGCCAAAGCCCCAAGAAAAGGGAAAGTTCTGCTCGGCTCAGGCCACAGGGCTCCGAC	36
Db	580	CGGGCCAAAGCCCCAAGAAAAGGGAAAGTTCTGCTCGGCTCAGGCCACAGGGCTCCGAC	63
QY	361	CACCATCTTTTCTCTCAAAATTGAGCCCTCTTCTCGGCACTGTGTGAAGAGATG	42
Db	640	CACCATCTTTTCTCTCAAAATTGAGCCCTCTTCTCGGCACTGTGTGAAGAGATG	69
QY	421	CCACCCCCCTCTGCAATGTGTTCTTCCAGCCCTTGCCCCAACCCCCACCTCCGAGTGA	48
Db	700	CCACCCCCCTCTGCAATGTGTTCTTCCAGCCCTTGCCCCAACCCCCACCTCCGAGTGA	75
QY	481	GTTTCTTCTGGGAGTCCCTTTTATCTGGGTAGGGAGCGGAGTCCGTCTCTTTGTT	54
Db	760	GTTTCTTCTGGGAGTCCCTTTTATCTGGGTAGGGAGCGGAGTCCGTCTCTTTGTT	81
QY	541	CCGTGTCAAAATTAAGAAAGAGCTCGGTAAACATTCTGAATTAATTAAGCTGACATG	60
Db	820	CCGTGTCAAAATTAAGAAAGAGCTCGGTAAACATTCTGAATTAATTAAGCTGACATG	87
QY	601	TTTTAGTATGTACTTGAAGAAAGAGGTGAGTGAATAAGTTCAACCCCATGTCTGTAA	66
Db	880	TTTTAGTATGTACTTGAAGAAAGAGGTGAGTGAATAAGTTCAACCCCATGTCTGTAA	93
QY	661	CGGAGTCAAGGCGCAGGTGCGAGAGTAGTCTTGAAGAATCAGTGAAGTGGGATCTGCC	72
Db	940	CGGAGTCAAGGCGCAGGTGCGAGAGTAGTCTTGAAGAATCAGTGAAGTGGGATCTGCC	99
QY	721	TTTTTAAAGCTCAGTGTCCATTCTCATCCCTGTAGTGGGGCATAGTTTGAGACTGCAG	78
Db	1000	TTTTTAAAGCTCAGTGTCCATTCTCATCCCTGTAGTGGGGCATAGTTTGAGACTGCAG	105
QY	781	GTGAGAGTGAAGTTTCTTGAGGGCTGAGAGGCGAGTCCCACTCAAGGCTCCCTGCTTG	84
Db	1060	GTGAGAGTGAAGTTTCTTGAGGGCTGAGAGGCGAGTCCCACTCAAGGCTCCCTGCTTG	111
QY	841	ACATTCAAACTCATGTCTCTGAAACCATTTCTGTGACAGAGAAATGAGCTGTTTCGGC	90
Db	1120	ACATTCAAACTCATGTCTCTGAAACCATTTCTGTGACAGAGAAATGAGCTGTTTCGGC	117
QY	901	CTGAGTTGGGCTGTAGTGTGAGACTCGAGACTCAATAGTGGGACTTAAAGTGGGCTCTG	96
Db	1180	CTGAGTTGGGCTGTAGTGTGAGACTCGAGACTCAATAGTGGGACTTAAAGTGGGCTCTG	123
QY	961	CGCTCTAAAGTGTCTTAAGAAAATCTTCTCAGTTCTCTTGACAGAGACTGCGCGCGG	102
Db	1240	CGCTCTAAAGTGTCTTAAGAAAATCTTCTCAGTTCTCTTGACAGAGACTGCGCGCGG	129
QY	1021	ACGGGAAGACCAAGGGCGGTGCACAAACGGGGCGTGGCTGGTGGATGCGCATGTA	108
Db	1300	ACGGGAAGACCAAGGGCGGTGCACAAACGGGGCGTGGCTGGTGGATGCGCATGTA	135



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Db 1015 GTGAGATGACGTTTCTTCTAGAGGCTGAGAGGCGCAGTCCCATCTCAAGGCTCCCTGCTTG 1074
Oy 841 ACATTCAAACTTCATGCTCCTGAAACCAATTCCTGACAGAGAAATGGCTGGTTGGCCG 900
Db 1075 ACATTCAAACTTCATGCTCCTGAAACCAATTCCTGACAGAGAAATGGCTGGTTGGCCG 1134
Oy 901 CTGAGTTGGGCTTACGAGTACGAGTCAATGACTGGGACTTGAAGTGGGGCTGGCCCT 960
Db 1135 CTGAGTTGGGCTTACGAGTACGAGTCAATGACTGGGACTTGAAGTGGGGCTGGCCCT 1194
Oy 961 CGCTCTGAAAGTGTCTTAAGAAATCTTCTCAGTTCTCTTTCGACAGAGATCTGGCCGGG 1020
Db 1195 CGCTCTGAAAGTGTCTTAAGAAATCTTCTCAGTTCTCTTTCGACAGAGATCTGGCCGGG 1254
Oy 1021 ACCGCAAGAGCAACGGGGCTGACAAAGGGGGCTGCTGCTGGTGGAGTGGCATGTA 1080
Db 1255 ACCGCAAGAGCAACGGGGCTGACAAAGGGGGCTGCTGCTGGTGGAGTGGCATGTA 1314
Oy 1081 CGCGAGGCGCTTCTGCTGGTGGGCTGCTGACGAGAGCGGCGACAGCACACCTTGC 1140
Db 1315 CGCGAGGCGCTTCTGCTGGTGGGCTGCTGACGAGAGCGGCGACAGCACACCTTGC 1373
Oy 1141 ACCGACACCCCGGAACTGCTGCTGACAGACACCGCTGACAGAGGGGTTGATACCGAG 1200
Db 1374 ACCGACACCCCGGAACTGCTGCTGACAGACACCGCTGACAGAGGGGTTGATACCGAG 1433
Oy 1201 CTGAGGTAGAAAGTCTCTCGAAGAGGGAGAGATCATGTACGCCCGGAAGTAGAGAC 1260
Db 1434 CTGAGGTAGAAAGTCTCTCGAAGAGGGAGAGATCATGTACGCCCGGAAGTAGAGAC 1493
Oy 1261 CTGCTCAAGTCTGCTGGTGGTGGCCGACGACATGATCTCCGAAATGCTGGTGGCATC 1320
Db 1494 CTGCTCAAGTCTGCTGGTGGTGGCCGACGACATGATCTCCGAAATGCTGGTGGCATC 1553
Oy 1321 CAGCATACGGCCATGATGACAAACATCAGCCCTGGGCAACACAGAGAGAGAGAGAC 1380
Db 1554 CAGCATACGGCCATGATGACAAACATCAGCCCTGGGCAACACAGAGAGAGAGAGAC 1613
Oy 1381 AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGAAATGAAATGAAATGAAATG 1440
Db 1614 AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGAAATGAAATGAAATGAAATG 1673
Oy 1441 CCCCTCTGCTGCTGCTTACTGTCGCAAGAAATGTTACAAATTTTTCAGTGGTGAATGA 1500
Db 1674 CCCCTCTGCTGCTGCTTACTGTCGCAAGAAATGTTACAAATTTTTCAGTGGTGAATGA 1733
Oy 1501 CAGCTTCTTTTGCACAGCAAGAGAGATTTTAACTGTTTCAACCCCGGGGAGTTGG 1560
Db 1734 CAGCTTCTTTTGCACAGCAAGAGAGATTTTAACTGTTTCAACCCCGGGGAGTTGG 1793
Oy 1561 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGT 1599
Db 1794 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGT 1832

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RESULT 11
PCT-US01-45395-214
; Sequence 214, Application PC/TUS0145395
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jlangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Filing, Steven P.
; APPLICANT: Molesh, David Alan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214

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; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-214

Query Match
Best local similarity 99.8%; Pred. No. 4,4e-259;
Matches 1616; Conserved 0; Mismatches 2; Indels 1; Gaps 1;

Oy 1 GGCACATTTTGGCGATTTGTTCTTCTTCCAGGCTTGGGCTGCAATCCAGTCTACCA 60
Db 280 GGCACATTTTGGCGATTTGTTCTTCTTCCAGGCTTGGGCTGCAATCCAGTCTACCA 339
Oy 61 GGTGAAGATTTCCAGTGAACAGACTGCTCCCTCCCGAGTCTATTGTAATTCAC 120
Db 340 GGTGAAGATTTCCAGTGAACAGACTGCTCCCTCCCGAGTCTATTGTAATTCAC 399
Oy 121 GGTGAAGATTTCAAGCATGTCTCAGAAAGATGATGAGCAAGTCCGGGATCATGTA 180
Db 400 GGTGAAGATTTCAAGCATGTCTCAGAAAGATGATGAGCAAGTCCGGGATCATGTA 459
Oy 181 CGGCAAGTCTGTCATATCATAGGCGCTGTCATCGCTCTGCGGGATACAGTCTT 240
Db 460 CGGCAAGTCTGTCATATCATAGGCGCTGTCATCGCTCTGCGGGATACAGTCTT 519
Oy 241 CTGCTCCCGAGGAGAACTGAACTAGTTGATCATGCTGCTGCAACACCCCTCTTTGTA 300
Db 520 CTGCTCCCGAGGAGAACTGAACTAGTTGATCATGCTGCTGCAACACCCCTCTTTGTA 579
Oy 301 CGGCGCAAGGCGCCAGAAAGGGGAATTCGCTCGGCGCTCAGGCGGAGGCTCCGAC 360
Db 580 CGGCGCAAGGCGCCAGAAAGGGGAATTCGCTCGGCGCTCAGGCGGAGGCTCCGAC 639
Oy 361 CACCATCTGTTCTCAATTAAGCCCTCTTCTGCGACACTGCTGAGCTGAAGAGATG 420
Db 640 CACCATCTGTTCTCAATTAAGCCCTCTTCTGCGACACTGCTGAGCTGAAGAGATG 699
Oy 421 CCAACCCCTCTGCAATTTCTTCCAGGCTTGGCCCGCAACCCCGACCTCCCTGAGTA 480
Db 700 CCAACCCCTCTGCAATTTCTTCCAGGCTTGGCCCGCAACCCCGACCTCCCTGAGTA 759
Oy 481 GTTCTCTGCGGTCCTTTTATCTGGGTAGGAGCGGAGTCCGTCTCTTTTGT 540
Db 760 GTTCTCTGCGGTCCTTTTATCTGGGTAGGAGCGGAGTCCGTCTCTTTTGT 819
Oy 541 CCTGTCAAAATATGAAGAGCTCGTAAAGCATTTGTGAATTAATCACCCAGTCAAT 600
Db 820 CCTGTCAAAATATGAAGAGCTCGTAAAGCATTTGTGAATTAATCACCCAGTCAAT 879
Oy 601 TTTCAATATGACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATGCTGTGTAC 660
Db 880 TTTCAATATGACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATGCTGTGTAC 939
Oy 661 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTTGAAGTCACTGAGAGTGGCATCTGCC 720
Db 940 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTTGAAGTCACTGAGAGTGGCATCTGCC 999
Oy 721 TTTGTAAAGCTCCAGTGTCTCATTCATCCGATGAGGGGCAATGTTGAGACTCAGA 780
Db 1000 TTTGTAAAGCTCCAGTGTCTCATTCATCCGATGAGGGGCAATGTTGAGACTCAGA 1059
Oy 781 GTGAGAGTGAAGTTTCTTGAAGGCTGAGGCGCAGTTCCCACTCAAGAGCTCCCTG 840
Db 1060 GTGAGAGTGAAGTTTCTTGAAGGCTGAGGCGCAGTTCCCACTCAAGAGCTCCCTG 1119
Oy 841 ACATTCAAACTTCATGCTCCTGAAACCAATTCCTGACAGAGAAATGGCTGGTTGGCCG 900
Db 1120 ACATTCAAACTTCATGCTCCTGAAACCAATTCCTGACAGAGAAATGGCTGGTTGGCCG 1179
Oy 901 CTGAGTTGGGCTTACGAGTACGAGTCAATGACTGGGACTTGAAGTGGGGCTGGCCCT 960
Db 1180 CTGAGTTGGGCTTACGAGTACGAGTCAATGACTGGGACTTGAAGTGGGGCTGGCCCT 1239

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Db 541 CCTGTGCAATATATGAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCCTGACTGAAT 600  
QY 601 TTTCAGTATGACTTGAAGAGAGGAGTGAAGTGAAGTTCACCCCATCTCTGTGTAAAC 660  
Db 601 TTTCAGTATGACTTGAAGAGAGGAGTGAAGTGAAGTTCACCCCATCTCTGTGTAAAC 660  
QY 661 CGGAGTCAGAGCCAGGCTGGCAGAGTCTCTTAGAAGTCACTGAGAGTGGGATCTGGC 720  
Db 661 CGGAGTCAGAGCCAGGCTGGCAGAGTCTCTTAGAAGTCACTGAGAGTGGGATCTGGC 720  
QY 721 TTTTGTAAAGCTTCCAGTCTGATTCATCTCCATGAGGAGGCAATGTTGAGACTGAGA 780  
Db 721 TTTTGTAAAGCTTCCAGTCTGATTCATCTCCATGAGGAGGCAATGTTGAGACTGAGA 780  
QY 781 GTGAGAGTGAAGTCTTCTTGAAGGCTGGAGGAGGCTCCACATCAAGAGGCTCCCTGCTG 840  
Db 781 GTGAGAGTGAAGTCTTCTTGAAGGCTGGAGGAGGCTCCACATCAAGAGGCTCCCTGCTG 840  
QY 841 ACATTTCAACTTCACTGCTCTGAAACCATCTCTGACAGAGAAATGGCTGTTGCGCG 900  
Db 841 ACATTTCAACTTCACTGCTCTGAAACCATCTCTGACAGAGAAATGGCTGTTGCGCG 900  
QY 901 CTGAGTTGGGCTCTGAGAGTCAATGAGTGGAGTGAAGTGAAGTGGGCTCGGCT 960  
Db 901 CTGAGTTGGGCTCTGAGAGTCAATGAGTGGAGTGAAGTGAAGTGGGCTCGGCT 960  
QY 961 CGCTCTGAAAGTCTTGAAGAAATCTTCTCACTCTCTGAGAGGAGTGGGCTCGGCT 1020  
Db 961 CGCTCTGAAAGTCTTGAAGAAATCTTCTCACTCTCTGAGAGGAGTGGGCTCGGCT 1020  
QY 1021 ACCGGAAGAGCAAGGCGGCTGCAAAAGGCGGCTGTCGAGTGGAGTGGAGTGGAGTGA 1080  
Db 1021 ACCGGAAGAGCAAGGCGGCTGCAAAAGGCGGCTGTCGAGTGGAGTGGAGTGGAGTGA 1080  
QY 1081 CGGCGAGGCGCTTCTGTGGTGGGCTGCTGCTGAGAGGAGGCGGAGCAGACAGCTTGC 1140  
Db 1081 CGGCGAGGCGCTTCTGTGGTGGGCTGCTGCTGAGAGGAGGCGGAGCAGACAGCTTGC 1140  
QY 1141 ACAGAAACCCCGGAAAGTCTGCGAGAGACCCGCTGACAGAGCGGCTGATGACCGAG 1200  
Db 1141 ACAGAAACCCCGGAAAGTCTGCGAGAGACCCGCTGACAGAGCGGCTGATGACCGAG 1200  
QY 1201 CTGAGGTAGAAAGAGTCTCCGAGAGGAGGAGGAGTATGAGCCCGGAGAGTAAAGAG 1260  
Db 1201 CTGAGGTAGAAAGAGTCTCCGAGAGGAGGAGGAGTATGAGCCCGGAGAGTAAAGAG 1260  
QY 1261 CTGCTCACTGCTGCTGCTGGGTTGGCCAGCCATGATCTCGAATCTGTTGGGCAATC 1320  
Db 1261 CTGCTCACTGCTGCTGCTGGGTTGGCCAGCCATGATCTCGAATCTGTTGGGCAATC 1320  
QY 1321 CAGCATAGGCGCAATGTCACAAACATCAGCCCTGGCAGACACAGAGAGAGAGAGAC 1380  
Db 1321 CAGCATAGGCGCAATGTCACAAACATCAGCCCTGGCAGACACAGAGAGAGAGAGAC 1380  
QY 1381 AGAGAAAG 1440  
Db 1381 AGAGAAAG 1440  
QY 1441 CCCCTCTGTTGCTGCTTACTGGCAGAGAAATGTAACAAATTTTCAAGTGGAGCTTGA 1500  
Db 1441 CCCCTCTGTTGCTGCTTACTGGCAGAGAAATGTAACAAATTTTCAAGTGGAGCTTGA 1500  
QY 1501 CAGGCTTCTTGGCAG 1560  
Db 1501 CAGGCTTCTTGGCAG 1560  
QY 1561 CTGTGTAAAG 1619  
Db 1561 CTGTGTAAAG 1619

RESULT 10  
US-10-108-260A-197

; Sequence 197, Application US/10108260A  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108, 260A  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 197  
; LENGTH: 1832  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-197  
  
Query Match 88.1%; Score 1427; DB 40; Length 1832;  
Best Local Similarity 99.9%; Pred. No. 5e-265;  
Matches 1597; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 GGCACCTTTTTCGGATTTGTTCTTCTTCCAGGCTTTCGCTGCAAAATCCAGTGTACCA 60  
Db 235 GGCACCTTTTTCGGATTTGTTCTTCTTCCAGGCTTTCGCTGCAAAATCCAGTGTACCA 294  
QY 61 GTGTGAAGATTCAGCTGAGCAAGCAAGTCTCCCTCCCGAGTTCAATTTGATTTGAC 120  
Db 295 GTGTGAAGATTCAGCTGAGCAAGCAAGTCTCCCTCCCGAGTTCAATTTGATTTGAC 354  
QY 121 GGTGAACCTTCAAGCATGTGTGAGAAAGAGTGTGAGAGCAAGTGGCGGATCATGTA 180  
Db 355 GGTGAACCTTCAAGCATGTGTGAGAAAGAGTGTGAGAGCAAGTGGCGGATCATGTA 414  
QY 181 CGGCAAGTCTGTGATATCATGAGGCGCTGTCTATGCTCTGCGGAGTACAGTCTT 240  
Db 415 CGGCAAGTCTGTGATATCATGAGGCGCTGTCTATGCTCTGCGGAGTACAGTCTT 474  
QY 241 CTGCTCCCGAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300  
Db 475 CTGCTCCCGAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 534  
QY 301 CGGCGCAGGCGCCAAAGAAAGGAGGAGTTCGCTCGGCTTCAAGGCGAGGCTCCGAC 360  
Db 535 CGGCGCAGGCGCCAAAGAAAGGAGGAGTTCGCTCGGCTTCAAGGCGAGGCTCCGAC 594  
QY 361 CACCATCTGTTCTCAAAATTAAGCCCTTCTGCGCACAGTCTGGAAGTGAAGGAGATG 420  
Db 595 CACCATCTGTTCTCAAAATTAAGCCCTTCTGCGCACAGTCTGGAAGTGAAGGAGATG 654  
QY 421 CCACCCCTCTGCAATGTTCTTCCAGCCCTCGCCCAACCCCCCACTCCCTGAGTGA 480  
Db 655 CCACCCCTCTGCAATGTTCTTCCAGCCCTCGCCCAACCCCCCACTCCCTGAGTGA 714  
QY 481 GTTTCCTTGGGTTGCTCTTATCTGAGTGAAGAGGAGGAGTCCGTTCTCTTTTGT 540  
Db 715 GTTTCCTTGGGTTGCTCTTATCTGAGTGAAGAGGAGGAGTCCGTTCTCTTTTGT 774  
QY 541 CCTGTGCAAAATTAAGAGAGCTGCTAAAGCATTTGAAATTAATTCAGCTGAGTGAAT 600  
Db 775 CCTGTGCAAAATTAAGAGAGCTGCTGAAAGCATTTGAAATTAATTCAGCTGAGTGAAT 834  
QY 601 TTTCAGTATGACTTGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660  
Db 835 TTTCAGTATGACTTGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 894  
QY 661 CGGAGTCAGAGCCAGGCTGGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720  
Db 895 CGGAGTCAGAGCCAGGCTGGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 954  
QY 721 TTTTGTAAAGCTTCCAGTCTGATTCATCTCCATGAGGAGGAGTGAAGTGAAGTGAAG 780  
Db 955 TTTTGTAAAGCTTCCAGTCTGATTCATCTCCATGAGGAGGAGTGAAGTGAAGTGAAG 1014  
QY 781 GTGAGTGAAGCTTTTCTTGGGCTGGAGGCGAGTTCACATCAAGGCTCCCTGCTTG 840

Oy	421	CCACCCCCTCCGCAATGTTCTTCCAGGCCCTGGCCCCAACCCCCAACCCCTCCCTGAGTA	480
Db	421	CCACCCCCTCCGCAATGTTCTTCCAGGCCCTGGCCCCAACCCCCAACCCCTCCCTGAGTA	480
Oy	481	GTTTCTCTGGGGTGCCTTTATTCCTGGGGTGGAGAGCGGGAGTCCGTCTCTTTTGT	540
Db	481	GTTTCTCTGGGGTGCCTTTATTCCTGGGGTGGAGAGCGGGAGTCCGTCTCTTTTGT	540
Oy	541	CCGTGCAATTAATGAAAGCTCCGCTAAAGCATTTCTGAATAAATTACGCTTACAGAT	600
Db	541	CCGTGCAATTAATGAAAGCTCCGCTAAAGCATTTCTGAATAAATTACGCTTACAGAT	600
Oy	601	TTTTCAGTATCTTGAAGAGAGAGGTGAGTGAAGTTACCCCCCATCTCTGTATAAC	660
Db	601	TTTTCAGTATCTTGAAGAGAGAGGTGAGTGAAGTTACCCCCCATCTCTGTGTAAAC	660
Oy	661	CGAGTCMAAGCCAGGCTGGCAGAGTCACTCTTGAAGTCACTGAGGTGGCATCTGCC	720
Db	661	CGAGTCMAAGCCAGGCTGGCAGAGTCACTCTTGAAGTCACTGAGGTGGCATCTGCC	720
Oy	721	TTTTGTAAACCTCCAGTGCATTCCTCATCCCTGATGGGGGCATAGTTTGAAGTCAAGA	780
Db	721	TTTTGTAAACCTCCAGTGCATTCCTCATCCCTGATGGGGGCATAGTTTGAAGTCAAGA	780
Oy	781	GTCGAGTCGACGTTTTCTTAGGGCTGGAGGGCCAGTTCCACATCAAGGCTCCCTCGCTT	840
Db	781	GTCGAGTCGACGTTTTCTTAGGGCTGGAGGGCCAGTTCCACATCAAGGCTCCCTCGCTT	840
Oy	841	ACATTCAAACTTCATCTCTCTGAAACCATTCTCGACAGCAAAATTGGCTGTTTGGCGC	900
Db	841	ACATTCAAACTTCATCTCTCTGAAACCATTCTCGACAGCAAAATTGGCTGTTTGGCGC	900
Oy	901	CTGAGTTGGGCTCTAGTACCTCAGACACTCAATGACTGGGACTTGACTGGGGGCTCGGCT	960
Db	901	CTGAGTTGGGCTCTAGTACCTCAGACACTCAATGACTGGGACTTGACTGGGGGCTCGGCT	960
Oy	961	CGCTCTGAAAAGTCTTAGAATAATTCTTCAGTCTCTCTTCGACAGAGACTGGCGCGGG	1020
Db	961	CGCTCTGAAAAGTCTTAGAATAATTCTTCAGTCTCTCTTCGACAGAGACTGGCGCGGG	1020
Oy	1021	ACGGGAAGACACGGGCGCTGTCACAAACGGGGCCTCGTGGTGTGAGTGGCCATGTA	1080
Db	1021	ACGGGAAGACACGGGCGCTGTCACAAACGGGGCCTGTGCTGTGTGAGTGGCCATGTA	1080
Oy	1081	CGCGCAGGCGTCTCTGCTGTTGGCTGCTGCACGACACAGCGGCGACACAGCACTTCC	1140
Db	1081	CGCGCAGGCGTCTCTGCTGTTGGCTGCTGTCGACGACAGCGGCGACACAGCACTTCC	1140
Oy	1141	ACGAACACCCCGCAAACTCTCGAGAGACACCGTGTACAGGAGCGGGTTATATACGAG	1200
Db	1141	ACGAACACCCCGCAAACTCTCTCGAGAGACACCGTGTACAGGAGCGGGTTATATACGAG	1200
Oy	1201	CTGAGTGTAGAAAACGTCTCCGAAAGGGAGGAGATCATTTACGCCGGAAGTAGAC	1260
Db	1201	CTGAGTGTAGAAAACGTCTCCGAAAGGGAGGAGATCATTTACGCCGGAAGTAGAC	1260
Oy	1261	CTTCCTCAGTCTGCTTGGGTTTGGCCGACGCATATCTCTCGAATCTGGTGGGATC	1320
Db	1261	CTTCCTCAGTCTGCTTGGGTTTGGCCGACGCATATCTCTCGAATCTGGTGGGATC	1320
Oy	1321	CAGCATACGGCCATGTGCACAAACATAGCCCTGGGSCAACAACGAGACGAGGAGAGAC	1380
Db	1321	CAGCATACGGCCATGTGCACAAACATAGCCCTGGGSCAACAACGAGACGAGGAGAGAC	1380
Oy	1381	AGAGAAAAGAAAACACAGCATGAGAACACGTTAAATGAATAAAAACATAAATATTAG	1440
Db	1381	AGAGAAAAGAAAACACAGCATGAGAACACGTTAAATGAATAAAAACATAAATATTAG	1440
Oy	1441	CCCCCTCTCTCTGCTTACTGCGCCAGGAATGTATACAAATTTTTCAGTGTGGACTCTGA	1500
Db	1441	CCCCCTCTCTCTGCTTACTGCGCCAGGAATGTATACAAATTTTTCAGTGTGGACTCTGA	1500

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      0;
    Oy   1501 CAGCTTCTTTTGCCCAACGACAGAGAAATTAACACTGTTCACACC6GGGGAGTTGG   1560
        Db   1501 CAGCTTCTTTTGCCCAACGACAGAGAAATTAACACTGTTCACACC6GGGGAGTTGG   1560
    Oy   1561 CTGTGTTAAGAACAACCATTTAAATGCTTTAGACAGTGTAAAAA          1619
        Db   1561 CTGTGTTAAGAACAACCATTTAAATGCTTTAGACAGTGTAAAAA          1619

RESULT 9
US-10-212-677-211
: Sequence 211, Application US/10212677
: GENERAL INFORMATION:
: APPLICANT: Chenaule, Ruth A.
: APPLICANT: Xu, Jlangchun
: APPLICANT: Fanger, Gary R.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.4867
: CURRENT APPLICATION NUMBER: US/10/212,677
: CURRENT FILING DATE: 2002-08-02
: NUMBER OF SEQ ID NOS: 288
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 211
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-212-677-211

Query Match           100.0%; Score 1619; DB 42; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7.9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

Oy       1 GGCACATTTTGGCGAGATTGTTCTTGCTTCCAGGCTTTGGCGTGCACAAATCCAGTGTCTACCA   60
Db       1 GGCAACATTTTGGCGAGATTGTTCTTGCTTCCAGGCTTTGGCGTGCACAAATCCAGTGTCTACCA   60
Oy       61 GTGTGAAGATTTCACACTGACGTAACAACAGTCGTCCTCCCGGATTCATTGTGAATTGAC   120
Db       61 GTGTGAAGATTTCACACTGACGTAACAACAGTCGTCCTCCCGGATTCATTGTGAATTGAC   120
Oy      121 GGTGAACGTTCAAGACATGTGTGAGAAAAGTGTATGAGAACAAAGTCCGGGATCATGTGA   180
Db      121 GGTGAACGTTCAAGACATGTGTGAGAAAAGTGTATGAGAACAAAGTCCGGGATCATGTGA   180
Oy      181 CGCGAAGTCTGTGTCATCATCAGCGGCTGTCTCATCGCTCTGCCGGGGTACCAAGTCTT   240
Db      181 CGCGAAGTCTGTGTCATCATCAGCGGCTGTCTCATCGCTCTGCCGGGGTACCAAGTCTT   240
Oy      241 CTGCTCCCCAAGGAAACTGAACTCAGTTTGCATCAGTGTGTCGACACCCCTTTGTGA   300
Db      241 CTGCTCCCCAAGGAAACTGAACTCAGTTTGCATCAGTGTGTCGACACCCCTTTGTGA   300
Oy      301 CGGGCCAAAGCCCAAGAAAAGGGGAAGTTTGCTGTGGCTTCAAGGCCAAGGCTCCGGCAC   360
Db      301 CGGGCCAAAGCCCAAGAAAAGGGGAAGTTTGCTGTGGCTTCAAGGCCAAGGCTCCGGCAC   360
Oy      361 CACCATCTCTTCTCCTCAAAATTAAGCCCTCTTCTGTGGGACACACTGCTGAAAGCTGAAGGAGATG   420
Db      361 CACCATCTCTTCTCCTCAAAATTAAGCCCTCTTCTGTGGGACACACTGCTGAAAGCTGAAGGAGATG   420
Oy      421 CCAACCCCCTCTCGATTTGTTCTTCACAGCCCTCGGCCCAAACCCCCCACTCCCTGAGTGA   480
Db      421 CCAACCCCCTCTCGATTTGTTCTTCACAGCCCTCGGCCCAAACCCCCCACTCCCTGAGTGA   480
Oy      481 GTTTCTTCTGGGTGCTCTTTTATTTCTGGGTATGGAGAGGGGAAGTCCGTGTTCTCTTTTGT   540
Db      481 GTTTCTTCTGGGTGCTCTTTTATTTCTGGGTATGGAGAGGGGAAGTCCGTGTTCTCTTTTGT   540
Oy      541 CCTGTGAATAATGAAGAAGCTGGTGAAGCATTTGAATTAATTCAGCTGACTGAAT   600

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Qy	241	CTGTCTCCCAAGGAAAC	TGAAC	TCA	CTTTGGATCAG	TGCTGCAAC	ACCCCTCTTTGAA	300	
Db	241	CTCTCTCCCAAGGAAAC	TGAAC	TCA	CTTTGGATCAG	TGCTGCAAC	ACCCCTCTTTGAA	300	
Qy	301	CGGGCCAAAGGCCAAGAA	AGGAGG	AGTTTC	TGCTCGGCTC	TAGGCC	ACGAGGCTCCGAC	360	
Db	301	CGGGCCAAAGGCCAAGAA	AGGAGG	AGTTTC	TGCTCGGCTC	TAGGCC	ACGAGGCTCCGAC	360	
Qy	361	CACCATCTCTTCTCAAT	TA	T	TAGCCCTCTT	TCGGGC	ACACTGCTGAAGCTGAAGGAGATG	420	
Db	361	CACCATCTCTTCTCAAT	TA	T	TAGCCCTCTT	TCGGGC	ACACTGCTGAAGCTGAAGGAGATG	420	
Qy	421	CCACCCCTCTCTCAT	T	TTCTTCCAG	CCCTCGCCCCA	ACCCCCAC	CCCTCGTAGTGA	480	
Db	421	CCACCCCTCTCTCAT	T	TTCTTCCAG	CCCTCGCCCCA	ACCCCCAC	CCCTCGTAGTGA	480	
Qy	481	GTTCCTTCTGGGTGTC	CTTTAT	T	TCGGGTAGGAG	CGGAGTCCGTTC	TTCTTTGT	540	
Db	481	GTTCCTTCTGGGTGTC	CTTTAT	T	TCGGGTAGGAG	CGGAGTCCGTTC	TTCTTTGT	540	
Qy	541	CCGTGCAAAATAT	TA	TA	TAAGAGCTCGTAAT	TCGTAATTAAT	TAGAGCTGACTGAAT	600	
Db	541	CCGTGCAAAATAT	TA	TA	TAAGAGCTCGTAAT	TCGTAATTAAT	TAGAGCTGACTGAAT	600	
Qy	601	TTTTCAGTATGACT	TGAAG	AGAGAG	TGAGTGAAT	TACCCCACTG	CTGTGTAA	660	
Db	601	TTTTCAGTATGACT	TGAAG	AGAGAG	TGAGTGAAT	TACCCCACTG	CTGTGTAA	660	
Qy	661	CGGAGTCAGAGCC	CAGGCTGG	CAGAGTCA	CTCTTGAAG	TGAC	TGAGAGTGGAGTCTGGC	720	
Db	661	CGGAGTCAGAGCC	CAGGCTGG	CAGAGTCA	CTCTTGAAG	TGAC	TGAGAGTGGAGTCTGGC	720	
Qy	721	TTTTTAAAGCCTC	CAGTGTGC	ATTCAT	CCCTGATG	TGGGGCAT	AGTTTGAAGACTGACAG	780	
Db	721	TTTTTAAAGCCTC	CAGTGTGC	ATTCAT	CCCTGATG	TGGGGCAT	AGTTTGAAGACTGACAG	780	
Qy	781	GTGAGATGAC	GT	TTT	T	TAGGGCTG	AGAGGCCAGT	TCCCACTAAAGGTCCTCGCTG	840
Db	781	GTGAGATGAC	GT	TTT	T	TAGGGCTG	AGAGGCCAGT	TCCCACTAAAGGTCCTCGCTG	840
Qy	841	ACATTC	CAAACT	CA	TGCTCCTG	GA	AAAC	CAATCTCTG	900
Db	841	ACATTC	CAAACT	CA	TGCTCCTG	GA	AAAC	CAATCTCTG	900
Qy	901	CTGAGTGGGCT	CT	T	TAGACTCG	AGACTCA	TATGACTT	GGGAGCTCGGCT	960
Db	901	CTGAGTGGGCT	CT	T	TAGACTCG	AGACTCA	TATGACTT	GGGAGCTCGGCT	960
Qy	961	CGCTCTG	AAATGCTT	T	T	T	T	T	1020
Db	961	CGCTCTG	AAATGCTT	T	T	T	T	T	1020
Qy	1021	ACGCGAAG	AGCA	ACGGGCGCTG	CA	CAAAAGCGGGCGCTG	CGTGGTGTGA	GTGCGCATGTA	1080
Db	1021	ACGCGAAG	AGCA	ACGGGCGCTG	CA	CAAAAGCGGGCGCTG	CGTGGTGTGA	GTGCGCATGTA	1080
Qy	1081	CGGCGAGG	CGGCTTCT	CTGCTGTGTG	GC	GTGCGGTGA	CGACAGCGGCGGAGCA	ACGACCTTGC	1140
Db	1081	CGGCGAGG	CGGCTTCT	CTGCTGTGTG	GC	GTGCGGTGA	CGACAGCGGCGGAGCA	ACGACCTTGC	1140
Qy	1141	ACGAAAC	ACCCGCGAA	CTGCTG	CGAGAG	ACCGTGTGA	CAGAGCGGGTGTGA	CCGAG	1200
Db	1141	ACGAAAC	ACCCGCGAA	CTGCTG	CGAGAG	ACCGTGTGA	CAGAGCGGGTGTGA	CCGAG	1200
Qy	1201	CTGAGGT	AGAAAAAC	GTCTCCG	AGAAAGGAGAGATCA	TGTAGGCCCGCGGA	AGTAGAGAC	1260	
Db	1201	CTGAGGT	AGAAAAAC	GTCTCCG	AGAAAGGAGAGATCA	TGTAGGCCCGCGGA	AGTAGAGAC	1260	
Qy	1261	CTGTCTC	AGTCGTGTGGGTTT	T	T	T	T	T	1320
Db	1261	CTGTCTC	AGTCGTGTGGGTTT	T	T	T	T	T	1320
Qy	1321	CAGCAT	ATGCGCCAT	TTCA	CAAC	CAAT	T	T	1380
Db	1321	CAGCAT	ATGCGCCAT	TTCA	CAAC	CAAT	T	T	1380

Accession	Sequence	Length
Dp 1321	CAGATTCGGCCCATGTGCACCAACCAATTCAGCCCTGGGCGACACGAGCGAGGGGAGAGAC	1380
Qy 1381	AGAGAAAAAGAAAAACACAGATGAGAAACACAGTAAATGAATTAACCACTPAAAAATTTTAG	1440
Dp 1381	AGAGAAAAAGAAAAACACAGATGAGAAACACAGTAAATGAATTAACCACTPAAAAATTTTAG	1440
Qy 1441	CCCCCTGTTCTGTGTTACTGTCGCCAGGAATGTCACAAATTTTCAGTGTGGACCTGA	1500
Dp 1441	CCCCCTGTTCTGTGTTACTGTCGCCAGGAATGTCACAAATTTTCAGTGTGGACCTGA	1500
Qy 1501	CAGCTCTTTTGGCCACAAGACAAGAGAAATTTAACTGTTCAAACCCCGGGGAGTTGG	1560
Dp 1501	CAGCTCTTTTGGCCACAAGACAAGAGAAATTTAACTGTTCAAACCCCGGGGAGTTGG	1560
Qy 1561	CTGTGTTAAAGAAAGACCATTTAAATGCTTTAGACAGCTGTAAAAAATTTTTTTTTTTTTTTT	1619
Dp 1561	CTGTGTTAAAGAAAGACCATTTAAATGCTTTAGACAGCTGTAAAAAATTTTTTTTTTTTTTTT	1619

[illegible]

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OY 61 GTGTGAAGAAATTCACAGTCAAGACGACGCTCTCCCGGAGTTTCATTGTGAATTCAC 120
    |||
Db 61 GTGTGAAGAAATTCACAGTCAAGACGACGCTCTCCCGGAGTTTCATTGTGAATTCAC 120
OY 121 GGTGAACGTTTCAAGACATGTGTGACAAAGAGATGATGAGCAAAAGTCCGGATCATGTA 180
    |||
Db 121 GGTGAACGTTTCAAGACATGTGTGACAAAGAGATGATGAGCAAAAGTCCGGATCATGTA 180
OY 181 CCGCAAGTCCTGTGATCATCAGCGGCGTGTCTATCGCCCTCCGGGTACCACTCTT 240
    |||
Db 181 CCGCAAGTCCTGTGATCATCAGCGGCGTGTCTATCGCCCTCCGGGTACCACTCTT 240
OY 241 CTGTCTCCCAAGGAAATGAACTCAATGTTGATCATGAGTGTGTAACACCCCTTTGTA 300
    |||
Db 241 CTGTCTCCCAAGGAAATGAACTCAATGTTGATCATGAGTGTGTAACACCCCTTTGTA 300
OY 301 CCGGCAAGGCGCCAGAAAGAGGAGGAGTTCCTCGGCGCTCAGGCGAGGCTCCGAC 360
    |||
Db 301 CCGGCAAGGCGCCAGAAAGAGGAGGAGTTCCTCGGCGCTCAGGCGAGGCTCCGAC 360
OY 361 CACCATCTGTTCCTCAAAATTAAGCCCTTCTCGGACACAGTGTGAAGTGAAGAGATG 420
    |||
Db 361 CACCATCTGTTCCTCAAAATTAAGCCCTTCTCGGACACAGTGTGAAGTGAAGATG 420
OY 421 CCACCCCTCCCTGCAATTTCTTCCAGCCCTCCGCCCCAACCCCGCACCTCTGAGTGA 480
    |||
Db 421 CCACCCCTCCCTGCAATTTCTTCCAGCCCTCCGCCCCAACCCCGCACCTCTGAGTGA 480
OY 481 GTTTCCTCTGGGTGTCTCTTTATCTCTGAGTGAAGGAGGAGGAGTCCGGTCTCTTTGTT 540
    |||
Db 481 GTTTCCTCTGGGTGTCTCTTTATCTCTGAGTGAAGGAGGAGGAGTCCGGTCTCTTTGTT 540
OY 541 CCTGTGCAATTAATGAAGAGCTCGTAAAGCAATTCGTAATTAATTCAGCTGACTGAAT 600
    |||
Db 541 CCTGTGCAATTAATGAAGAGCTCGTAAAGCAATTCGTAATTAATTCAGCTGACTGAAT 600
OY 601 TTTCAATGATGATCTGAAGAGAGAGTGAAGTGAAGTCAACCCCATGTCTGTCTAAC 660
    |||
Db 601 TTTCAATGATGATCTGAAGAGAGAGTGAAGTGAAGTCAACCCCATGTCTGTCTAAC 660
OY 661 CCGAGTCAAGGCCAGGCTGCGACAGTCAAGTCTTAGAAGTCACTGAGTGGGATCTGCC 720
    |||
Db 661 CCGAGTCAAGGCCAGGCTGCGACAGTCAAGTCTTAGAAGTCACTGAGTGGGATCTGCC 720
OY 721 TTTTGTAAAGCTCCAGTCTCCATTCATTCCTGATGGGGCATAGTTTGAAGTGCAGA 780
    |||
Db 721 TTTTGTAAAGCTCCAGTCTCCATTCATTCCTGATGGGGCATAGTTTGAAGTGCAGA 780
OY 781 GTGAGAGTGAAGTCTTCTTAAAGGCTGAGGCGAGTTCACATCAAGGCTCCCTGCTTG 840
    |||
Db 781 GTGAGAGTGAAGTCTTCTTAAAGGCTGAGGCGAGTTCACATCAAGGCTCCCTGCTTG 840
OY 841 ACATTCAAACTTATGCTCTCTGAAAAACATTCCTGACAGACAAATTTGGCTGTGTCGCG 900
    |||
Db 841 ACATTCAAACTTATGCTCTCTGAAAAACATTCCTGACAGACAAATTTGGCTGTGTCGCG 900
OY 901 CTAGATTGGGCTCTAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 960
    |||
Db 901 CTAGATTGGGCTCTAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 960
OY 961 CCGTCTGAAAAAGTCTTAAAGAAATCTTCTCAGTTCTCTTTCAGAGAGAGTGGGCGGG 1020
    |||
Db 961 CCGTCTGAAAAAGTCTTAAAGAAATCTTCTCAGTTCTCTTTCAGAGAGAGTGGGCGGG 1020
OY 1021 AGCGGAAGAGCAAGCGGCGCTCACAAGACGCGGCTGTGCGGTGGTGAAGTGCATGTA 1080
    |||
Db 1021 AGCGGAAGAGCAAGCGGCGCTCACAAGACGCGGCTGTGCGGTGGTGAAGTGCATGTA 1080
OY 1081 CCGCGAGGCGCTTCTGAGTGTGGGTGCTGAGGAGAGAGCGGCGAGCAGCAGCCTTGC 1140
    |||
Db 1081 CCGCGAGGCGCTTCTGAGTGTGGGTGCTGAGGAGAGAGCGGCGAGCAGCAGCCTTGC 1140
OY 1141 ACGAACAACCCCGCGCAACTGTCTGCGAGAGACACGCTGTAACAGAGAGGTTGATACCGAG 1200

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Db 1141 ACGAACAACCCCGCGCAACTGTCTGCGAGAGACACCGTGTACAGAGAGGGGTGTATACCGAG 1200
OY 1201 CTGAGGTAGAAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAATAGAC 1260
    |||
Db 1201 CTGAGGTAGAAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAATAGAC 1260
OY 1261 CTGCTCCAGTCTGCTGTGGTGTGGGCTCCGACCATATGATCTCCGAATCTGGTGGCATC 1320
    |||
Db 1261 CTGCTCCAGTCTGCTGTGGTGTGGGCTCCGACCATATGATCTCCGAATCTGGTGGCATC 1320
OY 1321 CAGCATAGGCGCAATGTACAAACAATACCCCTGGGAGACAGCAGAGAGAGAGAC 1380
    |||
Db 1321 CAGCATAGGCGCAATGTACAAACAATACCCCTGGGAGACAGCAGAGAGAGAGAC 1380
OY 1381 AGAGAAAAAGAAAAACACAGCATGAGAAACAGTAAATGAATTAATTAATTTAG 1440
    |||
Db 1381 AGAGAAAAAGAAAAACACAGCATGAGAAACAGTAAATGAATTAATTAATTTAG 1440
OY 1441 CCCCTCTGTCTGTCTTACTGTGCGCAGGAAATGTACCAATTTTTCAGTGTGACTTGA 1500
    |||
Db 1441 CCCCTCTGTCTGTCTTACTGTGCGCAGGAAATGTACCAATTTTTCAGTGTGACTTGA 1500
OY 1501 CAGCTTCTTTTGCACAGAGAGAGAAATTAACATCTTTTAAACCCGGGAGTGG 1560
    |||
Db 1501 CAGCTTCTTTTGCACAGAGAGAGAAATTAACATCTTTTAAACCCGGGAGTGG 1560
OY 1561 CTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTAAAAA 1619
    |||
Db 1561 CTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTAAAAA 1619

RESULT 7
US-09-970-966-211
: Sequence 211, Application US/09970966
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesb, David Alan
: APPLICANT: Fling, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.484C6
: CURRENT APPLICATION NUMBER: US/09/970,966
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 211
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-970-966-211

Query Match          100.0%; Score 1619; DB 36; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7, 9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGCACATTTTTCGCGATGTTTCTTCTTCAGGCTTTTCGCTGCAATTCAGTCTACCA 60
    |||
Db 1 GGCACATTTTTCGCGATGTTTCTTCTTCAGGCTTTTCGCTGCAATTCAGTCTACCA 60
OY 61 GTGTGAAGAAATTCAGAGTCAAGACGACGCTCCCGGAGTTCATTGTGAATTCAC 120
    |||
Db 61 GTGTGAAGAAATTCAGAGTCAAGACGACGCTCCCGGAGTTCATTGTGAATTCAC 120
OY 121 GGTGAACGTTTCAAGACATGTGTGACAAAGAGATGATGAGCAAAAGTCCGGATCATGTA 180
    |||
Db 121 GGTGAACGTTTCAAGACATGTGTGACAAAGAGATGATGAGCAAAAGTCCGGATCATGTA 180
OY 181 CCGCAAGTCCTGTGATCATCAGCGGCGTGTCTATCGCCCTCCGGGTACCACTCTT 240
    |||
Db 181 CCGCAAGTCCTGTGATCATCAGCGGCGTGTCTATCGCCCTCCGGGTACCACTCTT 240

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TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-970-966-211

Query Match 100.0%; Score 1619; DB 31; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 7.9e-302;  
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTCCGAGATGTTCTTCCAGGCTTTGGCGTCAAAATCCAGTGTACCA 60  
DB 1 GGCACCTTTTCCGAGATGTTCTTCCAGGCTTTGGCGTCAAAATCCAGTGTACCA 60  
QY 61 GTGTGAAGATTCACAGTCAACAGAGCTCTCCGCCGAGTTCAATGTGAATTCAC 120  
DB 61 GTGTGAAGATTCACAGTCAACAGAGCTCTCCGCCGAGTTCAATGTGAATTCAC 120  
QY 121 GGTGAACGTTCAAGACATGTCTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180  
DB 121 GGTGAACGTTCAAGACATGTCTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180  
QY 181 CCGCAAGTCTGTGATCATACAGCGGCTGTCTCATCGGCTTCCGCGGTACAGTCCCT 240  
DB 181 CCGCAAGTCTGTGATCATACAGCGGCTGTCTCATCGGCTTCCGCGGTACAGTCCCT 240  
QY 241 CTGCTCCCAAGGAAACAGTCACTAGTTGATGATGATGATGATGATGATGATGAT 300  
DB 241 CTGCTCCCAAGGAAACAGTCACTAGTTGATGATGATGATGATGATGATGATGAT 300  
QY 301 CGGCGCAAGGCGCCCAAGAAAGGGAAGTTCTGCGCGGCTCCAGGCGGCTCCGAC 360  
DB 301 CGGCGCAAGGCGCCCAAGAAAGGGAAGTTCTGCGCGGCTCCAGGCGGCTCCGAC 360  
QY 361 CACCATCTCTGTTCTCAAAATTAAGCCCTCTCTGCGCACAGTCTGAAGAGATG 420  
DB 361 CACCATCTCTGTTCTCAAAATTAAGCCCTCTCTGCGCACAGTCTGAAGAGATG 420  
QY 421 CCACCCCTCTGATGTTCTTCCAGCCCTCCGCCACACCCCTCCCTGATGATG 480  
DB 421 CCACCCCTCTGATGTTCTTCCAGCCCTCCGCCACACCCCTCCCTGATGATG 480  
QY 481 GTTCTCTGAGGCTCTTATCTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
DB 481 GTTCTCTGAGGCTCTTATCTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
QY 541 CCTGTCAATATATGAAGAGCTCGTAAAGCATCTGAATTAATTCAGCTGATGAT 600  
DB 541 CCTGTCAATATATGAAGAGCTCGTAAAGCATCTGAATTAATTCAGCTGATGAT 600  
QY 601 TTTTCAGTATGTTCTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
DB 601 TTTTCAGTATGTTCTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
QY 661 CGAGATCAAGGCGAGGCTGCGAGATCAGTCTTGAAGTCACTAGGAGGAGGAGGAG 720  
DB 661 CGAGATCAAGGCGAGGCTGCGAGATCAGTCTTGAAGTCACTAGGAGGAGGAGGAG 720  
QY 721 TTTTAAAGCCTCAAGTGTCCATTCATCCCTGATGGGGGATGTTGAGAGTCA 780  
DB 721 TTTTAAAGCCTCAAGTGTCCATTCATCCCTGATGGGGGATGTTGAGAGTCA 780  
QY 781 GTGAGAGTACCTTTTCTTGAAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
DB 781 GTGAGAGTACCTTTTCTTGAAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
QY 841 ACATTCAAATTCATGCTCTGTAAGAAACCATCTCTGAGAGAGAAATGGCTGTTGGCG 900  
DB 841 ACATTCAAATTCATGCTCTGTAAGAAACCATCTCTGAGAGAGAAATGGCTGTTGGCG 900  
QY 901 CTGAGTGGGCTCTGAGTCACTGAGATCAATGAGTGGAGTGGAGTGGAGTGGAGT 960  
DB 901 CTGAGTGGGCTCTGAGTCACTGAGATCAATGAGTGGAGTGGAGTGGAGTGGAGT 960  
QY 961 CGCTGTGAAGATGCTTGAAGAAATCTTCTCAGTTCCTCTGAGAGGAGTGGCGCGG 1020

DB 961 CGCTGTGAAGATGCTTGAAGAAATCTTCTCAGTTCCTCTGAGAGGAGTGGCGCGG 1020  
QY 1021 ACAGGAGAGACACAGGCGCTGCAACAGCGGCGCTGTGTTGTTGAGTGGCATGTA 1080  
DB 1021 ACAGGAGAGACACAGGCGCTGCAACAGCGGCGCTGTGTTGTTGAGTGGCATGTA 1080  
QY 1081 CGCGAGAGGCTCTGTTGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
DB 1081 CGCGAGAGGCTCTGTTGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
QY 1141 AGAACAACCGCGCAACAGTCTGAGAGACAGGATGATGATGATGATGATGATGAT 1200  
DB 1141 AGAACAACCGCGCAACAGTCTGAGAGACAGGATGATGATGATGATGATGATGAT 1200  
QY 1201 CTGAGGTGAAGAAACGTTCTCCGAGAAAGGAGAGAGATCATATACCGCCGAGT 1260  
DB 1201 CTGAGGTGAAGAAACGTTCTCCGAGAAAGGAGAGAGATCATATACCGCCGAGT 1260  
QY 1261 CTGCTCCAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320  
DB 1261 CTGCTCCAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320  
QY 1321 CAGCATACGCGCAATGTCACACATCAGCCCTGGGAGACAGAGAGAGAGAGAGAC 1380  
DB 1321 CAGCATACGCGCAATGTCACACATCAGCCCTGGGAGACAGAGAGAGAGAGAGAC 1380  
QY 1381 AGAAGAAAGAAACACAGATGAGACAGATGAATGAATGAATGAATGAATGAATGA 1440  
DB 1381 AGAAGAAAGAAACACAGATGAGACAGATGAATGAATGAATGAATGAATGAATGA 1440  
QY 1441 CCCCTCTGTTCTGTTCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
DB 1441 CCCCTCTGTTCTGTTCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
QY 1501 CAGCTTTTTCACAGAGAGAGATTAACATGTTTCAACCCCGGGAGTGG 1560  
DB 1501 CAGCTTTTTCACAGAGAGAGATTAACATGTTTCAACCCCGGGAGTGG 1560  
QY 1561 CTGTTTAAAGAAAGACATTAATGCTTGAACAGTGAATGAATGAATGAATGAATGA 1619  
DB 1561 CTGTTTAAAGAAAGACATTAATGCTTGAACAGTGAATGAATGAATGAATGAATGA 1619

RESULT 6  
US-09-970-966-205  
Sequence 205, Application US/09970966  
GENERAL INFORMATION:  
APPLICANT: Stolck, John A.  
APPLICANT: Molesch, David Alan  
APPLICANT: Fling, Steven P.  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.484C6  
CURRENT APPLICATION NUMBER: US/09/970,966  
CURRENT FILING DATE: 2001-10-02  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 205  
LENGTH: 1619  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-970-966-205

Query Match 100.0%; Score 1619; DB 36; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 7.9e-302;  
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Filing, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 205
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-825-294-205

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Query Match      100.0%; Score 1619; DB 31; Length 1619;
Best Local Similarity 100.0%; Pred. No. 7,9e-302;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGCACCTTTTGGGATGTTCTTCTCCAGGCTTTGCGTCAAAATCCAGTGTACCA 60
DB 1 GGCACCTTTTGGGATGTTCTTCTCCAGGCTTTGCGTCAAAATCCAGTGTACCA 60
QY 61 GTGTGAAGATTCAGCTGAACAAAGACTGCTCTCCCGAGTTCATTGTAATTCAC 120
DB 61 GTGTGAAGATTCAGCTGAACAAAGACTGCTCTCCCGAGTTCATTGTAATTCAC 120
QY 61 GTGTGAAGATTCAGCTGAACAAAGACTGCTCTCCCGAGTTCATTGTAATTCAC 120
DB 61 GTGTGAAGATTCAGCTGAACAAAGACTGCTCTCCCGAGTTCATTGTAATTCAC 120
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATA 180
DB 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATA 180
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATA 180
DB 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATA 180
QY 181 CGGCAAGTCGTGTGATATCAGGGGCTGTCTACGCTCTGCGGGGTACAGTCTT 240
DB 181 CGGCAAGTCGTGTGATATCAGGGGCTGTCTACGCTCTGCGGGGTACAGTCTT 240
QY 181 CGGCAAGTCGTGTGATATCAGGGGCTGTCTACGCTCTGCGGGGTACAGTCTT 240
DB 181 CGGCAAGTCGTGTGATATCAGGGGCTGTCTACGCTCTGCGGGGTACAGTCTT 240
QY 241 CTGCTCCCGAGGAAATCTGAATCTGATGATGATGATGATGATGATGATGATGAT 300
DB 241 CTGCTCCCGAGGAAATCTGAATCTGATGATGATGATGATGATGATGATGATGAT 300
QY 301 CGGGCCAGAGGCCCAAGAAAGGGAAGTCTGCGGCGCTCAGGCGCAAGGCTCCGAC 360
DB 301 CGGGCCAGAGGCCCAAGAAAGGGAAGTCTGCGGCGCTCAGGCGCAAGGCTCCGAC 360
QY 301 CGGGCCAGAGGCCCAAGAAAGGGAAGTCTGCGGCGCTCAGGCGCAAGGCTCCGAC 360
DB 301 CGGGCCAGAGGCCCAAGAAAGGGAAGTCTGCGGCGCTCAGGCGCAAGGCTCCGAC 360
QY 361 CACCATCTCTCTCAATATGAGCCCTCTGCGGCACTGCTGATGATGATGATGATGAT 420
DB 361 CACCATCTCTCTCAATATGAGCCCTCTGCGGCACTGCTGATGATGATGATGATGAT 420
QY 421 CCAGCCCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 CCAGCCCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 GTTCTCTCTGAGGCTCTTATTTCTGGGTAGGAGCGGAGTCCGTTCTCTTTTGT 540
DB 481 GTTCTCTCTGAGGCTCTTATTTCTGGGTAGGAGCGGAGTCCGTTCTCTTTTGT 540
QY 481 GTTCTCTCTGAGGCTCTTATTTCTGGGTAGGAGCGGAGTCCGTTCTCTTTTGT 540
DB 481 GTTCTCTCTGAGGCTCTTATTTCTGGGTAGGAGCGGAGTCCGTTCTCTTTTGT 540
QY 541 CCTGTGAATATATGAAGAGCTCGTAAAGCATCTGAATATATATATATATATATAT 600
DB 541 CCTGTGAATATATGAAGAGCTCGTAAAGCATCTGAATATATATATATATATATAT 600
QY 601 TTTTCAGTATGATGATGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
DB 601 TTTTCAGTATGATGATGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
QY 601 TTTTCAGTATGATGATGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
DB 601 TTTTCAGTATGATGATGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
QY 661 CGGAGTCAAGGCGGAGGCTGAGAGTCAAGTCTTGAAGTCAAGTCAAGTCAAGTCA 720
DB 661 CGGAGTCAAGGCGGAGGCTGAGAGTCAAGTCTTGAAGTCAAGTCAAGTCAAGTCA 720
QY 721 TTTTGAAGAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 780
DB 721 TTTTGAAGAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 780
QY 781 GTGAGAGTGAAGCTTTTCTTGAAGGCTGAGAGGCAATTCCTCAAGGCTCTCTGCTTG 840

```

```

DB 781 GTGAGAGTGAAGCTTTTCTTGAAGGCTGAGAGGCGGAGTCCCACTCAAGGCTCTGCTTG 840
QY 841 ACATTCAACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 ACATTCAACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 CTGAGTGGGCTCTAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 960
DB 901 CTGAGTGGGCTCTAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 960
QY 961 CGCTCTGAAAGTGTCTTGAAGAAATCTTCTCAATCTCTCTCTCTCTCTCTCTCTCT 1020
DB 961 CGCTCTGAAAGTGTCTTGAAGAAATCTTCTCAATCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1021 ACCGGAAGACCAAGGCGCTGCAACAAAGCGGCGCTGTGCTGTGTGTGTGTGTGT 1080
DB 1021 ACCGGAAGACCAAGGCGCTGCAACAAAGCGGCGCTGTGCTGTGTGTGTGTGTGT 1080
QY 1081 CGGCGAGGCGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1081 CGGCGAGGCGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 1141 ACAGAACCCCGGAAATCTGCTGAGAGACCGGTGTACAGAGCGGCTGTGTGTGTGTGT 1200
DB 1141 ACAGAACCCCGGAAATCTGCTGAGAGACCGGTGTACAGAGCGGCTGTGTGTGTGTGT 1200
QY 1201 CTGAGGTAGAAAACGCTCTCGAGAGGAGAGAGATCTGTACGCGCGGAAATGTAGAC 1260
DB 1201 CTGAGGTAGAAAACGCTCTCGAGAGGAGAGAGATCTGTACGCGCGGAAATGTAGAC 1260
QY 1261 CTGCTCCAGTCGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
DB 1261 CTGCTCCAGTCGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 1321 CAGCATAGGCGCAATGTCTACAGCAATGAGCCCTGCGGAGACAGAGAGAGAGAGAC 1380
DB 1321 CAGCATAGGCGCAATGTCTACAGCAATGAGCCCTGCGGAGACAGAGAGAGAGAGAC 1380
QY 1381 AGAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 AGAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 CCCCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1500
DB 1441 CCCCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1500
QY 1501 CAGCTCTTTTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1501 CAGCTCTTTTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 CTGTGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1619
DB 1561 CTGTGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1619

```

```

RESULT 5
US-09-825-294-211
: Sequence 211, Application US/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Filing, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 211
: LENGTH: 1619

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Query 1501 CACCTCTTTTGGCCACAGACAGAGAAATTAACACTGTTTCAACCCGGGGAGTTGG 1560  
1501 CACCTCTTTTGGCCACAGACAGAGAAATTAACACTGTTTCAACCCGGGGAGTTGG 1560  
1561 CTTGTGTTAAAGAAAGACATTAATGCTTTAGACACTGTAAAAAATTTTTTTTTT 1619  
1561 CTTGTGTTAAAGAAAGACATTAATGCTTTAGACACTGTAAAAAATTTTTTTTTT 1619

RESULT 3  
US-09-713-550-205  
Sequence 205 Application US/09713550  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
FILE REFERENCE: 210121.484C4  
CURRENT APPLICATION NUMBER: US/09/713,550  
CURRENT FILING DATE: 2000-11-14  
NUMBER OF SEQ ID NOS: 205  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 205  
LENGTH: 1619  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-713-550-205

Query Match 100.0%; Score 1619; DB 28; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 7,9e-302;  
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 GGCACCTTTTGGCGATGTTCTTCTGCTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA 60  
1 GGCACCTTTTGGCGATGTTCTTCTGCTCCAGGCTTTGGCTGCAAAATCCAGTGTACCA 60  
61 GGTGGAAGATTCACAGTCAACAGACAGTGTCTCCCGGAGTTCATTTGTAATTTGCAC 120  
61 GGTGGAAGATTCACAGTCAACAGACAGTGTCTCCCGGAGTTCATTTGTAATTTGCAC 120  
121 GGTGGAAGATTCACAGTGTCTCCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180  
121 GGTGGAAGATTCACAGTGTCTCCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180  
121 GGTGGAAGATTCACAGTGTCTCCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180  
181 CGGCAAGTCTGTGATCATCAAGCGGCTGTCTATGCTTCCCGGGTACAGTCTCT 240  
181 CGGCAAGTCTGTGATCATCAAGCGGCTGTCTATGCTTCCCGGGTACAGTCTCT 240  
241 CTGCTCCCCAGGAAACTGAACAGTGTGATGATGATGATGATGATGATGATGATGAT 300  
241 CTGCTCCCCAGGAAACTGAACAGTGTGATGATGATGATGATGATGATGATGATGAT 300  
301 CGGGCCCAAGGCCCCAAGAAAGGGGAAATTCCTGCTCCGCTCCAGGCAAGGCTCCGAC 360  
301 CGGGCCCAAGGCCCCAAGAAAGGGGAAATTCCTGCTCCGCTCCAGGCAAGGCTCCGAC 360  
361 CAGCATTCCTGCTCCCAATTAATGAGCCCTCTCTCGGCACTCTGAAGTGAAGAGATG 420  
361 CAGCATTCCTGCTCCCAATTAATGAGCCCTCTCTCGGCACTCTGAAGTGAAGAGATG 420  
421 CCACCCCTCTGATGATGTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTAGAGA 480  
421 CCACCCCTCTGATGATGTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTAGAGA 480  
481 GTTCTTCTGGGCTGCTCTTATCTGAGGATGAGGAGCGGAGTCCGTTCTTTTGT 540  
481 GTTCTTCTGGGCTGCTCTTATCTGAGGATGAGGAGCGGAGTCCGTTCTTTTGT 540  
541 CCTGTGCAATATATGAAAGAGCTCGGTAAGCATTTCTGAATTAATTCAGCTGAT 600  
541 CCTGTGCAATATATGAAAGAGCTCGGTAAGCATTTCTGAATTAATTCAGCTGAT 600  
601 TTTCAATATGATGATGAAAGAGAGGATGAGTGAAGTTCACCCCACTGCTGTGAAC 660

Db 601 TTTCAATATGATGATGAAAGAGAGGATGAGTGAAGTTCACCCCACTGCTGTGAAC 660  
661 CGGATCAAGGCGGAGCTGCGACAGTCACTCTTAAGATCACTGAGTGGGCTCTGCC 720  
661 CGGATCAAGGCGGAGCTGCGACAGTCACTCTTAAGATCACTGAGTGGGCTCTGCC 720  
721 TTTTGTAAAGCCTCCAGTGTCCATTCCTGATGGGGGATGATGATGATGATGATGAT 780  
721 TTTTGTAAAGCCTCCAGTGTCCATTCCTGATGGGGGATGATGATGATGATGATGAT 780  
781 GTGAGATGAGCTTTCTTAAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCT 840  
781 GTGAGATGAGCTTTCTTAAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCT 840  
841 ACATTCAACTCAATGCTCCCTGCAAAACCATCTCTGCAAGAAATTTGGTCTTCCGC 900  
841 ACATTCAACTCAATGCTCCCTGCAAAACCATCTCTGCAAGAAATTTGGTCTTCCGC 900  
901 CTGAGTTGGGCTAGTACTGAGACTCAATGACTGAGTGGGCTGAGTGGGCTGAGT 960  
901 CTGAGTTGGGCTAGTACTGAGACTCAATGACTGAGTGGGCTGAGTGGGCTGAGT 960  
961 CGCTGTGAAAGTGTCTTAAGAAATCTTCTCAATGCTCTTCTGAGAGAGTGGCGGG 1020  
961 CGCTGTGAAAGTGTCTTAAGAAATCTTCTCAATGCTCTTCTGAGAGAGTGGCGGG 1020  
1021 ACGGAAAGAGCAAGGCGGCTGCAAAAGCGGCGCTGTGAGTGTGAGTGGGCTGAGT 1080  
1021 ACGGAAAGAGCAAGGCGGCTGCAAAAGCGGCGCTGTGAGTGTGAGTGGGCTGAGT 1080  
1081 CGCGAGGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
1081 CGCGAGGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
1141 ACGAACAACCCCGCAAACTGCTGCGAGACACGCTGTACAGAGAGCGGCTGTATACC 1200  
1141 ACGAACAACCCCGCAAACTGCTGCGAGACACGCTGTACAGAGAGCGGCTGTATACC 1200  
1201 CTGAGATGAAAGAAAGTCTCCGAGAGGAGGAGGAGTCAATGATGATGATGATGAT 1260  
1201 CTGAGATGAAAGAAAGTCTCCGAGAGGAGGAGGAGTCAATGATGATGATGATGAT 1260  
1261 CTGCTCAAGTGTGCTTGGGTTTGGCGCAGCCATGATGATGATGATGATGATGAT 1320  
1261 CTGCTCAAGTGTGCTTGGGTTTGGCGCAGCCATGATGATGATGATGATGATGAT 1320  
1321 CAGCATACGGCATGTCACAAATCAAGCCCTGCGCAGACAGAGAGAGAGAGAG 1380  
1321 CAGCATACGGCATGTCACAAATCAAGCCCTGCGCAGACAGAGAGAGAGAGAGAG 1380  
1381 AGAGAAAGAAAGAAACAGATGAGAACACAGTAAATGAATTAATTAATTAATTAAT 1440  
1381 AGAGAAAGAAAGAAACAGATGAGAACACAGTAAATGAATTAATTAATTAATTAAT 1440  
1441 CCCCTCTGCTGCTGCTTACTGCGCAGGAAATGATGATGATGATGATGATGATGAT 1500  
1441 CCCCTCTGCTGCTGCTTACTGCGCAGGAAATGATGATGATGATGATGATGATGAT 1500  
1501 CAGCTTCTTTTGGCAAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1560  
1501 CAGCTTCTTTTGGCAAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1560  
1561 CTTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTT 1619  
1561 CTTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTT 1619

RESULT 4  
US-09-825-294-205  
Sequence 205 Application US/09825294  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun







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c 22 1377 85.1 1925 28 US-09-710-281-4458 Sequence 4458, Ap
c 23 1377 85.1 1925 29 US-09-726-805-1608 Sequence 1608, Ap
24 1299 80.2 1917 17 US-09-371-168-7188 Sequence 7188, Ap
25 1299 80.2 1917 25 US-09-644-873-9077 Sequence 9077, Ap
26 1299 80.2 1917 25 US-09-652-109-9370 Sequence 9370, Ap
27 1299 80.2 1917 25 US-09-652-121-6191 Sequence 6191, Ap
28 1299 80.2 1917 25 US-09-652-128-7518 Sequence 7518, Ap
29 1299 80.2 1917 25 US-09-652-355-9112 Sequence 9112, Ap
30 1299 80.2 1917 25 US-09-652-914-8473 Sequence 8473, Ap
31 1299 80.2 1917 25 US-09-652-917-2477 Sequence 2477, Ap
32 1299 80.2 1917 31 US-09-801-833-7188 Sequence 7188, Ap
33 1264 78.1 1524 40 US-10-119-480-15 Sequence 15, Ap
34 1264 78.1 1524 42 US-10-216-159A-15 Sequence 15, Ap
35 1264 78.1 1524 42 US-10-216-160-15 Sequence 15, Ap
36 1264 78.1 1524 42 US-10-216-162-15 Sequence 15, Ap
37 1264 78.1 1524 42 US-10-216-163-15 Sequence 15, Ap
38 1264 78.1 1524 42 US-10-216-164-15 Sequence 15, Ap
39 1264 78.1 1524 42 US-10-216-165-15 Sequence 15, Ap
40 1264 78.1 1524 42 US-10-216-166-15 Sequence 15, Ap
41 1264 78.1 1524 42 US-10-216-167-15 Sequence 15, Ap
42 1264 78.1 1524 42 US-10-216-168-15 Sequence 15, Ap
43 1264 78.1 1524 42 US-10-218-612-15 Sequence 15, Ap
44 1264 78.1 1524 42 US-10-218-631-15 Sequence 15, Ap
45 1264 78.1 1524 42 US-10-218-765-15 Sequence 15, Ap

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## ALIGNMENTS

RESULT 1  
PCT-US01-45395-205  
Sequence 205, Application PC/TUS0145395

## GENERAL INFORMATION:

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: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 205
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
: PCT-US01-45395-205

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Query Match 100.0%; Score 1619; DB 1; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 7,9e-302;  
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

c 1 GGCACATTTTGGGATGTTCTTGGCTTCCAGGCTTTGGCGTCGAATCCAGTGTACCA 60
Db 1 GGCACATTTTGGGATGTTCTTGGCTTCCAGGCTTTGGCGTCGAATCCAGTGTACCA 60
c 61 GTGTGAAGATTCAGCTGAGCAACAGACTGCTCCCTCCCGAGTTCTTGTGAATTCAC 120
Db 61 GTGTGAAGATTCAGCTGAGCAACAGACTGCTCCCTCCCGAGTTCTTGTGAATTCAC 120
c 121 GGTAAAGTTCAACATGATGTGAGAAAGATGATGAGACAAAGTCCGGATCATGTA 180
Db 121 GGTAAAGTTCAACATGATGTGAGAAAGATGATGAGACAAAGTCCGGATCATGTA 180
c 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTATCGCTTGGCGGATACAGTCTTT 240
Db 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTATCGCTTGGCGGATACAGTCTTT 240
c 241 CTGCTCCCGAGGAACTGAACACTGATGATGATGCTGCTGCAACCCCTCTTTGTA 300

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Db 241 CTGCTCCCGAGGAACTGAACACTGATGATGATGCTGCTGCAACCCCTCTTTGTA 300
c 301 CGGGCCAAAGCCCAAGAAAGGGGAATTTCTGCTCGGCCCTCAGGCGAGGCTCCGCAC 360
Db 301 CGGGCCAAAGCCCAAGAAAGGGGAATTTCTGCTCGGCCCTCAGGCGAGGCTCCGCAC 360
c 361 CACATATCTGTTCTCAATTAAGCCCTTCTCGGCAACATGCTGTAAGCTGAAGAGATG 420
Db 361 CACATATCTGTTCTCAATTAAGCCCTTCTCGGCAACATGCTGTAAGCTGAAGAGATG 420
c 421 CCACCCCTCTGCTGATTTCTTCCAGCCCTCGCCCAACCCCTCCTGAGTGA 480
Db 421 CCACCCCTCTGCTGATTTCTTCCAGCCCTCGCCCAACCCCTCCTGAGTGA 480
c 481 GTTCTCTGCTGCTGCTTCTTATCTGCTGAGAGAGAGGAGTCCGCTCTTTTGT 540
Db 481 GTTCTCTGCTGCTGCTTCTTATCTGCTGAGAGAGAGGAGTCCGCTCTTTTGT 540
c 541 CCGTGTCAATTAATGAAGAGCTGCTGAAGCAATTCGAATTAATTCAGCTGAGTAA 600
Db 541 CCGTGTCAATTAATGAAGAGCTGCTGAAGCAATTCGAATTAATTCAGCTGAGTAA 600
c 601 TTTTCAATGATGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 TTTTCAATGATGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
c 661 CGAGTCAAGGCTCAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 CGAGTCAAGGCTCAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
c 721 TTTTGAAGGCTCAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 TTTTGAAGGCTCAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
c 781 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
c 841 ACATTCAAACTCATGCTCTGAAACCATTCTGACAGCAAGAAATGGCTGCTTCCGC 900
Db 841 ACATTCAAACTCATGCTCTGAAACCATTCTGACAGCAAGAAATGGCTGCTTCCGC 900
c 901 CTGAGTGGGCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 CTGAGTGGGCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
c 961 CGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 CGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
c 1021 ACGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 ACGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
c 1081 CGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 CGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
c 1141 ACGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 ACGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
c 1201 CTGAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1201 CTGAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
c 1261 CTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1261 CTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
c 1321 CAGCATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 CAGCATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:02:33 ; Search time 3626.06 Seconds

(without alignments)  
11225.881 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619  
Sequence: 1 ggcacatttcgcatgtt.....aaaaaaaaaaaaaaaaaaaaa 1619

Scoring table: OLIGO.MNC

Gapop 60.0, Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size: 10

Total number of hits satisfying chosen parameters: 19445921

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3	1619	100.0	1619	28 US-09-713-550-205	Sequence 205, App
4	1619	100.0	1619	31 US-09-825-294-205	Sequence 205, App
5	1619	100.0	1619	31 US-09-825-294-211	Sequence 211, App
6	1619	100.0	1619	36 US-09-970-966-205	Sequence 205, App
7	1619	100.0	1619	36 US-09-970-966-211	Sequence 211, App
8	1619	100.0	1619	42 US-10-212-677-205	Sequence 205, App
9	1619	100.0	1619	42 US-10-212-677-211	Sequence 211, App
10	1427	88.1	1832	40 US-10-108-260A-197	Sequence 197, App
11	1396	86.2	1897	1 PCT-US01-45395-214	Sequence 214, App
12	1396	86.2	1897	31 US-09-825-294-214	Sequence 214, App
13	1396	86.2	1897	36 US-09-970-966-214	Sequence 214, App
14	1388	85.7	1967	1 PCT-US02-29964-16	Sequence 16, App
15	1384	85.5	1918	17 US-09-397-022-4454	Sequence 4454, App
16	1384	85.5	1918	31 US-09-808-383-4454	Sequence 4454, App
17	1377	85.1	1925	25 US-09-652-121-7293	Sequence 7293, App
18	1377	85.1	1925	25 US-09-652-128-9375	Sequence 9375, App
19	1377	85.1	1925	25 US-09-652-917-3346	Sequence 3346, App
20	1377	85.1	1925	27 US-09-699-997-11085	Sequence 11085, App
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES



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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,966B
FILING DATE: 01-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997.
REFERENCE/DOCKET NUMBER: FHCRI7694
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: clone 19; see Figure 26
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-252-966B-15
```

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Best Local Similarity 100.0%; Score 23; DB 1; Length 1008;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAA 1619
DB 975 TGTAAAAA 997
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RESULT 43
US-09-173-300-21
Sequence 21, Application US/09173300
Patent No. 6451581
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/09/173,300
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 60/063,423
EARLIER FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 21
LENGTH: 1162
TYPE: DNA
ORGANISM: Glycine max
US-09-173-300-21
```

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Query Match
Best Local Similarity 100.0%; Score 23; DB 4; Length 1162;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAA 1619
DB 1132 TGTAAAAA 1154
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```
RESULT 44
US-07-869-933-10
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Sequence 10, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19970416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..880
US-07-869-933-10
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 1174;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1597 TGTAAAAA 1619
DB 1150 TGTAAAAA 1172
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```
RESULT 45
US-09-103-663-10
Sequence 10, Application US/09103663D
Patent No. 6171803
GENERAL INFORMATION:
APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: subunit of the high affinity receptor for
FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 1174
TYPE: DNA
ORGANISM: Homo sapiens
```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/575,602
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,086
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1915/Reg
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "cdna sequence for
DESCRIPTION: female-preferential transcript designated B20014-2"
HYPOTHETICAL: NO
US-09-575-602-1

```

```

Query Match 1.4%; Score 23; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAAAAAAAAAAAAAAAAAA 1619
DB 747 TGTAAAAAAAAAAAAAAAAAAAAA 769

```

```

RESULT 41
US-08-032-393-5
Sequence 5, Application US/08032393
Patent No. 5332660
GENERAL INFORMATION:
APPLICANT: Osamu TAKEDA et al.
TITLE OF INVENTION: Gene of Candida Yeast
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,393
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/729,414
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856

```

```

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 933 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Candida albicans
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-032-393-5

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Query Match 1.4%; Score 23; DB 1; Length 933;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1597 TGTAAAAAAAAAAAAAAAAAAAAA 1619
DB 911 TGTAAAAAAAAAAAAAAAAAAAAA 933

```

```

RESULT 42
US-08-252-966B-15
Sequence 15, Application US/08252966B
Patent No. 5624818
GENERAL INFORMATION:
APPLICANT: Eisenman, Robert N.
APPLICANT: Hurlin, Peter J.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessPLLC
STREET: 1420 Fifth Ave., Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,383
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,884
; FILING DATE: 31-DEC-1991
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/756,211
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: SCH 1359
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-206-185-5
```

```

Query Match          1.4%; Score 23; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 508 TGTAAAAAAAAAAAAAAAAAAAA 530
```

```

RESULT 37
US-09-433-248A-7
; Sequence 7, Application US/09433248A
; Patent No. 6355462
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Disease Resistance Factors
; FILE REFERENCE: B1252 US NA
; CURRENT APPLICATION NUMBER: US/09/433,248A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,242
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Trillium aestivum
; US-09-433-248A-7
```

```

Query Match          1.4%; Score 23; DB 4; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 563 TGTAAAAAAAAAAAAAAAAAAAA 585
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```

RESULT 38
US-09-385-982-262/C
; Sequence 262, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
```

```

; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 262
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(593)
; OTHER INFORMATION: n = A,T,C or G
; US-09-385-982-262
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Query Match          1.4%; Score 23; DB 4; Length 593;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 75 TGTAAAAAAAAAAAAAAAAAAAA 53
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```

RESULT 39
5212073-1
; Patent No. 5212073
; APPLICANT: ROLINS, BARRETT,STILES, CHARLES,WONG, GORDON G.
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/351,008
; FILING DATE:12-MAY-1989
; SEQ ID NO:1:
; LENGTH: 752
; 5212073-1
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Query Match          1.4%; Score 23; DB 6; Length 752;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 730 TGTAAAAAAAAAAAAAAAAAAAA 752
```

```

RESULT 40
US-09-575-602-1
; Sequence 1, Application US/09575602
; Patent No. 6392123
; GENERAL INFORMATION:
; APPLICANT: Crossland, Lyle D
; APPLICANT: Harper, Stacy M
; TITLE OF INVENTION: Method of Hybrid Seed Production Using
; TITLE OF INVENTION: Conditional Female Sterility
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 6392123artis Corporation - Patent & Trademark
; ADDRESSEE: Dept.
; STREET: P.O. Box 12257
; CITY: Research Triangle Park
; STATE: NCNY
; COUNTRY: USA
; ZIP: 22057
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

## RESULT 34

US-09-186-188B-29/C  
Sequence 29, Application US/09186188B  
Patent No. 6455672  
GENERAL INFORMATION:  
APPLICANT: Benfey et al.  
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses  
FILE REFERENCE: 5914-074-999  
CURRENT APPLICATION NUMBER: US/09/186,188B  
PRIOR FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: 08/842,445  
PRIOR FILING DATE: 1997-04-24  
PRIOR APPLICATION NUMBER: 08/538,617  
PRIOR FILING DATE: 1996-04-26  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 29  
LENGTH: 502  
TYPE: DNA  
ORGANISM: Plant  
US-09-186-188B-29

Query Match 1.4%; Score 23; DB 4; Length 502;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

## RESULT 35

US-08-462-894-5  
Sequence 5, Application US/08462894  
Patent No. 5723312  
GENERAL INFORMATION:  
APPLICANT: NOESKE-JUNGBLUT, CHRISTIANE  
APPLICANT: HAENDLER, BERNHARD  
APPLICANT: KRAETZSCHMAR, JOERN  
APPLICANT: SCHLEUNING, WOLF-DIETER  
APPLICANT: ALAGON, ALEJANDRO  
APPLICANT: POSSANI, LOURIVAL  
APPLICANT: CUEVAS-AGUIRRE, DELIA  
TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION  
TITLE OF INVENTION: INHIBITOR  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD., SUITE 1400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,894  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/206,185  
FILING DATE: 07-MAR-1994  
APPLICATION NUMBER: US 08/116,889  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP92/02052  
FILING DATE: 04-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/914,383

FILING DATE: 17-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,884

FILING DATE: 31-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/756,211

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 530 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-462-894-5

Query Match 1.4%; Score 23; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
Db 508 TGTAAAAAAAAAAAAAAAAAAAA 530

## RESULT 36

US-08-206-185-5  
Sequence 5, Application US/08206185  
Patent No. 5756454  
GENERAL INFORMATION:  
APPLICANT: NOESKE-JUNGBLUT, CHRISTIANE  
APPLICANT: HAENDLER, BERNHARD  
APPLICANT: KRAETZSCHMAR, JOERN  
APPLICANT: SCHLEUNING, WOLF-DIETER  
APPLICANT: ALAGON, ALEJANDRO  
APPLICANT: POSSANI, LOURIVAL  
APPLICANT: CUEVAS-AGUIRRE, DELIA  
TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION  
TITLE OF INVENTION: INHIBITOR  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD., SUITE 1400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/206,185  
FILING DATE: 07-MAR-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,889  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP92/02052  
FILING DATE: 04-SEP-1992

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;; CURRENT APPLICATION NUMBER: US/09/439,313
;; CURRENT FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 575
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 353
;; LENGTH: 436
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-439-313-353

Query Match
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 29 TGTAAAAAAAAAAAAAAAAAAAA 7

RESULT 30
US-09-352-616A-353/C
; Sequence 353, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiaqichun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.4278
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 353
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-353

Query Match
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 29 TGTAAAAAAAAAAAAAAAAAAAA 7

RESULT 31
US-09-372-422A-35
; Sequence 35, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Bartheu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(257)
```

```
US-09-372-422A-35

Query Match
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 406 TGTAAAAAAAAAAAAAAAAAAAA 428

RESULT 32
US-09-186-276B-29/C
; Sequence 29, Application US/09186276B
; Patent No. 6388173
; GENERAL INFORMATION:
; APPLICANT: Benfey, Phillip
; APPLICANT: Dilaurenzio, Laura
; APPLICANT: Wysocka-Diller, Joanna
; APPLICANT: Malamy, Jocelyn E.
; APPLICANT: Pysch, Leonard
; APPLICANT: Helariutta, Yrjo
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
; FILE REFERENCE: 5914-075-999
; CURRENT APPLICATION NUMBER: US/09/186,276B
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 08/842,445
; PRIOR FILING DATE: 1997-04-24
; PRIOR APPLICATION NUMBER: 08/638,617
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Oryza sp.
US-09-186-276B-29

Query Match
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 33
US-08-842-445-29/C
; Sequence 29, Application US/08842445A
; Patent No. 6441270
; GENERAL INFORMATION:
; APPLICANT: Benfey et al.
; TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5914-056-999
; CURRENT APPLICATION NUMBER: US/08/842,445A
; CURRENT FILING DATE: 1997-04-24
; EARLIER APPLICATION NUMBER: 08/638,617
; EARLIER FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Plant
US-08-842-445-29

Query Match
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619
```



APPLICANT: Dillon, Davin C.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang, Yuqi  
APPLICANT: Xu, Jiangchun  
APPLICANT: Mitcham, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.427C8  
CURRENT APPLICATION NUMBER: US/09/352, 616A  
CURRENT FILING DATE: 1999-07-13  
NUMBER OF SEQ ID NOS: 472  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 357  
LENGTH: 393  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-352-616A-357

Query Match 1.4%; Score 23; DB 4; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAA 1619  
DB 34 TGTAAAAA 12

RESULT 27  
US-09-014-969-5  
Sequence 5, Application US/09014969  
Patent No. 5965397  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: Lavallee, Edward R.  
APPLICANT: Racie, Lisa A.  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Spaulding, Vikki  
APPLICANT: Agostino, Michael J.  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014, 969  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne A.  
REGISTRATION NUMBER: 41,323  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 413 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-014-969-5

Query Match 1.4%; Score 23; DB 2; Length 413;  
Best Local Similarity 100.0%; Pred. No. 0.66;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAA 1619  
DB 387 TGTAAAAA 409

RESULT 28  
US-09-605-785-353/C  
Sequence 353, Application US/09605785  
Patent No. 6321716  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolck, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darriack  
APPLICANT: Li, Samuel

APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C16

CURRENT APPLICATION NUMBER: US/09/605,785  
CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 835  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 353

LENGTH: 436  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-605-785-353

Query Match 1.4%; Score 23; DB 4; Length 436;  
Best Local Similarity 100.0%; Pred. No. 0.66;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1597 TGTAAAAA 1619  
DB 29 TGTAAAAA 7

RESULT 29  
US-09-439-313-353/C  
Sequence 353, Application US/09439313  
Patent No. 6329505  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang Yuqi  
APPLICANT: Reed, Steven G.  
APPLICANT: Kalos, Michael  
APPLICANT: Fanger, Gary  
APPLICANT: Retter, Mark

APPLICANT: Soik, John  
APPLICANT: Day, Craig

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C9

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||

Db 43 TGTAAAAAAAAAAAAAAAAAAAA 21

RESULT 23  
US-08-361-441B-14/C  
; Sequence 14, Application US/08361441B  
; Patent No. 6077948  
; GENERAL INFORMATION:  
; APPLICANT: Russell, Mary E.  
; APPLICANT: Utans, Ulrike  
; TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/361,441B  
; FILING DATE: 21-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/171,385  
; FILING DATE: 21-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 05433/014001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 350 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-361-441B-14

Query Match 1.4%; Score 23; DB 3; Length 350;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||

Db 43 TGTAAAAAAAAAAAAAAAAAAAA 21

RESULT 24  
US-09-605-785-357/C  
; Sequence 357, Application US/09605785  
; Patent No. 6321716  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C16  
; CURRENT APPLICATION NUMBER: US/09/605,785  
; CURRENT FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 835  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 357  
; LENGTH: 393  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; US-09-605-785-357

Query Match 1.4%; Score 23; DB 4; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||

Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 25  
US-09-439-313-357/C  
; Sequence 357, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqi  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 357  
; LENGTH: 393  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; US-09-439-313-357

Query Match 1.4%; Score 23; DB 4; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||

Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 26  
US-09-352-616A-357/C  
; Sequence 357, Application US/09352616A  
; Patent No. 6395278  
; GENERAL INFORMATION:

REGISTRATION NUMBER: 34, 819  
REFERENCE/DOCKET NUMBER: 05433/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-361-441B-20

Query Match 1.4%; Score 23; DB 3; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
DB 23 TGTAAAAAAAAAAAAAAAAAAAA 1

RESULT 21  
US-08-104-072B-2  
Sequence 2, Application US/08104072B  
Patent No. 5639948  
GENERAL INFORMATION:  
APPLICANT: Michiels, Frank  
APPLICANT: Morioka, Shinji  
APPLICANT: Scheerlinck, Trees  
APPLICANT: Komari, Toshiko  
TITLE OF INVENTION: Stamen-specific Promoters from Rice  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 No. 5639948west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/104, 072B  
FILING DATE: 05-AUG-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 9200272  
FILING DATE: 06-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 91403352.7  
FILING DATE: 10-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 91402590.3  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 91400318.1  
FILING DATE: 08-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kowalchuk, Katherine M.  
REGISTRATION NUMBER: 36,848  
REFERENCE/DOCKET NUMBER: 8076, 93USMO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 347 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: rice  
TISSUE TYPE: anther  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 1..322  
OTHER INFORMATION: /product="cDNA T23"  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 333..347  
OTHER INFORMATION: /product="cloning adaptor  
US-08-104-072B-2

Query Match 1.4%; Score 23; DB 1; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
DB 284 TGTAAAAAAAAAAAAAAAAAAAA 306

RESULT 22  
US-08-171-385-14/C  
Sequence 14, Application US/08171385  
Patent No. 5527884  
GENERAL INFORMATION:  
APPLICANT: Mary E. Russell  
APPLICANT: Urike Utans  
TITLE OF INVENTION: Mediators of Chronic Allograft  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171, 385  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34, 819  
REFERENCE/DOCKET NUMBER: 05433/006001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-171-385-14

Query Match 1.4%; Score 23; DB 1; Length 350;  
Best Local Similarity 100.0%; Pred. No. 0.67;

US-08-171-385-27

Query Match 1.4%; Score 23; DB 1; Length 340;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
DB 40 TGTAAAAAAAAAAAAAAAAAAAA 18

RESULT 18

US-08-361-441B-27/c  
Sequence 27, Application US/08361441B  
Patent No. 6077948

GENERAL INFORMATION:  
APPLICANT: Russell, Mary E.  
APPLICANT: Utans, Ulrike  
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,441B  
FILING DATE: 21-DEC-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/171,385

FILING DATE: 21-DEC-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/014001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:

LENGTH: 340 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

US-08-361-441B-27

Query Match 1.4%; Score 23; DB 3; Length 340;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
DB 40 TGTAAAAAAAAAAAAAAAAAAAA 18

RESULT 19  
US-08-171-385-20/c

Sequence 20, Application US/08171385  
Patent No. 5527884

GENERAL INFORMATION:  
APPLICANT: Mary E. Russell  
APPLICANT: Ulrike Utans  
TITLE OF INVENTION: Mediators of Chronic Allograft  
REJECTION  
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 555X

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/171,385

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 05433/006001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 345

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-171-385-20

Query Match 1.4%; Score 23; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAAAAAAAAAAAAAAAAA 1619  
|||||  
DB 23 TGTAAAAAAAAAAAAAAAAAAAA 1

RESULT 20

US-08-361-441B-20/c  
Sequence 20, Application US/08361441B  
Patent No. 6077948

GENERAL INFORMATION:  
APPLICANT: Russell, Mary E.

APPLICANT: Utans, Ulrike  
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION

NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street

CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,441B  
FILING DATE: 21-DEC-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/171,385

FILING DATE: 21-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.

Patent No. 5527884  
GENERAL INFORMATION:  
APPLICANT: Mary E. Russell  
APPLICANT: Ulrike Utans  
TITLE OF INVENTION: Mediators of Chronic Allograft  
TITLE OF INVENTION: Rejection  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171.385  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/006001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-171-385-22  
Query Match 1.4%; Score 23; DB 1; Length 321;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1597 TGTAAAAA 1619  
DB 24 TGTAAAAA 2  
RESULT 16  
US-08-361-441B-22/c  
Sequence 22, Application US/08361441B  
GENERAL INFORMATION:  
PATENT NO. 6077948  
APPLICANT: Russell, Mary E.  
APPLICANT: Utans, Ulrike  
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/361,441B  
FILING DATE: 21-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/171.385  
FILING DATE: 21-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-361-441B-22  
Query Match 1.4%; Score 23; DB 3; Length 321;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1597 TGTAAAAA 1619  
DB 24 TGTAAAAA 2  
RESULT 17  
US-08-171-385-27/c  
Sequence 27, Application US/08171385  
PATENT NO. 5527884  
GENERAL INFORMATION:  
APPLICANT: Mary E. Russell  
APPLICANT: Ulrike Utans  
TITLE OF INVENTION: Mediators of Chronic Allograft  
TITLE OF INVENTION: Rejection  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171.385  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/006001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 340  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

TITLE OF INVENTION: Neuronal PAS Domain Protein  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/785,310A  
FILING DATE: 21-JAN-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: UTSD:1226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4184 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-785-310A-4

Query Match 1.5%; Score 24; DB 2; Length 4184;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAACAAAAA 1619  
|||||  
DB 4138 GTGTAACAAAAA 4161

RESULT 12  
US-09-128-155-17/C  
; Sequence 17, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 176373  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(176373)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-17

Query Match 1.5%; Score 24; DB 3; Length 176373;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAACAAAAA 1619  
|||||  
DB 68491 GTGTAACAAAAA 68468

RESULT 13  
US-09-306-290-11/C  
; Sequence 11, Application US/09306290  
; Patent No. 6221635  
; GENERAL INFORMATION:  
; APPLICANT: Rovera, Giovanni  
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE  
; FILE REFERENCE: 09924-10  
; CURRENT APPLICATION NUMBER: US/09/306,290  
; CURRENT FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer RGP  
US-09-306-290-11

Query Match 1.4%; Score 23; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619  
|||||  
DB 23 TGTAAAAA 1

RESULT 14  
US-09-306-290-16/C  
; Sequence 16, Application US/09306290  
; Patent No. 6221635  
; GENERAL INFORMATION:  
; APPLICANT: Rovera, Giovanni  
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE  
; FILE REFERENCE: 09924-10  
; CURRENT APPLICATION NUMBER: US/09/306,290  
; CURRENT FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PrimerRGP  
US-09-306-290-16

Query Match 1.4%; Score 23; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 TGTAAAAA 1619  
|||||  
DB 23 TGTAAAAA 1

RESULT 15  
US-08-171-385-22/C  
; Sequence 22, Application US/08171385

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 01-MAR-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3073 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1111  
US-08-206-1888-31

Query Match 1.5%; Score 24; DB 3; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
DB 1520 GTGTAAAAA 1543

RESULT 9  
PCT-US91-02714-30  
Sequence 30, Application PC/TUS9102714  
GENERAL INFORMATION:  
APPLICANT: Wajler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02714  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25447  
REFERENCE/DOCKET NUMBER: 27805/30197

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3073 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1111  
PCT-US91-02714-30

Query Match 1.5%; Score 24; DB 5; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
DB 1520 GTGTAAAAA 1543

RESULT 10  
US-09-511-6258-67  
Sequence 67, Application US/095116258  
Patent No. 6368828  
GENERAL INFORMATION:  
APPLICANT: Laroche, William J.  
APPLICANT: Patel, Bhavlin H.  
APPLICANT: Pierce, Jacalyn H.  
TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVE VARIANT  
TITLE OF INVENTION: CDNAS OF STAT6: STAT6D AND STAT6C  
FILE REFERENCE: 14014.030001  
CURRENT APPLICATION NUMBER: US/09/511,6258  
CURRENT FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: PCT/US98/17821  
PRIOR FILING DATE: 1998-08-27  
PRIOR APPLICATION NUMBER: 60/070,397  
PRIOR FILING DATE: 1998-01-05  
PRIOR APPLICATION NUMBER: 60/056,075  
PRIOR FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 67  
LENGTH: 3375  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial Sequence: /No. 6368828e -  
OTHER INFORMATION: synthetic construct  
NAME/KEY: CDS  
LOCATION: (115)...(2655)  
US-09-511-6258-67

Query Match 1.5%; Score 24; DB 4; Length 3375;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
DB 3321 GTGTAAAAA 3344

RESULT 11  
US-08-785-310A-4  
Sequence 4, Application US/08785310A  
Patent No. 5840532  
GENERAL INFORMATION:  
APPLICANT: McKnight, Steven L.  
APPLICANT: Russell, David W.

Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
Db 1520 GTGTAAAAA 1543

## RESULT 6

US-08-474-379C-31  
; Sequence 31, Application US/08474379C  
; Patent No. 5977305  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED  
; NUMBER OF INVENTION: PROCESSES  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,379C  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/206,188  
; FILING DATE: 01-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,352  
; FILING DATE: 19-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 27866/32771  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3073 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1109  
; US-08-474-379C-31

Query Match 1.5%; Score 24; DB 2; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
Db 1520 GTGTAAAAA 1543

## RESULT 7

US-09-146-249A-31

; Sequence 31, Application US/09146249A  
; Patent No. 6069240

; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: Cloning by Complementation and Related  
; NUMBER OF INVENTION: PROCESSES  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/146,249A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448

; INFO: 25-3856  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3073 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1111  
; US-09-146-249A-31

Query Match 1.5%; Score 24; DB 3; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
Db 1520 GTGTAAAAA 1543

## RESULT 8

US-08-206-188B-31  
; Sequence 31, Application US/08206188B  
; Patent No. 6100025

; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: Cloning by Complementation and Related  
; NUMBER OF INVENTION: PROCESSES  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/146,249A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448



SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/068,140A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/04807  
FILING DATE: NO. 6281409ember 4, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dinner, Dara L.  
REGISTRATION NUMBER: 33,680  
REFERENCE/DOCKET NUMBER: C70237  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5017  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1046 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
HYPOHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Ribes nigrum  
STRAIN: Ben Alder  
US-09-068-140A-5

Query Match 1.5%: Score 24; DB 4; Length 1046;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAATAAAAAAAAAAAAAA 1619  
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DB 1015 GTGTAATAAAAAAAAAAAAAA 1038

RESULT 3  
US-09-413-574-1  
Sequence 1, Application US/09413574  
Patent No. 6235972  
GENERAL INFORMATION:  
APPLICANT: Mahajan, Pramod B.  
APPLICANT: Tagliani, Laura  
TITLE OF INVENTION: Maize Rad23 Genes and Uses Thereof  
FILE REFERENCE: 0964  
CURRENT APPLICATION NUMBER: US/09/413,574  
CURRENT FILING DATE: 1999-10-06  
EARLIER APPLICATION NUMBER: 60/109,728  
EARLIER FILING DATE: 1998-11-23  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 1522  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (58) ... (1272)  
US-09-413-574-1

Query Match 1.5%: Score 24; DB 4; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAATAAAAAAAAAAAAAA 1619  
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DB 1456 GTGTAATAAAAAAAAAAAAAA 1479

RESULT 4

5168051-9  
Patent No. 5168051  
APPLICANT: DERYNCK, RIK M.A.; GOEDDELE, DAVID V.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/389,929  
FILING DATE: 04-AUG-1989  
SEQ ID NO: 9  
LENGTH: 2671  
5168051-9

Query Match 1.5%: Score 24; DB 6; Length 2671;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAATAAAAAAAAAAAAAA 1619  
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DB 2577 GTGTAATAAAAAAAAAAAAAA 2600

RESULT 5  
US-07-688-352C-31  
Sequence 31, Application US/07688352C  
Patent No. 5527896  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/688,352C  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25447  
REFERENCE/DOCKET NUMBER: 27805/30197  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3073 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3...1111  
US-07-688-352C-31

Query Match 1.5%: Score 24; DB 1; Length 3073;

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:00:33 ; Search time 60.6676 Seconds  
(without alignments)  
6184.096 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619  
Sequence: 1 ggcacatttcgagattgt.....aaaaaaaaaaaaaaaaaa 1619

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size: 10

Total number of hits satisfying chosen parameters: 153595

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

- 1: Issued Patents\_NA.\*
- 2: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	24	1.5	1532	4	US-09-413-574-1
4	24	1.5	2671	6	5168051-9
5	24	1.5	3073	1	US-07-688-352C-31
6	24	1.5	3073	2	US-08-474-379C-31
7	24	1.5	3073	3	US-09-146-249A-31
8	24	1.5	3073	3	US-08-206-188B-31
9	24	1.5	3073	5	PCT-US91-02714-30
10	24	1.5	3375	4	US-09-511-625B-67
11	24	1.5	4184	2	US-08-785-310A-4
12	24	1.5	176373	3	US-09-128-155-17
13	24	1.4	40	4	US-09-306-290-11
14	24	1.4	40	4	US-09-306-290-11
15	24	1.4	321	1	US-08-171-385-22
16	24	1.4	321	1	US-08-361-441B-22
17	24	1.4	340	1	US-08-171-385-27
18	24	1.4	340	1	US-08-361-441B-27
19	24	1.4	345	1	US-08-171-385-20
20	24	1.4	345	1	US-08-171-385-14
21	24	1.4	347	1	US-08-104-072B-2
22	24	1.4	350	3	US-08-361-441B-14
23	24	1.4	350	3	US-08-361-441B-14
24	24	1.4	393	4	US-09-605-785-357
25	24	1.4	393	4	US-09-439-313-357
26	24	1.4	393	4	US-09-352-616A-357
27	24	1.4	413	2	US-09-014-969-5

C 28	23	1.4	436	4	US-09-605-785-353	Sequence 353, App
C 29	23	1.4	436	4	US-09-439-313-353	Sequence 353, App
C 30	23	1.4	436	4	US-09-352-616A-353	Sequence 353, App
C 31	23	1.4	442	4	US-09-372-422A-35	Sequence 35, App
C 32	23	1.4	502	4	US-09-186-276B-29	Sequence 29, App
C 33	23	1.4	502	4	US-08-842-445-29	Sequence 29, App
C 34	23	1.4	502	4	US-09-186-188B-29	Sequence 29, App
C 35	23	1.4	530	1	US-08-462-894-5	Sequence 5, App
C 36	23	1.4	530	1	US-08-206-185-5	Sequence 5, App
C 37	23	1.4	588	4	US-09-433-248A-7	Sequence 7, App
C 38	23	1.4	593	4	US-09-385-982-262	Sequence 262, App
C 39	23	1.4	752	6	5212073-1	Patent No. 5212073
C 40	23	1.4	772	4	US-09-575-602-1	Sequence 1, App
C 41	23	1.4	933	1	US-08-032-393-5	Sequence 5, App
C 42	23	1.4	1008	4	US-08-252-966B-15	Sequence 15, App
C 43	23	1.4	1162	4	US-09-173-300-21	Sequence 21, App
C 44	23	1.4	1174	1	US-07-869-933-10	Sequence 10, App
C 45	23	1.4	1174	4	US-09-103-663-10	Sequence 10, App

ALIGNMENTS

RESULT 1  
US-09-248-335-59  
; Sequence 59, Application US/09248335  
; Patent No. 6096504  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEF, DANIEL  
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CI-1128-A  
; CURRENT APPLICATION NUMBER: US/09/248,335  
; EARLIER FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 08/924,759  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Word Version 7.0A  
; SEQ ID NO 59  
; LENGTH: 967  
; TYPE: DNA  
; ORGANISM: maize  
US-09-248-335-59

Query Match 1.5% Score 24; DB 3; Length 967;  
Best Local Similarity 100.0% Pred. No. 0.23;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619  
DB 943 GTGTAAAAAAAAAAAAAAAAAAAA 966

RESULT 2  
US-09-068-140A-5  
; Sequence 5, Application US/09068140A  
; Patent No. 6281409  
; GENERAL INFORMATION:  
; APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor  
; APPLICANT: and Rex Michael Brennan  
; TITLE OF INVENTION: Blackcurrant Promoters and Genes  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESSES:  
; ADDRESS: Smithline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

562

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 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/089908  
 ; PRIOR FILING DATE: 1998-06-18  
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 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182

; PRIOR FILING DATE: 1998-07-09  
 Query Match 15%; Score 24; DB 10; Length 1337;  
 Best Local Similarity 100.0%; Pred. No. 0.67;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619  
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 Db 1298 GTGTAAAAAAAAAAAAAAAAAAAA 1321

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 Job time : 101.36 secs

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Query Match          1.5%  Score 24;  DB 10;  Length 1337;
Best Local Similarity 100.0%;  Pred. No. 0.67;
Matches 24;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy  1596 GTGTAAAAAAAAAAAAAAAAAAAA 1619
Db  1298 GTGTAAAAAAAAAAAAAAAAAAAA 1321

RESULT 45
US-09-990-442-286
: Sequence 286, Application US/09990442
: Patent No. US20020132252A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaud, J Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumes, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730PIC8
: CURRENT APPLICATION NUMBER: US/09/990,442
: CURRENT FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
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: PRIOR FILING DATE: 1997-11-24
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: PRIOR FILING DATE: 1998-02-25
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: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
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: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: PRIOR APPLICATION NUMBER: 60/087607
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: PRIOR APPLICATION NUMBER: 60/087827
: PRIOR FILING DATE: 1998-06-03
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;; PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;  
Best Local Similarity 100.0%; Pred.No. 0.67;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1596 GTGTAAAAA 1619  
Db 1298 GTGTAAAAA 1321

RESULT 44  
US-09-991-073-286  
Sequence 286, Application US/09991073  
Patent No. US20020127576A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlson, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091526  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;  
 Best Local Similarity 100.0%; Pred. No. 0.67; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0;

OY 1596 GTGTAAAAA 1619  
 Db 1298 CTGTAAAAA 1321

RESULT 43  
 US-09-989-732-286  
 Sequence 286, Application US/09989732  
 Patent No. US20020123463A1

GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bolstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavich, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumes, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C57  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13  
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 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
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 PRIOR FILING DATE: 1998-03-20  
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 PRIOR FILING DATE: 1998-06-16



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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690

PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619  
Db 1298 GTGTAAAAA 1321

RESULT 42  
US-09-969-731-286  
Sequence 286, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
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PRIOR FILING DATE: 1998-06-26  
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PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
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PRIOR APPLICATION NUMBER: 60/091519  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 24; DB 10; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1596 GTGTAAAAA 1619  
Db 1298 GTGTAAAAA 1321

RESULT 41  
US-09-989-727-286  
Sequence 286, Application US/09989727  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989, 279  
PRIOR FILING DATE: 2001-11-19  
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 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gueney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.

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: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
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: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
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: APPLICANT: Gerritsen, Mary E.
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: APPLICANT: Napier, Mary A.
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: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C62
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APPLICANT: Zhang, Zemin  
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 PRIOR APPLICATION NUMBER: 60/089538  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089598  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089599  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089600  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089653  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089801  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089907  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089908  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089947  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/089948  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/089952  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/090246  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090252  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090254  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090349

PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090355  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090429  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090431  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090435  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090444  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090445  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090472  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090535  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090540  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090542  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090557  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090676  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090678  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090690  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090694  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090695  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090696  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 1.58; Score 24; DB 9; Length 1337;  
 Best Local Similarity 100.0%; Pred. No. 0.67;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAATAAAAAAAAAAAAAA 1619  
 |||  
 Db 1298 GTGTAATAAAAAAAAAAAAAA 1321

RESULT 38  
 US-09-989-722-286  
 ; Sequence 286, Application US/09989722  
 ; Patent No. US20020072067A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.



RESULT 35  
US-09-764-870-15  
; Sequence 15, Application US/09764870  
; Patent No. US20020042386A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT214  
; CURRENT APPLICATION NUMBER: US/09/764, 870  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 646  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 1066  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-870-15

Query Match 1.5%; Score 24; DB 10; Length 1066;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1596 GTGTAAAAA 1619  
Db 1043 GTGTAAAAA 1066

RESULT 36  
US-09-410-194-14  
; Sequence 14, Application US/09410194  
; Patent No. US20020095030A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jurg  
; APPLICANT: Burns, Margot  
; APPLICANT: Immler, Marten  
; APPLICANT: Hanne, Michael  
; APPLICANT: Schreier, Michael  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Bodmer, Jean- Luc  
; APPLICANT: Steiner, Veronique  
; APPLICANT: Rimoldi, Donata  
; APPLICANT: Hoffmann, Kay  
; APPLICANT: French, E. Lais  
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
; FILE REFERENCE: 11141-002001  
; CURRENT APPLICATION NUMBER: US/09/410,194  
; CURRENT FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: PCT/EP98/01857  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 1190  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (394)...(1056)  
US-09-410-194-14

Query Match 1.5%; Score 24; DB 10; Length 1190;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1596 GTGTAAAAA 1619  
Db 1121 GTGTAAAAA 1144

RESULT 37  
US-09-992-598-286  
; Sequence 286, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, V. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumes, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087609  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087827  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: 60/088021  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088025  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088028  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088029  
; PRIOR FILING DATE: 1998-06-04



APPLICANT: Haas, William David  
APPLICANT: Garcia, Carlos A.  
APPLICANT: Krickler, Maja  
APPLICANT: Slader, Ted  
APPLICANT: Davis, Keith R.  
APPLICANT: Allen, Keith  
APPLICANT: Hoffman, Neil  
APPLICANT: Hurban, Patrick  
TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
FILE REFERENCE: 2029 (PAPA-018PRV)  
CURRENT APPLICATION NUMBER: US/09/770,791  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/178,480  
PRIOR FILING DATE: 2000-01-27  
NUMBER OF SEQ ID NOS: 999  
SOFTWARE: fastseq for windows version 4.0  
SEQ ID NO 315  
LENGTH: 373  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-770-791-315

Query Match 1.5%; Score 24; DB 10; Length 373;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
DB 24 GTGTAAAAA 1

RESULT 29  
US-09-924-035A-439/C  
Sequence 439, Application US/09924035A  
Patent No. US20020142319A1  
GENERAL INFORMATION:  
APPLICANT: Grlach, Jtn  
TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
FILE REFERENCE: 2011US  
CURRENT APPLICATION NUMBER: US/09/924,035A  
CURRENT FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: US 60/148,784  
PRIOR FILING DATE: 1999-08-13  
NUMBER OF SEQ ID NOS: 900  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 439  
LENGTH: 419  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-924-035A-439

Query Match 1.5%; Score 24; DB 10; Length 419;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
DB 45 GTGTAAAAA 22

RESULT 30  
US-10-062-254-125  
Sequence 125, Application US/10062254  
Patent No. US2002013882A1  
GENERAL INFORMATION:  
APPLICANT: Cahoon, Edgar B  
APPLICANT: Cahoon, Rebecca E  
APPLICANT: Falco, Saverio Carl  
APPLICANT: Fang, Ylwen  
APPLICANT: Hanke, Sabine S.  
APPLICANT: Lee, Jian-Ming

APPLICANT: Li, Zhongsen  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Morgante, Michele  
APPLICANT: Niu, Xiping  
APPLICANT: Odell, Joan  
APPLICANT: Rafalski, Antoni  
APPLICANT: Sakai, Hajime  
APPLICANT: Zheng, Peizhong  
APPLICANT: Zhu, Qun  
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/062,254  
CURRENT FILING DATE: 2002-02-01  
PRIOR APPLICATION NUMBER: 09/630,346  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/146511  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: 60/156006  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: 60/156899  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 60/157287  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/169767  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/171054  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: 60/172958  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/171515  
PRIOR FILING DATE: 1999-12-22  
PRIOR APPLICATION NUMBER: 60/173535  
PRIOR FILING DATE: 1999-12-29  
NUMBER OF SEQ ID NOS: 375  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 125  
LENGTH: 766  
TYPE: DNA  
ORGANISM: Plectrantha pentandra  
US-10-062-254-125

Query Match 1.5%; Score 24; DB 12; Length 766;  
Best Local Similarity 100.0%; Pred. No. 0.69;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1596 GTGTAAAAA 1619  
DB 734 GTGTAAAAA 757

RESULT 31  
US-09-925-300-627  
Sequence 627, Application US/09925300  
Patent No. US20020151681A1  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruden,  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 627  
LENGTH: 871  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature

OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-301-584

Query Match  
Best Local Similarity 1.5%; Score 25; DB 10; Length 2968;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGTGTAAAAA 1619  
DB 2886 AGTGTAAAAA 2910

## RESULT 25

US-09-770-696-104  
Sequence 104, Application US/09770696  
Patent No. US2001004940A1  
GENERAL INFORMATION:  
APPLICANT: Gorlach, Jörn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameaka, Joshua G.  
APPLICANT: Page, Amy  
APPLICANT: Ledford, Brooke L.  
APPLICANT: Moessner, Jeffrey P.  
APPLICANT: Haas, William David  
APPLICANT: Garcia, Carlos A.  
APPLICANT: Krickler, Maja  
APPLICANT: Slader, Ted  
APPLICANT: Davis, Keith R.  
APPLICANT: Allen, Keith  
APPLICANT: Hoffman, Neil  
APPLICANT: Hurban, Patrick  
TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
FILE REFERENCE: 2031US (PARA-0208RV)  
CURRENT APPLICATION NUMBER: US/09/770,696  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/178,278  
PRIOR FILING DATE: 2000-01-27  
NUMBER OF SEQ ID NOS: 911  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 104  
LENGTH: 208  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-770-696-104

Query Match  
Best Local Similarity 1.5%; Score 24; DB 10; Length 208;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619  
DB 169 GTGTAAAAA 192

## RESULT 26

US-09-920-300A-58  
Sequence 58, Application US/09920300A  
Patent No. US20020136728A1  
GENERAL INFORMATION:  
APPLICANT: King, Gordon E.  
APPLICANT: Meagher, Madeleine Joy  
APPLICANT: Xu, Jiangchun  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121,547  
CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31  
NUMBER OF SEQ ID NOS: 1789  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 58  
LENGTH: 258  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 258  
OTHER INFORMATION: n = A,T,C or G  
US-09-920-300A-58

Query Match  
Best Local Similarity 1.5%; Score 24; DB 10; Length 258;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619  
DB 228 GTGTAAAAA 251

## RESULT 27

US-10-033-528-58  
Sequence 58, Application US/10033528  
Patent No. US20020131971A1  
GENERAL INFORMATION:  
APPLICANT: King, Gordon E.  
APPLICANT: Meagher, Madeleine Joy  
APPLICANT: Xu, Jiangchun  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121,547C1  
CURRENT APPLICATION NUMBER: US/10/033,528  
CURRENT FILING DATE: 2001-12-26  
NUMBER OF SEQ ID NOS: 1896  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 58  
LENGTH: 258  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 258  
OTHER INFORMATION: n = A,T,C or G  
US-10-033-528-58

Query Match  
Best Local Similarity 1.5%; Score 24; DB 12; Length 258;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 GTGTAAAAA 1619  
DB 228 GTGTAAAAA 251

## RESULT 28

US-09-770-791-315/C  
Sequence 315, Application US/09770791  
Patent No. US20020062014A1  
GENERAL INFORMATION:  
APPLICANT: Gorlach, Jörn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameaka, Joshua G.  
APPLICANT: Page, Amy  
APPLICANT: Ledford, Brooke L.  
APPLICANT: Moessner, Jeffrey P.

```
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9079
LENGTH: 152
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 39-LIB3058-009-Q1-K1-B12
US-09-960-352-9079

Query Match
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGTGTAAAAA 1619
DB 52 AGTGTAAAAA 28

RESULT 21
US-09-867-701-4911/c
Sequence 4911, Application US/09867701
Patent No. US2002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4911
LENGTH: 363
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-4911

Query Match
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGTGTAAAAA 1619
DB 27 AGTGTAAAAA 3

RESULT 22
US-09-867-701-5174/c
Sequence 5174, Application US/09867701
Patent No. US2002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5174
LENGTH: 395
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-5174

Query Match
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGTGTAAAAA 1619
DB 27 AGTGTAAAAA 3

RESULT 23
US-09-919-580-143/c
Sequence 143, Application US/09919580
Patent No. US20020110832A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.552
CURRENT APPLICATION NUMBER: US/09/919,580
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 143
LENGTH: 568
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 62, 74, 231, 357, 405, 499, 510, 532, 564
OTHER INFORMATION: n = A,T,C or G
US-09-919-580-143

Query Match
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGTGTAAAAA 1619
DB 35 AGTGTAAAAA 11

RESULT 24
US-09-925-301-584
Sequence 584, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 584
LENGTH: 2968
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (454)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (1437)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (2961)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (2964)
```

NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7826  
LENGTH: 381  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-867-701-7826

Query Match  
Best Local Similarity 100.0%; Score 125; DB 10; Length 381;  
Pred. No. 1.7e-42;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 959 CTCGCTGTAAGAAAGCTTAGAAATCTTCTCAGTCTCTCTGACAGAGACTGGCCG 1018  
DB 116 CTCGCTGTAAGAAAGCTTAGAAATCTTCTCAGTCTCTCTGACAGAGACTGGCCG 175  
QY 1019 GGACGCGAAGACAGACGGCGCTGCACAAAGCGGCGCTGCGGTGGTGGAGTCCGATG 1078  
DB 176 GGACGCGAAGACAGACGGCGCTGCACAAAGCGGCGCTGCGGTGGTGGAGTCCGATG 235  
QY 1079 TACGC 1083  
DB 236 TACGC 240

## RESULT 17

US-09-867-701-4251  
Sequence 4251, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4251  
LENGTH: 430  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-867-701-4251

Query Match  
Best Local Similarity 100.0%; Score 120; DB 10; Length 430;  
Pred. No. 2e-40;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 CTCGATGTTCTTCAGACCCCTGCGCCCAACCCCACTCCCTGAGTGGTCTTCTG 490  
DB 182 CTCGATGTTCTTCAGACCCCTGCGCCCAACCCCACTCCCTGAGTGGTCTTCTG 241  
QY 491 GGTGTCTTTATCTGGGTAGGAGCGGAGTCCGTGTTCTTGTCTTCTGCGCAA 550  
DB 242 GGTGTCTTTATCTGGGTAGGAGCGGAGTCCGTGTTCTTGTCTTCTGCGCAA 301

## RESULT 18

US-09-867-701-2375  
Sequence 2375, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2375  
LENGTH: 558  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (1)...(358)  
OTHER INFORMATION: n = A,T,C or G  
US-09-867-701-2375

Query Match  
Best Local Similarity 100.0%; Score 112; DB 10; Length 558;  
Pred. No. 3.8e-37;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1138 TGCAGAACACCCCGCAACTGCTGCAGAGACCGGTACAGGAGCGGTGAGACC 1197  
DB 142 TGCAGAACACCCCGCAACTGCTGCAGAGACCGGTGAGAGCGGTTGATGACC 201  
QY 1198 GAGCTGAGGTGAGAAACGTTCCGAGAGGAGGAGGATCATGTACGCC 1249  
DB 202 GAGCTGAGGTGAGAAACGTTCCGAGAGGAGGAGGATCATGTACGCC 253

## RESULT 19

US-09-834-975-825  
Sequence 825, Application US/09834975  
Patent No. US20020110815A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Brown, Jeffrey  
APPLICANT: Bolt, Andrew  
APPLICANT: Van Hufel, Christophe  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS  
FILE REFERENCE: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
TITLE OF INVENTION: OF HUMAN CANCERS  
FILE REFERENCE: MRI-0168  
CURRENT APPLICATION NUMBER: US/09/834,975  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/197,538  
PRIOR FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 1046  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 825  
LENGTH: 1368  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (1)...(1368)  
OTHER INFORMATION: n = A,T,C or G  
US-09-834-975-825

Query Match  
Best Local Similarity 100.0%; Score 27; DB 10; Length 1368;  
Pred. No. 0.039;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 ACAGGTGTAAGAAAGCTTAGAAATCTTCTCAGTCTCTCTGACAGAGACTGGCCG 1619  
DB 459 ACAGGTGTAAGAAAGCTTAGAAATCTTCTCAGTCTCTCTGACAGAGACTGGCCG 485

## RESULT 20

US-09-960-352-9079/C  
Sequence 9079, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Ningbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan  
TITLE OF INVENTION: NOCTIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

OY 1525 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAACCCATTAA 1584  
 |||||||  
 DB 75 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAACCCATTAA 16  
 |||||||  
 OY 1585 TGCTTTAGACACTGT 1599  
 |||||||  
 DB 15 TGCTTTAGACACTGT 1

## RESULT 13

US-09-867-701-8894/c  
 ; Sequence 8894, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jones, Robert  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8894  
 ; LENGTH: 201  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-867-701-8894

Query Match 10.3%; Score 166; DB 10; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-59;  
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1223 AGAAGGGAGAGAGATCATGTAGCCCGGAAGTAGAGACCTGTCAGTGTGCTGGGTT 1282  
 |||||||  
 DB 181 AGAAGGGAGAGAGATCATGTAGCCCGGAAGTAGAGACCTGTCAGTGTGCTGGGTT 122  
 |||||||  
 OY 1283 TGCCCCGACCATATGCTCTCGAATCTGTGGGCAATCCGATACGGCCATGTACAA 1342  
 |||||||  
 DB 121 TGCCCCGACCATATGCTCTCGAATCTGTGGGCAATCCGATACGGCCATGTACAA 62  
 |||||||  
 OY 1343 CAATCAGCCCTGGGCGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1388  
 |||||||  
 DB 61 CAATCAGCCCTGGGCGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 16  
 |||||||

## RESULT 14

US-09-867-701-1532  
 ; Sequence 1532, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1532  
 ; LENGTH: 390  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(390)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-867-701-1532

Query Match 9.5%; Score 154; DB 10; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;  
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1358 AGACAGCAGCAG 1417  
 |||||||  
 DB 147 AGACAGCAGCAG 206  
 |||||||  
 OY 1418 GATTAACCAATTAATTTTATAGCCCTGTGCTGTGCTTACTGCGCAGAAATGTAC 1477  
 |||||||  
 DB 207 GATTAACCAATTAATTTTATAGCCCTGTGCTGTGCTTACTGCGCAGAAATGTAC 266  
 |||||||  
 OY 1478 CAATTTTCAGTGTGAGACTTGACAGCTTCTTTT 1511  
 |||||||  
 DB 267 CAATTTTCAGTGTGAGACTTGACAGCTTCTTTT 300  
 |||||||

## RESULT 15

US-09-825-294-213  
 ; Sequence 213, Application US/09825294  
 ; Patent No. US20020004491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Fling, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; FILE REFERENCE: 210121.484C5  
 ; CURRENT APPLICATION NUMBER: US/09/825,294  
 ; CURRENT FILING DATE: 2001-04-03  
 ; NUMBER OF SEQ ID NOS: 215  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 213  
 ; LENGTH: 480  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-825-294-213

Query Match 9.0%; Score 146; DB 10; Length 480;  
 Best Local Similarity 99.5%; Pred. No. 3.8e-51;  
 Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGAAGCTTTTGGCGGATTTCTTCTCCAGGCTTTGGCGTCAATCCAGTGTACCA 60  
 |||||||  
 DB 280 GCGAAGCTTTTGGCGGATTTCTTCTCCAGGCTTTGGCGTCAATCCAGTGTACCA 339  
 |||||||  
 OY 61 GTGTGAAGATTTCCAGCTGAACAACGACTGCTCTCCCGAGTTCATTGTGATTCAC 120  
 |||||||  
 DB 340 GTGTGAAGATTTCCAGCTGAACAACGACTGCTCTCCCGAGTTCATTGTGATTCAC 399  
 |||||||  
 OY 121 GGTGAAGCTTTAAGACATGTCTCAAGAAAGATGATGAGCAAGTGGCGGATCATGA 180  
 |||||||  
 DB 400 GGTGAAGCTTTAAGACATGTCTCAAGAAAGATGATGAGCAAGTGGCGGATCATGA 459  
 |||||||  
 OY 181 CCGCAAGTCTGTGCAT 197  
 |||||||  
 DB 460 CCGCAAGTCTGTGCAT 476  
 |||||||

## RESULT 16

US-09-867-701-7826  
 ; Sequence 7826, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29

```

QY 241 CTGCTCCCGAGGAACTGAACTGAGTTCATGCTGCTGCAACACCCCTTTGTA 300
    |||||||
Db 251 CTGCTCCCGAGGAACTGAACTGAGTTCATGCTGCTGCAACACCCCTTTGTA 310
QY 301 CGGGCCAGG 310
    |||||||
Db 311 CGGGCCAGG 320

```

## RESULT 10

```

US-09-867-701-2409/c
; Sequence 2409, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2409
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-2409

```

```

Query Match          19.0%; Score 307; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1292 CCATGATCTCCGAACTGCTGGGATCCAGCATCGGCAATGTCACAAATCAGCC 1351
    |||||||
Db 310 CCATGATCTCCGAACTGCTGGGATCCAGCATCGGCAATGTCACAAATCAGCC 251
QY 1352 CTGGGCGACAGCAGCAGGAGGAGACAGACAGAAAAAGAAAAACACAGCATGAGACACA 1411
    |||||||
Db 250 CTGGGCGACAGCAGCAGGAGGAGAGACAGAAAAAGAAAAACACAGCATGAGACACA 191
QY 1412 GTAATGTAATAAACCATTAATATTATTCACCCCTGCTCTGCTTACTGCGCCAGGAAA 1471
    |||||||
Db 190 GTAATGTAATAAACCATTAATATTATTCACCCCTGCTCTGCTTACTGCGCCAGGAAA 131
QY 1472 TGGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAGAGAAATT 1531
    |||||||
Db 130 TGGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAGAGAAATT 71
QY 1532 TAACACTGTTTCAAAACCGGGGAGTGGCTGTTAAGAAAGACCATTAATGCTTTA 1591
    |||||||
Db 70 TAACACTGTTTCAAAACCGGGGAGTGGCTGTGTAAAGAAAGCCATTAAATGCTTTA 11
QY 1592 GACAGTG 1598
    |||||||
Db 10 GACAGTG 4

```

## RESULT 11

```

US-09-825-294-212
; Sequence 212, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03

```

```

; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 212
; LENGTH: 1010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-212

```

```

Query Match          16.7%; Score 271; DB 10; Length 1010;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 31 AGGCTTCCGCTGCAATTCAGTCTACAGTGTGAAGAAATTCAGCTGACAGACTG 90
    |||||||
Db 258 AGGCTTCCGCTGCAATTCAGTCTACAGTGTGAAGAAATTCAGCTGACAGACTG 317
QY 91 CTCTCCCGGAGTTCATTTGAAATTCAGGTTGAAAGCTTCAAGACATGTGCAGAAAGA 150
    |||||||
Db 318 CTCTCCCGGAGTTCATTTGAAATTCAGGTTGAAAGCTTCAAGACATGTGCAGAAAGA 377
QY 151 AGTATGAGCAAGAGTCCGCGATCATGTACCGCAAGTCCGTGTCATCATCGCGGCTG 210
    |||||||
Db 378 AGTATGAGCAAGAGTCCGCGATCATGTACCGCAAGTCCGTGTCATCATCGCGGCTG 437
QY 211 TCTCATGCGCTCTGCGCGGATACAGTCTTCTCTCCAGGAACTGAACTGATTG 270
    |||||||
Db 438 TCTCATGCGCTCTGCGCGGATACAGTCTTCTCTCCAGGAACTGAACTGATTG 497
QY 271 CATCAGCTGCTGCAACACCCCTTTGTAC 301
    |||||||
Db 498 CATCAGCTGCTGCAACACCCCTTTGTAC 528

```

## RESULT 12

```

US-09-867-701-4240/c
; Sequence 4240, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4240
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4240

```

```

Query Match          16.3%; Score 264; DB 10; Length 409;
Best Local Similarity 99.7%; Pred. No. 9e-100;
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1285 GCCGAGCCATGATCTCTCGAATCTGTTGGGATCCAGCATACGGCCATGTACAAACA 1344
    |||||||
Db 315 GCCGAGCCATGATCTCTCGAATCTGTTGGGATCCAGCATACGGCCATGTACAAACA 256
QY 1345 ATCAGCCCTGGGCGACACGAGCAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGA 1404
    |||||||
Db 255 ATCAGCCCTGGGCGACACGAGCAGGAGGAGAGAGACAGAGAAAAAGAAAAACACAGCATGA 196
QY 1405 GAACACAGTAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1464
    |||||||
Db 195 GAACACAGTAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 136
QY 1465 CAGGAAATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAAGA 1524
    |||||||
Db 135 CAGGAAATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAAGA 76

```



```

APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Filing, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.4845
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 199
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(369)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

```

Query Match 19.5%; Score 315; DB 10; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-121;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 30 CAGGCTTTGGCTGCAAAATCCAGTGTACCAAGTGTGAAGATTCAGCTGAACAGCACT 89
    |||||||
DB 30 CAGGCTTTGGCTGCAAAATCCAGTGTACCAAGTGTGAAGATTCAGCTGAACAGCACT 89
OY 90 GCTCTCTCCCGAGTGTATGTGATGACGGGTGAACGTTCAAGACATGTGCAGAAAG 149
    |||||||
DB 90 GCTCTCTCCCGAGTGTATGTGATGACGGGTGAACGTTCAAGACATGTGTCAAAAG 149
OY 150 AAGTATGAGCAAAAGTCCGGGATGATGATGACCGCAAGCTCTGTGATCATCAGCGGCT 209
    |||||||
DB 150 AAGTATGAGCAAAAGTCCGGGATGATGATGACCGCAAGCTCTGTGATCATCAGCGGCT 209
OY 210 GCTGTATGCTCTGCGGGGTGACAGTCTCTGCTCCCGAGGAACTGACTGAGTTT 269
    |||||||
DB 210 GCTGTATGCTCTGCGGGGTGACAGTCTCTGCTCCCGAGGAACTGACTGAGTTT 269
OY 270 GCATCAGCTGCTGCAAAACCCCTCTTTGTAAAGGGCCAGGCGCCCAAGAAAGGGAGTT 329
    |||||||
DB 270 GCATCAGCTGCTGCAAAACCCCTCTTTGTAAAGGGCCAGGCGCCCAAGAAAGGGAGTT 329
OY 330 CTGCTCTGGGCTCTCA 344
    |||||||
DB 330 CTGCTCTGGGCTCTCA 344

```

RESULT 8  
 US-09-867-701-1516/c  
 ; Sequence 1516, Application US/09867701  
 ; Patent No. US2002013237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1516  
 ; LENGTH: 373  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-09-867-701-1516

Query Match 19.5%; Score 315; DB 10; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-121;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1285 GCCGAGCCATGATCTCTCCGATCTGTTGGGCAATCCAGCATACGGCATTGTCACAA 1344
    |||||||
DB 315 GCCGAGCCATGATCTCTCCGATCTGTTGGGCAATCCAGCATACGGCATTGTCACAA 256
OY 1345 ATCAGCCCTGGGCGACGACGACGAGGAGAGACAGAGAGAGAGAGAGAGAGAGAG 1404
    |||||||
DB 255 ATCAGCCCTGGGCGACGACGACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
OY 1405 GAGCACTGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1464
    |||||||
DB 195 GAGCACTGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 136
OY 1465 GAGCACTGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1524
    |||||||
DB 135 GAGCACTGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 76
OY 1525 GAGCACTGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1584
    |||||||
DB 75 GAGCACTGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 16
OY 1585 TGCTTTAGACATGT 1599
    |||||||
DB 15 TGCTTTAGACATGT 1

```

RESULT 9  
 US-09-825-294-9  
 ; Sequence 9, Application US/09825294  
 ; Patent No. US2002004491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Filing, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; FILE REFERENCE: 210121.4845  
 ; CURRENT APPLICATION NUMBER: US/09/825,294  
 ; CURRENT FILING DATE: 2001-04-03  
 ; NUMBER OF SEQ ID NOS: 215  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 396  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (1)...(396)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-825-294-9

Query Match 19.1%; Score 310; DB 10; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 1e-118;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 GGCACATTTTGGCGATTTCTTCTTCCAGGCTTTCGCTGCAAAATCCAGTCTACCA 60
    |||||||
DB 11 GGCACATTTTGGCGATTTCTTCTTCCAGGCTTTCGCTGCAAAATCCAGTCTACCA 70
OY 61 GTGTGAAGATTCACAGTCAACAGACTGCTCTCCCGAGTTCATTTGAATTCAC 120
    |||||||
DB 71 GTGTGAAGATTCACAGTCAACAGACTGCTCTCCCGAGTTCATTTGAATTCAC 130
OY 121 GGTGAAGTTCACAGATGTGTCAAGAAAGATGATGAGCAAGTGTGCGGAGATCATGTA 180
    |||||||
DB 131 GGTGAAGTTCACAGATGTGTCAAGAAAGATGATGAGCAAGTGTGCGGAGATCATGTA 190
OY 181 CCGGAGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
    |||||||
DB 191 CCGGAGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250

```

Db 600 GACAGTG 606

## RESULT 5

US-09-867-701-10876  
 ; Sequence 10876, Application US/09867701  
 ; Patent No. US2002013237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 10876  
 ; LENGTH: 625  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 607  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-867-701-10876

Query Match 30.0%; Score 486; DB 10; Length 625;  
 Best Local Similarity 99.8%; Pred. No. 2,9e-191;  
 Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 992 AGTCTCTCTTCGACAGAGACTGCGCGCGGAGACGCGGAGACAAACGCGCTGTCACAAAGCG 1051  
 Db 1 AGTCTCTCTTCGACAGAGACTGCGCGCGGAGACGCGGAGACAAACGCGCTGTCACAAAGCG 60  
 QY 1052 GCGCGTGTGCGTGTGAGAGCGCATGTACGCGGAGCGCTTCTGTGGTTGGCGTGTG 1111  
 Db 61 GCGCGTGTGCGTGTGAGAGCGCATGTACGCGGAGCGCTTCTGTGGTTGGCGTGTG 120  
 QY 1112 CAGCGACAGCGCGGACAGACAGCCTTTCAGACAAACCGCGGAGAACTGTGCGAGGACA 1171  
 Db 121 CAGCGACAGCGCGGACAGACAGCCTTTCAGACAAACCGCGGAGAACTGTGCGAGGACA 179  
 QY 1172 CCGTGTACAGAGCGGCGTGTGATGACGAGCTAGTAAAGAAACGCTTCGAGAGAGGGA 1231  
 Db 180 CCGTGTACAGAGCGGCGTGTGATGACGAGCTAGTAAAGAAACGCTTCGAGAGAGGGA 239  
 QY 1232 GAGAGATCATGTACGCGCGGAGAGTAGAGACTGTCAGTGTGCGTGGTTGGCGGAG 1291  
 Db 240 GAGAGATCATGTACGCGCGGAGAGTAGAGACTGTCAGTGTGCGTGGTTGGCGGAG 299  
 QY 1292 CCATGATCTCGGAAATGTGTTGGGATTCAGCATACGCGCAATGTACAAATTCAGCC 1351  
 Db 300 CCATGATCTCGGAAATGTGTTGGGATTCAGCATACGCGCAATGTACAAATTCAGCC 359  
 QY 1352 CTGGGACAGACAG 1411  
 Db 360 CTGGGACAGACAG 419  
 QY 1412 GTAATGTAATAAACAATAAATTTAGCCCTGTCTGTGCTTACTGCGCAGAGAA 1471  
 Db 420 GTAATGTAATAAACAATAAATTTAGCCCTGTCTGTGCTTACTGCGCAGAGAA 479  
 QY 1472 TGTACCAATTTTTCAGTGTGAGCTGACAGCTTCTTTTCCACAGAGAGAGAGAGAG 1531  
 Db 480 TGTACCAATTTTTCAGTGTGAGCTGACAGCTTCTTTTCCACAGAGAGAGAGAGAG 539  
 QY 1532 TAAACAGTGTTCACAAACCGGAGAGTGTGCTGTGTTAAAGAGAGAGAGAGAGAGAG 1591  
 Db 540 TAAACAGTGTTCACAAACCGGAGAGTGTGCTGTGTTAAAGAGAGAGAGAGAGAGAG 599

QY 1592 GACAGTG 1598  
 Db 600 GACAGTG 606

## RESULT 6

US-09-825-294-208/c  
 ; Sequence 208, Application US/09825294  
 ; Patent No. US20020004491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Fling, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; FILE REFERENCE: 210121.484C5  
 ; CURRENT APPLICATION NUMBER: US/09/825,294  
 ; NUMBER OF SEQ ID NOS: 215  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 208  
 ; LENGTH: 1362  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-825-294-208

Query Match 23.8%; Score 386; DB 10; Length 1362;  
 Best Local Similarity 99.8%; Pred. No. 4.5e-150;  
 Matches 506; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 845 TCAACTTCTGCTCTGAAACCATCTCTGACAGAGAAATGGCTGTTGCGCCTGA 904  
 Db 1362 TCAACTTCTGCTCTGAAACCATCTCTGACAGAGAAATGGCTGTTGCGCCTGA 1303  
 QY 905 GTTGGGCTTAGTACGAGCTGCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964  
 Db 1302 GTTGGGCTTAGTACGAGCTGCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1243  
 QY 965 CTGAAAGTCTTTAGAAATCTTCTGAGTTCTCTTCAGAGAGAGAGAGAGAGAGAGAG 1024  
 Db 1242 CTGAAAGTCTTTAGAAATCTTCTGAGTTCTCTTCAGAGAGAGAGAGAGAGAGAGAG 1183  
 QY 1025 GAAGAGCAACGGGCGGTGACAAACGCGGCTGTGCTGTGAGAGAGAGAGAGAGAGAG 1084  
 Db 1182 GAAGAGCAACGGGCGGTGACAAACGCGGCTGTGCTGTGAGAGAGAGAGAGAGAGAG 1123  
 QY 1085 CAGGCGCTTCTGTGTTGGCTGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1144  
 Db 1122 CAGGCGCTTCTGTGTTGGCTGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1064  
 QY 1145 ACACCGCGGAAATGCTGCGAGAGACCGTGTACAGAGAGAGAGAGAGAGAGAGAGAG 1204  
 Db 1063 ACACCGCGGAAATGCTGCGAGAGACCGTGTACAGAGAGAGAGAGAGAGAGAGAGAG 1004  
 QY 1205 GGTAAGAAAGAGTCTCCAG 1264  
 Db 1003 GGTAAGAAAGAGTCTCCAG 944  
 QY 1265 TCCATGCTGTGTTGGGTTGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1324  
 Db 943 TCCATGCTGTGTTGGGTTGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 884  
 QY 1325 ATACGCGCAATGTACAAACATCAGCC 1351  
 Db 883 ATACGCGCAATGTACAAACATCAGCC 857

## RESULT 7

US-09-825-294-199  
 ; Sequence 199, Application US/09825294  
 ; Patent No. US20020004491A1  
 ; GENERAL INFORMATION:



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QY 421 CCACCCCTCTGATTTGTTCTTCACAGCCCTCGCCCAACCCCCACCTCCCTAGTGA 480
DB 421 CCACCCCTCTGATTTGTTCTTCACAGCCCTCGCCCAACCCCCACCTCCCTAGTGA 480
QY 481 GTTTCCTCTGGGTGCTCTTTTATTTCTGGGTAGGAGCGGGAGTCCGTGTTCTTTGTT 540
DB 481 GTTTCCTCTGGGTGCTCTTTTATTTCTGGGTAGGAGCGGGAGTCCGTGTTCTTTGTT 540
QY 541 CCTGTGCAATTAATGAAGAGCTCGGTAAAGCATCTGTAATTAATTCACCTGACCTGAAT 600
DB 541 CCTGTGCAATTAATGAAGAGCTCGGTAAAGCATCTGTAATTAATTCACCTGACCTGAAT 600
QY 601 TTTTACGATGATCTTGAAGAGAGAGGTGAGTAAAGTTCAACCCCACTGCTGTGTAAAC 660
DB 601 TTTTACGATGATCTTGAAGAGAGAGGTGAGTAAAGTTCAACCCCACTGCTGTGTAAAC 660
QY 661 CGAGGTCAAGGCGGAGGTGAGTCAAGTCACTGATGAGTGGGATGTTGAGACTGCA 720
DB 661 CGAGGTCAAGGCGGAGGTGAGTCAAGTCACTGATGAGTGGGATGTTGAGACTGCA 720
QY 721 TTTTGTAAAGCTTCAGATGTCATTCATCCGATGGGGGATGTTGAGACTGCA 780
DB 721 TTTTGTAAAGCTTCAGATGTCATTCATCCGATGGGGGATGTTGAGACTGCA 780
QY 781 GTGAGAGTGAAGTCTTTCTTAGGGCTGAGGCGCAAGTCCCACTCAAGGCTCCCTGCTTG 840
DB 781 GTGAGAGTGAAGTCTTTCTTAGGGCTGAGGCGCAAGTCCCACTCAAGGCTCCCTGCTTG 840
QY 841 ACATTCAAACTTCATGCTCTGCTGAAAAACATCTCTGCAAGCAAAATGGCTGTTTCCGCC 900
DB 841 ACATTCAAACTTCATGCTCTGCTGAAAAACATCTCTGCAAGCAAAATGGCTGTTTCCGCC 900
QY 901 CTGAGTGGGCTCTGATGACTGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCT 960
DB 901 CTGAGTGGGCTCTGATGACTGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCT 960
QY 961 CGCTGGAAGAGTCTTGAAGAAATCTTCTCAAGTCTCTTTCAGAGAGAGTGGCGCGG 1020
DB 961 CGCTGGAAGAGTCTTGAAGAAATCTTCTCAAGTCTCTTTCAGAGAGAGTGGCGCGG 1020
QY 1021 ACGCGAAGAGCAAGGCGCTGCAACAAAGCGGCGCTGCGGTGGTGGAGTGGCAATGTA 1080
DB 1021 ACGCGAAGAGCAAGGCGCTGCAACAAAGCGGCGCTGCGGTGGTGGAGTGGCAATGTA 1080
QY 1081 CGCGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CGCGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 ACGAAGACCCCGCGCAAACTGCTGCGAGAGACACGCTGTAACAGAGAGCGGTGATGACCGAG 1200
DB 1141 ACGAAGACCCCGCGCAAACTGCTGCGAGAGACACGCTGTAACAGAGAGCGGTGATGACCGAG 1200
QY 1201 CTGAGGTGAAAAAGTCTGCGAAGAGGAGAGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 CTGAGGTGAAAAAGTCTGCGAAGAGGAGAGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 CTGCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 CTGCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 CAGCATACGCGCAATGTCACAACTACGCTGCGAGACAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 CAGCATACGCGCAATGTCACAACTACGCTGCGAGACAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 AGAAGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 AGAAGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 CCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 CCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

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QY 1501 CAGCTCTTTTGGCACAAGAGAGAGATTTAACAAGTCTTTTCAAAACCGGGGAGTTGG 1560
DB 1501 CAGCTCTTTTGGCACAAGAGAGAGATTTAACAAGTCTTTTCAAAACCGGGGAGTTGG 1560
QY 1561 CTGTGTAAGAAAGACCATTAATGCTTTAGACATGTAAGAAAAA 1619
DB 1561 CTGTGTAAGAAAGACCATTAATGCTTTAGACATGTAAGAAAAA 1619

RESULT 3
US-09-825-294-214
: Sequence 214, Application US/09825294
: Patent No. US2002000491A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stol, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: 210121.4845
: CURRENT APPLICATION NUMBER: US/09/825,294
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)-(1897)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

Query Match      86.2%; Score 1396; DB 10; Length 1897;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGCACACTTTTGGGATGTTGCTTTCAGAGCTTTGCGCTGCAAAATCCAGTGTCTACCA 60
DB 280 GGCACACTTTTGGGATGTTGCTTTCAGAGCTTTGCGCTGCAAAATCCAGTGTCTACCA 339
QY 61 GTGTGAAGAATTCAGCTGGAACAGCACTGCTCCGCCGAGTTCATTTGTAATTCAC 120
DB 340 GTGTGAAGAATTCAGCTGGAACAGCACTGCTCCGCCGAGTTCATTTGTAATTCAC 399
QY 121 GGTGAACGTTTAAGACATGTGTGAGAAAGAAAGATGATGAGCAAAAGTCCGAGATCATGTA 180
DB 400 GGTGAACGTTTAAGACATGTGTGAGAAAGAAAGATGATGAGCAAAAGTCCGAGATCATGTA 459
QY 181 CGGCAAGTCTGTGATCATCAGCGGCTGTCTATGCTGCTGCGGGATCAGATGCTT 240
DB 460 CGGCAAGTCTGTGATCATCAGCGGCTGTCTATGCTGCTGCGGGATCAGATGCTT 519
QY 241 CTGCTCCCAAGGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 300
DB 520 CTGCTCCCAAGGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 579
QY 301 CGGCGCAAGGCGCCAAAGAAAGGGGAAGTTCGCTGCGGCTCAGGCGCAGAGGCTCCGCAC 360
DB 580 CGGCGCAAGGCGCCAAAGAAAGGGGAAGTTCGCTGCGGCTCAGGCGCAGAGGCTCCGCAC 639
QY 361 CACCATCCTGTTCTCAAAATTAAGCCCTCTTCTGCGACACTGCTGAAGTGAAGAGATG 420
DB 640 CACCATCCTGTTCTCAAAATTAAGCCCTCTTCTGCGACACTGCTGAAGTGAAGAGATG 699
QY 421 CCACCCCTCTGATGTTCTTTCAGAGCCCTGCGCCCAACCCCACTCCCTGAGTGA 480
DB 700 CCACCCCTCTGATGTTCTTTCAGAGCCCTGCGCCCAACCCCACTCCCTGAGTGA 759
QY 481 GTTTCCTCTGGGTGCTCTTTTATTTCTGGGTAGGAGCGGGAGTCCGTGTTCTTTGTT 540

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Qy	241	CTGTCCTCCCAAGGAAACTGA	CTCACTGTTTGCATACAGTGTGCAACACCCCTTTGTA	300
Db	241	CTCTCTCCCAAGGAAACTGA	CTCACTGTTTGCATACAGTGTGCAACACCCCTTTGTA	300
Qy	301	CGGCGCAAGGCCAAGAA	AAAGGGGAAGTTCCTGCTCGCCCTCAGGCCAGGAGCTCGGAC	360
Db	301	CGGCGCAAGGCCCAAGAA	AAAGGGGAAGTTCCTGCTCGGCCCTCAGGCCAGGAGCTCGGAC	360
Qy	361	CACCAATCTGTCTTCA	AAATTAAGCCCTTTCTCGGCACTGCTGAAGCTGAAGAGATG	420
Db	361	CACCAATCTGTCTTCA	AAATTAAGCCCTTTCTCGGCACTGCTGAAGCTGAAGAGATG	420
Qy	421	CCACCCCTCTCATGTTG	TTCTTCAGGCTTCGGCCCAACCCCAACCTCCTGAGTGA	480
Db	421	CCACCCCTCTCATGTTG	TTCTTCAGGCTTCGGCCCAACCCCAACCTCCTGAGTGA	480
Qy	481	GTTCCTTCTGGGTGTC	CTTTATATCTGGGTAGGAGGCGGAGTCCGTCTCTTTGTT	540
Db	481	GTTCCTTCTGGGTGTC	CTTTATATCTGGGTAGGAGGCGGAGTCCGTCTCTTTGTT	540
Qy	541	CCCTGGAATTAATTA	GAAGAGCTCGTAAGACATTCATAATTAATTAATTAAGCTGACTGAAT	600
Db	541	CCCTGGAATTAATTA	GAAGAGCTCGGTAAAGAGCTCGGTAAAGACATTCATAATTAATTAAGCTGACTGAAT	600
Qy	601	TTTCAGTATGTACTTGA	AGGAAGAGGTGAGTGAAGTTACCCCACTGCTGTGTAAC	660
Db	601	TTTCAGTATGTACTTGA	AGGAAGAGGTGAGTGAAGTTACCCCACTGCTGTGTAAC	660
Qy	661	CGGAGTCAAGGCCAG	GCTGGCAGAGTCACTCTTTGAAGTACTGAGGTGGGATCGGC	720
Db	661	CGGAGTCAAGGCCAG	GCTGGCAGAGTCACTCTTTGAAGTACTGAGGTGGGATCGGC	720
Qy	721	TTTTGTAAGGCTTCA	GTGTCATTCCTCGATGGGGGCAATAGTTGAGACTGACGA	780
Db	721	TTTTGTAAGGCTTCA	GTGTCATTCCTCGATGGGGGCAATAGTTGAGACTGACGA	780
Qy	781	GTGAGAGTGACGTTT	CTTTAGGGCTGAGGGCCACTCCACTAAGGCTCCCTCGCTG	840
Db	781	GTGAGAGTGACGTTT	CTTTAGGGCTGAGGGCCACTCCACTAAGGCTCCCTCGCTG	840
Qy	841	ACATTCAAACTTCAT	TGCTCTGTGAAAACCAATCTCTGCAAGCAAAATGGCTGTTCGGCG	900
Db	841	ACATTCAAACTTCAT	TGCTCTGTGTGAAAACCAATCTCTGCAAGCAAAATGGCTGTTCGGCG	900
Qy	901	CTGAGTTGGGCTCTA	GTGACTCGAGACTCAATGACTGGGACTTAAAGTGGGGCTCGGCT	960
Db	901	CTGAGTTGGGCTCTA	GTGACTCGAGACTCAATGACTGGGACTTAAAGTGGGGCTCGGCT	960
Qy	961	CGCTCGAAAAGTGCT	TAAAGAAATCTTCCAGTTCTCTTCAAGAGACTGGCGCGG	1020
Db	961	CGCTCGAAAAGTGCT	TAAAGAAATCTTCCAGTTCTCTTCAAGAGACTGGCGCGG	1020
Qy	1021	ACGCGAAGAGCA	CGGGCGCTGCAAAACGGGCGCTGTCCGTTGTGAGTGCATGTA	1080
Db	1021	ACGCGAAGAGCA	CGGGCGCTGCAAAACGGGCGCTGTCCGTTGTGAGTGCATGTA	1080
Qy	1081	CGGCGAGGGCTTCT	CGTGTGGTGGCGTGTGCAACGACAGCGGCGGACACACACTTTC	1140
Db	1081	CGGCGAGGGCTTCT	CGTGTGGTGGCGTGTGCAACGACAGCGGCGGACACACACTTTC	1140
Qy	1141	ACGAACACCCGCG	CAAACTGCTCGGAGAGACCGGTAGAGAGCGGGTTGATGACCGAG	1200
Db	1141	ACGAACACCCGCG	CAAACTGCTCGGAGAGACCGGTAGAGAGCGGGTTGATGACCGAG	1200
Qy	1201	CTGAGGTAGAAAA	ACGTCCTCCGAAGAGGAGAGATCATGTAGCCCGGAAGTAGAGAC	1260
Db	1201	CTGAGGTAGAAAA	ACGTCCTCCGAAGAGGAGAGATCATGTAGCCCGGAAGTAGAGAC	1260
Qy	1261	CTGCTGCAGTCTG	CTGTTGGGTTTGGCGCAGACATGATCTCTCCGATCTGTGTTGGCATC	1320
Db	1261	CTGCTGCAGTCTG	CTGTTGGGTTTGGCGCAGACATGATCTCTCCGATCTGTGTTGGCATC	1320
Qy	1321	CAGCATACGGCC	AAATGTCAACAATCAAGCCCTTGGGCAACACAGCAAGGAGGAGAGAC	1380

Db	1321	CAGCATTCGGCCAAATGTCAACAAATCAGCCCTCGGGCAGACACGAGCAGGAGGAGAC	1380
QY	1381	AGAGAAAAGAAAAACACAGCATATGAAACACATAAATGAAATTAACCTAAATATATTAG	1440
Db	1381	AGAGAAAAGAAAAACACAGCATATGAAACACAGTAATGATATAAACCTTAATTAATRTTTAG	1440
QY	1441	CCCTCTGTTCTGTGCTTTACTGTGCCAGGAAATGATCCAAATTTTCAGTGTGGACTTGA	1500
Db	1441	CCCTCTGTTCTGTGCTTTACTGTGCCAGGAAATGATCCAAATTTTCAGTGTGGACTTGA	1500
QY	1501	CAGTCTCTTTGGCCACAGCAGAGAGAAATTTAACTCTTTCAAAACCCGGGGAGTTGG	1560
Db	1501	CAGTCTCTTTGGCCACAGCAGAGAGAAATTTAACTCTTTCAAAACCCGGGGAGTTGG	1560
QY	1561	CTGTGTTAAAGAAAGACCATTAATAGTGTATAGCAGTGTAAAAAATTTTTTTTTTTTTTTT	1619
Db	1561	CTGTGTTAAAGAAAGACCATTAATAGTGTATAGCAGTGTAAAAAATTTTTTTTTTTTTTTT	1619

RESULT 2

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1 Sequence 211, Application US/098252594
2
3 Patent No. US/2002004491A1
4
5 GENERAL INFORMATION:
6
7 APPLICANT: Xu, Jiangchun
8
9 APPLICANT: Stolk, John A.
10
11 APPLICANT: Algate, Paul A.
12
13 APPLICANT: Fling, Steven P.
14
15 TITLE OF INVENTION: COMPOSITIONS AND METHODS
16
17 FILE REFERENCE: 210121.48465
18
19 CURRENT APPLICATION NUMBER: US/09/825,294
20
21 CURRENT FILING DATE: 2001-04-03
22
23 NUMBER OF SEQ ID NOS: 215
24
25 SOFTWARE: FastSeq for Windows Version 3.0.0
26
27 SEQ. ID NO. 211
28
29 LENGTH: 1619
30
31 TYPE: DNA
32
33 ORGANISM: Homo sapiens
34
35 US-09-825-294-211

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Query Match	100.0%;	Score 1619;	DB 10;	Length 1619;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1619;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	1	GGGAACTTTTTCGGATTGTTCTTGCTTCCAGGGCTTTGGGTGTAATTCAGTGTCTACCA	60
QY	61	GGTGTGAAGAAATTCACGCTGCAACACGACTGGCTCCGCCGAGTTCAATTTGAAATTCAC	120
Db	61	GGTGTGAAGAAATTCACGCTGCAACACGACTGGCTCCGCCGAGTTCAATTTGAAATTCAC	120
QY	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAGCAAGTCCCGGATCATGTA	180
Db	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAGCAAGTCCCGGATCATGTA	180
QY	181	CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTCTGCGGGATACCAAGTCTT	240
Db	181	CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTCTGCGGGATACCAAGTCTT	240
QY	241	CTGCTCTCCCGAGGAAATCTAATCTCAAGTCTGCATCAGCTGTGTGCAACACCCTCTTTGTA	300
Db	241	CTGCTCTCCCGAGGAAATCTAATCTCAAGTCTGCATCAGCTGTGCAACACCCTCTTTGTA	300
QY	301	CGGGCCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCCCGGCGCTCAAGGCAGAGGCTCCGCAC	360
Db	301	CGGGCCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCCCGGCGCTCAAGGCAGAGGCTCCGCAC	360
QY	361	CACCATCTCTTCTCTCAAAATTAAGCCCTCTTCTCGGCACACTGTGAACTGAAGAGATG	420
Db	361	CACCATCTCTTCTCTCAAAATTAAGCCCTCTTCTCGGCACACTGTGAACTGAAGAGATG	420

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1619	100.0	1619	US-09-825-294-205	Sequence 205, App
2	1619	100.0	1619	US-09-825-294-211	Sequence 211, App
3	1396	86.2	1897	US-09-825-294-214	Sequence 214, App
4	486	30.0	625	US-09-825-294-210	Sequence 210, App
5	486	30.0	625	US-09-825-294-210	Sequence 210, App
6	386	23.8	1362	US-09-825-294-208	Sequence 10876, A
7	315	19.5	369	US-09-825-294-199	Sequence 208, App
8	315	19.5	373	US-09-825-294-199	Sequence 199, App
9	310	19.1	396	US-09-825-294-8	Sequence 1516, App
10	307	19.0	349	US-09-825-294-8	Sequence 9, App1
11	271	16.7	1010	US-09-825-294-212	Sequence 212, App
12	264	16.3	409	US-09-825-294-212	Sequence 212, App
13	156	10.3	201	US-09-825-294-212	Sequence 212, App
14	154	9.5	390	US-09-825-294-212	Sequence 8894, App
15	146	9.0	480	US-09-825-294-213	Sequence 1532, App
16	125	7.7	381	US-09-825-294-213	Sequence 213, App
17	120	7.4	430	US-09-825-294-213	Sequence 7826, App
18	112	6.9	558	US-09-825-294-213	Sequence 4251, App
19	27	1.7	1368	US-09-825-294-213	Sequence 2375, App

C 20	25	1.5	152	10	US-09-960-352-9079	Sequence 9079, App
C 21	25	1.5	363	10	US-09-867-701-4911	Sequence 4911, App
C 22	25	1.5	395	10	US-09-867-701-5174	Sequence 5174, App
C 23	25	1.5	568	10	US-09-919-580-143	Sequence 143, App
C 24	25	1.5	2968	10	US-09-925-301-584	Sequence 584, App
C 25	24	1.5	208	10	US-09-770-696-104	Sequence 104, App
C 26	24	1.5	258	10	US-09-920-300A-58	Sequence 58, App1
C 27	24	1.5	258	10	US-09-920-300A-58	Sequence 58, App1
C 28	24	1.5	258	10	US-09-920-300A-58	Sequence 58, App1
C 29	24	1.5	419	10	US-09-770-791-315	Sequence 315, App
C 30	24	1.5	466	10	US-09-924-035A-439	Sequence 439, App
C 31	24	1.5	871	10	US-10-062-254-125	Sequence 125, App
C 32	24	1.5	939	12	US-10-078-920-627	Sequence 627, App
C 33	24	1.5	1029	10	US-09-925-300-89	Sequence 89, App1
C 34	24	1.5	1046	10	US-09-800-528-5	Sequence 384, App
C 35	24	1.5	1066	10	US-09-764-870-15	Sequence 15, App1
C 36	24	1.5	1190	10	US-09-410-194-14	Sequence 14, App1
C 37	24	1.5	1337	9	US-09-992-598-286	Sequence 286, App
C 38	24	1.5	1337	10	US-09-989-722-286	Sequence 286, App
C 39	24	1.5	1337	10	US-09-989-723-286	Sequence 286, App
C 40	24	1.5	1337	10	US-09-989-723-286	Sequence 286, App
C 41	24	1.5	1337	10	US-09-989-727-286	Sequence 286, App
C 42	24	1.5	1337	10	US-09-989-731-286	Sequence 286, App
C 43	24	1.5	1337	10	US-09-989-732-286	Sequence 286, App
C 44	24	1.5	1337	10	US-09-991-073-286	Sequence 286, App
C 45	24	1.5	1337	10	US-09-990-442-286	Sequence 286, App

#### ALIGNMENTS

RESULT 1  
US-09-825-294-205  
Sequence 205, Application US/09825294  
Patent No. US2002004491A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Algate, Paul A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C5  
CURRENT APPLICATION NUMBER: US/09/825,294  
CURRENT FILING DATE: 2001-04-03  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 205  
LENGTH: 1619  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-825-294-205

Query Match	100.0%	Score 1619;	DB 10;	Length 1619;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1619;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY 1	GGCACTTTTGGGATTTGTTCTGCTCCAGGCTTTGGCTGCAATTCAGTCTACCA	60		
DB 1	GGCACTTTTGGGATTTGTTCTGCTCCAGGCTTTGGCTGCAATTCAGTCTACCA	60		
QY 61	GTTGGAAGATTCACAGCTGACAGACGCTGCTCCCGGAGTTCATTGGAATTCAC	120		
DB 61	GTTGGAAGATTCACAGCTGACAGACGCTGCTCCCGGAGTTCATTGGAATTCAC	120		
QY 121	GGTGAAGCTTCAAGACATGTGTCAGAAAGAGTGAAGCAAGTGGCGGATCATGTA	180		
DB 121	GGTGAAGCTTCAAGACATGTGTCAGAAAGAGTGAAGCAAGTGGCGGATCATGTA	180		
QY 181	CCGCAAGTCTGTCATATCAGCGCGCTGCTCATGCTGCTGCGGATACCAAGTCTCT	240		
DB 181	CCGCAAGTCTGTCATATCAGCGCGCTGCTCATGCTGCTGCGGATACCAAGTCTCT	240		

182

CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.

XX  
SQ Sequence 51 BP; 9 A; 5 C; 10 G; 27 T; 0 other;

Query Match 1.5%; Score 25; DB 22; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1393 AACACAGCATGAGACACAGTAAT 1417  
|||||  
DB 51 AACACAGCATGAGACACAGTAAT 27

Search completed: November 7, 2002, 18:15:59  
Job time : 343.774 secs

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

Query Match	1.6%	Score 26	DB 22	Length 50
Best Local Similarity	100.0%	Pred. No. 1.1		
Matches 26	Conservative 0	Mismatches 0	Indels 0	Gaps 0

RESULT 44  
AAC84571  
ID AAC84571 standard; cDNA; 2481 BP.  
XY

02-APR-2001 (first entry)

soybean; ss.

Key	Location/Qualifiers
EH	
FT	
CDS	9..2261

PD 14-DEC-2000

02-JUN-2000; 2000WO-US15351.

04-JUN-1999; 99US-0137461.

( DUFO ) DU PONT DE NEMOURS & CO E I.

buciel ah, Fainodu UU, Gutteridge S, Maxwell CA

P-P\$DB: AAB48252

Isolated nucleic acid fragments analyzed by electrophoresis

for traits linked to these genes, and in plant breeding for traits linked to these genes, as markers

Claim 2; Page 59-60; 103pp; English

Sequence 2481 BP; 783 A; 489 C; 589 G; 620 T; 0 other.

Query Match	1.68;	Score 26;	DB 22;	Length 2481;
Best Local Similarity	100.08;	Pred. No. 0.64;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1594	CAGTGTAAAAAAAAAAAAAAAA	1615
Db	2424	CAGTGTAAAAAAAAAAAAAAAA	2449

RESULT 45  
AAL27277/c  
ID AAL27277 standard; DNA; 51 BP

AC AAL27277

DI 44-JAN-2002 (first entry)  
XY

Human SNP oligonucleotide #485.

KW immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclic; polymerase; oncogene; histone; kinase; colony stimulating factor  
KW complement related protein; cyclochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001

28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.  
37 DEC 2000 0173419  
DE

AA  
PA (CIRBA-) CIRBAEN CORR

Shimkets BA Teach M

WPI: 2001-465210/50

Polymorphic nuclei

PT cancer, autoimmune diseases and infections -  
antibodies and "abnormal" useful for diagnosing and treating, e.g.

Claim 1; Page 1529; 4143pp; English

variants of proteins related to amylases, amyloid proteins, angiotensin



XX Shinkets RA, Leach M;  
 XX WPI: 2001-465210/50.  
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX  
 PS Claim 1: Page 3450; 4143pp: English.  
 CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.  
 CC  
 SQ Sequence 50 BP; 11 A; 16 C; 10 G; 13 T; 0 other;  
 Query Match 1.6%; Score 26; DB 22; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 933 GACTGGACTTAGCTGGGGCTCGGC 958  
 Db 50 GACTGGACTTAGCTGGGGCTCGGC 25  
 RESULT 42  
 AAL33985/c  
 ID AAL33985 standard; DNA; 50 BP.  
 XX  
 AC AAL33985:  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human SNP oligonucleotide #7193.  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US35498.  
 XX  
 PR 28-DEC-1999; 99US-0173419.  
 PR 27-DEC-2000; 2000US-0173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach M;  
 XX

DR WPI: 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX  
 PS Claim 1: Page 3451; 4143pp: English.  
 CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.  
 CC  
 SQ Sequence 50 BP; 14 A; 13 C; 17 G; 6 T; 0 other;  
 Query Match 1.6%; Score 26; DB 22; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1285 GCCGACCATGATCCTCGAATCTG 1310  
 Db 26 GCCGACCATGATCCTCGAATCTG 1  
 RESULT 43  
 AAL33986/c  
 ID AAL33986 standard; DNA; 50 BP.  
 XX  
 AC AAL33986:  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human SNP oligonucleotide #7194.  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US35498.  
 XX  
 PR 28-DEC-1999; 99US-0173419.  
 PR 27-DEC-2000; 2000US-0173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach M;  
 XX  
 DR WPI: 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,



PI Algate PA, Harlocker SL, Jones R;  
 XX WPI: 2002-122075/16.  
 XX  
 XX Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide -  
 XX  
 XX

PS Claim 1; SEQ ID 4251; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumor  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (II) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (S1) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient, where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumor protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumor polypeptides  
 CC and proteins in tumor cells; and to isolate a full length gene from a  
 CC suitable library e.g., a tumor cDNA library using well known  
 CC techniques.  
 CC  
 XX

SQ Sequence 430 BP: 92 A; 121 C; 108 G; 109 T; 0 other;

Query Match 7.4%; Score 120; DB 24; Length 430;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-38;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 431 CTGATGTTCTTCCAGCCGCGCCCAACCCCAACCTCCTGAGTGTCTTCTG 490  
 DB 182 CTGATGTTCTTCCAGCCGCGCCCAACCCCAACCTCCTGAGTGTCTTCTG 241  
 OY 491 GGTGTCCTTTATCTGAGGAGGAGGAGTCCGTTCTTTCTTCTGTCGAAA 550  
 DB 242 GGTGTCCTTTATCTGAGGAGGAGGAGTCCGTTCTTTCTTCTGTCGAAA 301

RESULT 38

ABL79397  
 ID ABL79397 standard; cDNA: 558 BP.

AC ABL79397;

DT 17-MAY-2002 (first entry)

XX Human ovarian cancer related cDNA clone SEQ ID NO:2375.

XX Human; ovarian cancer; ovarian tumor; cytosolic; gene: ss.

XX Homo sapiens.

XX WO200192581-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US17756.

XX 26-MAY-2000; 2000US-207484P.

XX (CORI-) CORIXA CORP.

XX Algate PA, Harlocker SL, Jones R;

XX WPI: 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide -  
 XX  
 XX

PS Claim 1; SEQ ID 2375; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumor  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (II) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (S1) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient, where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumor protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumor polypeptides  
 CC and proteins in tumor cells; and to isolate a full length gene from a  
 CC suitable library e.g., a tumor cDNA library using well known  
 CC techniques.  
 CC  
 XX

SQ Sequence 558 BP: 147 A; 133 C; 166 G; 106 T; 6 other;

Query Match 6.9%; Score 112; DB 24; Length 558;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1138 TGCAAGAACACCCCGCAACCTGCTGAGACACCGTACAGAGCGGTTGATGACC 1197  
 DB 142 TGCAAGAACACCCCGCAACCTGCTGAGACACCGTACAGAGCGGTTGATGACC 201  
 OY 1198 GAGCTGAGGTGAAAAGAGTCTCCGAGAGGAGGAGGATCATGTAGCC 1249  
 DB 202 GAGCTGAGGTGAAAAGAGTCTCCGAGAGGAGGAGGATCATGTAGCC 253

RESULT 39

ABN41977/C  
 ID ABN41977 standard; DNA: 60 BP.

AC ABN41977;

DT 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:14725.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

XX splice variant; transcriptome; oligonucleotide library: ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB01903.

XX 28-JUL-2000; 2000US-221607P.

XX 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.



PT polypeptide -  
XX  
PS Claim 1: SEQ ID 1532; 489pp; English.  
XX  
CC The present invention describes a composition (I) comprising: carriers  
CC and immunostimulants; and a polynucleotide (II) of an ovarian tumour  
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
CC population of (II), or antigen presenting cells that express (II).  
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
CC (S1) can be used for detecting ovarian cancer in a patient's biological  
CC sample preferably serum or ovarian tissue. The method comprises  
CC contacting a biological sample from a patient with (IV), detecting the  
CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
CC patient, where the amount of polynucleotide hybridising to (IV) is  
CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
CC specific for an ovarian tumour protein comprising contacting T cells  
CC with (III) or (II). (III) is useful in design and preparation of  
CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
CC and proteins in tumour cells; and to isolate a full length gene from a  
CC suitable library e.g., a tumour cDNA library using well known  
CC techniques.  
XX  
SQ Sequence 390 BP; 121 A; 82 C; 99 G; 86 T; 2 other:  
XX  
Query Match 9.5%; Score 154; DB 24; Length 390;  
Best Local Similarity 100.0%; Pred. No. 3.1e-52;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1358 AGACACGACGAGGAGGAGACAGAGAAAGAAACACAGATGAGACAGTAAT 1417  
DB 147 AGACACGACGAGGAGGAGACAGAGAAAGAAACACAGATGAGACAGTAAT 206  
QY 1418 GAATTAACCATTAATATTAGCCCTCTGTCTGTCTTACTGCGCAGGAATGTAC 1477  
DB 207 GAATTAACCATTAATATTAGCCCTCTGTCTGTCTTACTGCGCAGGAATGTAC 266  
QY 1478 CAATTTTCACTGTGACCTTGACAGCTTCTTT 1511  
DB 267 CAATTTTCACTGTGACCTTGACAGCTTCTTT 300  
RESULT 34  
ABT03283  
ID ABT03283 standard; cDNA; 480 BP.  
XX  
XX ABT03283;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 213.  
DE  
XX  
XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
KW  
XX  
XX cytosolic; gene; ss.  
OS  
XX  
XX Homo sapiens.  
PN  
XX  
XX WO200239885-A2.  
PD  
XX  
XX 23-MAY-2002.  
PF  
XX  
XX 13-NOV-2001; 2001WO-US45395.  
PR  
XX  
XX 14-NOV-2000; 2000US-0713550.  
PR  
XX  
XX 03-APR-2001; 2001US-0825294.  
PR  
XX  
XX 02-OCT-2001; 2001US-0970966.  
XX  
XX (CORI-) CORIXA CORP.  
PA  
XX  
XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;  
PI

XX  
DR WPI: 2002-500186/53.  
XX  
PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
PT detecting the presence of ovarian cancer in a patient, and in  
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
PT  
XX  
PS Claim 2: Page 196; 197pp; English.  
XX  
XX The present invention provides human ovarian cancer associated proteins  
XX and coding sequences. The sequences can be used in the diagnosis and  
XX treatment of ovarian cancers. The present sequence is a coding sequence  
XX of the invention.  
SQ Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other:  
XX  
Query Match 9.0%; Score 146; DB 24; Length 480;  
Best Local Similarity 99.5%; Pred. No. 5e-49;  
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGCACCTTTTGGGATGTCCTTCAGCTTCGCTGCAATTCAGTCTACCA 60  
DB 280 GGCACCTTTTGGGATGTCCTTCAGCTTCGCTGCAATTCAGTCTACCA 339  
QY 61 GTGTGAAGATTCACGCTGACACGACTGCTCCGCCGAGTTGATTTGAC 120  
DB 340 GTGTGAAGATTCACGCTGACACGACTGCTCCGCCGAGTTGATTTGAC 399  
QY 121 GGTGACGCTTCAGACATGTCGTCAGAAAGATGATGAGCAAGTGCAGATCATGTA 180  
DB 400 GGTGACGCTTCAGACATGTCGTCAGAAAGATGATGAGCAAGTGCAGATCATGTA 459  
QY 181 CCGCAAGTCTGTGCAT 197  
DB 460 CCGCAAGTCTGTGCAT 476  
RESULT 35  
ABLA0351  
ID ABLA0351 standard; cDNA; 480 BP.  
XX  
XX ABLA0351;  
AC  
XX  
XX 28-JUN-2002 (first entry)  
DT  
XX  
XX Ovarian carcinoma BE33607 nucleotide sequence.  
DE  
XX  
XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
KW  
XX  
XX ss.  
OS  
XX  
XX Homo sapiens.  
PN  
XX  
XX US2002004491-A1.  
PD  
XX  
XX 10-JAN-2002.  
PF  
XX  
XX 03-APR-2001; 2001US-0825294.  
PR  
XX  
XX 10-SEP-1999; 99US-0394374.  
PR  
XX  
XX 01-MAY-2000; 2000US-0561778.  
PR  
XX  
XX 15-AUG-2000; 2000US-0640173.  
PR  
XX  
XX 07-SEP-2000; 2000US-0656668.  
PR  
XX  
XX 14-NOV-2000; 2000US-0713550.  
XX  
XX (XUJ/) XU J.  
XX  
XX (STOLK/) STOLK J A.  
XX  
XX (ALGATE/) ALGATE P A.  
XX  
XX (FLING/) FLING S P.  
XX  
XX Xu J, Stolk JA, Algate PA, Fling SP;  
PI WPI: 2002-171027/22.



QY 211 TCTCATGCGCTCTGCGGGGTACCACTCTTGTCTCCCGAGGAAACTGAATCAGTTTG 270  
 |||  
 DB 438 TCTCATGCGCTCTGCGGGGTACCACTCTTGTCTCCCGAGGAAACTGAATCAGTTTG 497  
 QY 271 CATCAGCTCTGCACACCCCTCTTTGTAAC 301  
 |||  
 DB 498 CATCAGCTCTGCACACCCCTCTTTGTAAC 528

## RESULT 30

ABL81262/c  
 ID ABL81262 standard; cDNA; 409 BP.

AC ABL81262;

XX 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:4240.

XX Human: ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

XX MO200192581-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001MO-US17756.

XX 26-MAY-2000; 2000US-207484P.

XX (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

XX WPI: 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide

PS Claim 1; SEQ ID 4240; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (S1) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient, where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumour protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
 CC and proteins in tumour cells; and to isolate a full length gene from a  
 CC suitable library e.g., a tumour cDNA library using well known  
 CC techniques.

XX Sequence 409 BP; 89 A; 106 C; 87 G; 127 T; 0 other;

XX Query Match 16.3%; Score 264; DB 24; Length 409;

XX Best Local Similarity 99.7%; Pred. NO. 2e-96;  
 Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1285 GCCGACGACATATCTCTCGAATCTGTTGGGCAATCCAGCATAGCGGCAATGTCACAAACA 1344

DB |||  
 DB 315 GCCGACGACATATCTCTCGAATCTGTTGGGCAATCCAGCATAGCGGCAATGTCACAAACA 256  
 QY 1345 ATCAGCCCTGGGCGACACACGACGAGGAGAGACAGACAGAAAAAGAAAAACACACATGA 1404  
 |||  
 DB 255 ATCAGCCCTGGGCGACACACGACGAGGAGGAGAGACAGAAAAAGAAAAACACACATGA 196  
 QY 1405 GAGACAGTAATGAATTAACCATTAATATTTAGCCCTCTGTTGCTTACTGGC 1464  
 |||  
 DB 195 GAGACAGTAATGAATTAACCATTAATATTTAGCCCTCTGTTGCTTACTGGC 136  
 QY 1465 GAGAAATGTTACCAATTTTTCAGTTGAGCTTGACAGCTTCTTTGCGCAAGCAAGA 1524  
 |||  
 DB 135 CAGGAATGTTACCAATTTTTCAGTTGAGCTTGACAGCTTCTTTGCGCAAGCAAGA 76  
 QY 1525 GAGAAATTTAACCACTTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACCATTTAA 1584  
 |||  
 DB 75 GAGAAATTTAACCACTTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACCATTTAA 16  
 QY 1585 TGCTTTAGACAGTGT 1599  
 |||  
 DB 15 TGCTTTAGACAGTGT 1

## RESULT 31

AAF94044  
 ID AAF94044 standard; DNA; 591 BP.

AC AAF94044;

DT 23-MAY-2001 (first entry)

DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 478.

XX Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; PCR primer; ss.

XX Synthetic.

XX EP1067182-A2.

XX 10-JAN-2001.

XX 07-JUL-2000; 2000EP-0114090.

XX 08-JUL-1999; 99JP-0194179.

XX 11-JAN-2000; 2000JP-0118775.

XX 02-MAY-2000; 2000JP-0183766.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI: 2001-093989/11.

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development -

PS Claim 4; SEQ ID 478; 609pp + CD ROM; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by  
 CC AAB88317 - AAB88419. Included in the invention are primers  
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
 CC cDNA sequences of the invention. The invention also includes methods for  
 CC the production of antibodies directed against the proteins, and cDNA  
 CC sequences, which can be used in vaccines. The polynucleotide sequences  
 CC can be used in gene therapy. The polynucleotide sequences and the  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate secretory  
 CC protein/membrane protein expression. The nucleic acids and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays  
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the

ABT03282	
ID	ABT03282 standard; cDNA; 1010 BP.
XX	
AC	ABT03282:
XX	
DT	05-SEP-2002 (first entry)
XX	
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 212.
XX	
KW	Human; ovarian cancer; ovarian carcinoma; gene therapy; Immunotherapy;
XX	Cytosolic; gene; ss.
OS	Homo sapiens.
PX	
PN	M0200239885-A2.
XX	
PD	23-MAY-2002.
PF	
XX	13-NOV-2001; 2001WO-US45395.
XX	
PR	14-NOV-2000; 2000US-0713550.
XX	03-APR-2001; 2001US-0825284.
PR	02-OCT-2001; 2001US-0970966.
XX	(CORI-) CORIXA CORP.
PA	
XX	
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA.
XX	
DR	WPI; 2002-500186/53.
XX	
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for
PT	detecting the presence of ovarian cancer in a patient, and in
PT	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX	
PS	Claim 2: Page 195; 197pp; English.
XX	
CC	The present invention provides human ovarian cancer associated proteins
CC	and coding sequences. The sequences can be used in the diagnosis and
CC	treatment of ovarian cancers. The present sequence is a coding sequence
CC	of the invention.
XX	
SQ	Sequence 1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;
Query Match	16.7%; Score 271; DB 24; Length 1010;
Best Local Similarity	100.0%; Pred. No. 2.7e-99;
Matches 271; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	31 AGGCTTGCGGTGGGAATTCAGTGCACCAAGTGTAAAGATTCCAGCTGAACAACGACTG 90
DB	258 AGCGTTTCGCTGCATAATCCAGTGTACCAAGTGTAAAGAATTCCAGCTGAACAACGACTG 317
OY	91 CTCCTCCCCGAGTTGATTGTGAATTGCACGGGTGAACGTTCAAGCATTGTGCAGAAAGA 150
DB	318 CTCCTCCCCGAGTTGATTGTGAATTGCACGGGTGAACGTTCAAGCATTGTGTCAAGAAAG 377
OY	151 AGTATGAGACCAAGTGCAGGATCATGTACCGCAAGTCTGTGCATATCAGCGGCTG 210
DB	378 AGTATGAGACCAAGTGCAGGATCATGTACCGCAAGTCTGTGCATATCAGCGGCTG 437
OY	211 TCTCATGCCCTGCAGGAGTACAGACGCTTGTGCTCCCGACAGGAAATGAATCACTTTG 270
DB	438 TCTCATGCCCTGCAGGAGTACAGACGCTTGTGCTCCCGACAGGAAATGAATCACTTTG 497
OY	271 CATCAGCTGCTGCAACACCCTCTTTGTAAC 301
DB	498 CATCAGCTGCTGCAACACCCTCTTTGTAAC 528

AC	ABL40350;
XX	
DE	28-JUN-2002 (first entry)
DE	Ovarian carcinoma BF345141 nucleotide sequence.
XX	
KM	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX	ss.
OS	Homo sapiens.
PN	US2002004491-A1.
PD	
PF	10-JAN-2002.
XX	
PE	03-APR-2001; 2001US-0825294.
PR	
XX	10-SEP-1999; 99US-0394374.
PR	01-MAY-2000; 2000US-0561778.
PR	15-AUG-2000; 2000US-0640173.
PR	07-SEP-2000; 2000US-0656668.
PR	14-NOV-2000; 2000US-0713550.
PA	(XUJ/) XU J.
PA	(STOK/) STOLK J A.
PA	(ALCA/) ALGATE P A.
PI	(FLIN/) FLING S P.
XX	
PI	Xu J, Stolk JA, Algate PA, Fling SP;
XX	
XX	WPI; 2002-171027/22.
PT	
XX	Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX	prevention and/or treatment of cancer, especially ovarian cancer -
XX	
XX	Claim 1a; Page 126-127; 131pp; English.
CC	
CC	The invention relates to ovarian tumour polynucleotides and polypeptides
CC	that may be utilised in cancer therapy, for example in a vaccine or
CC	gene therapy. Polypeptides and polynucleotides of the invention are
CC	useful for detecting a cancer in a patient, for stimulating and/or
CC	expanding T-cells specific for a tumour protein, and for inhibiting the
CC	development of a cancer in a patient. They are also useful for
CC	stimulating an immune response in a patient, and for treating a cancer in
CC	a patient and for determining the presence of a cancer in a patient.
CC	The isolated polynucleotides of the invention are useful for their
CC	ability to selectively form duplex molecules with complementary stretches
CC	of the entire desired gene or gene fragments, and for designing and
CC	preparing ribozyme molecules for inhibiting expression of tumour
CC	polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC	invention are also useful in recombinant DNA molecules to direct
CC	expression of a polypeptide in appropriate host cells. The current
CC	sequence represents the ovarian carcinoma BF345141 nucleotide
CC	sequence.
SO	
Sequence	1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;
Query Match	16.7%; Score 271; DB 24; Length 1010;
Best Local Similarity	100.0%; Pred. No. 2,7e-99;
Matches 271; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Db	
258	AGGGTTGGCGCTGCATTCAGTGTGAAGAATTCCAGCTGAACAACGACTG 90
31	AGGGTTGGCGCTGCATTCAGTGTGAAGAATTCCAGCTGAACAACGACTG 90
Db	
258	AGGGTTGGCGCTGCATTCAGTGTGAAGAATTCCAGCTGAACAACGACTG 317
91	CCTCCTCCCCGAGTTCATGTGTAATGACGGGTGAACCTTGAAAGCATNGTGAGAAGA 150
318	CCTCCTCCCCGAGTTCATGTGTAATGACGGGTGAACCTTGAAAGCATNGTGAGAAGA 377
151	AGTAGTAGGAGCAAAAGTCCGGGAGTATGTACGCCAAGTCTGTGCATCATCACGGGCTG 210
378	AGTAGTAGGAGCAAAAGTCCGGGAGTATGTACGCCAAGTCTGTGCATCATCACGGGCTG 437



XX  
DR MPI: 2002-171027/22.  
XX  
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
PT prevention and/or treatment of cancer, especially ovarian cancer -  
XX  
XX  
PS Claim 1a: Page 41-42; 131pp; English.  
XX  
XX The invention relates to ovarian tumour polynucleotides and polypeptides  
CC that may be utilised in cancer therapy, for example in a vaccine or  
CC gene therapy. Polypeptides and polynucleotides of the invention are  
CC useful for detecting a cancer in a patient, for stimulating and/or  
CC expanding T-cells specific for a tumour protein, and for inhibiting the  
CC development of a cancer in a patient. They are also useful for  
CC stimulating an immune response in a patient, and for treating a cancer in  
CC a patient and for determining the presence of a cancer in a patient.  
CC The isolated polynucleotides of the invention are useful for their  
CC ability to selectively form duplex molecules, and for designing and  
CC preparing ribozyme molecules for inhibiting expression of tumour  
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
CC invention are also useful in recombinant DNA molecules to direct  
CC expression of a polypeptide in appropriate host cells. The sequences  
CC given in records ABL8760-ABL8956 represent polynucleotides encoding  
CC ovarian carcinoma proteins.  
XX  
XX  
SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other:  
Query Match 19.1%; Score 310; DB 24; Length 396;  
Best Local Similarity 100.0%; Pred. No. 6.7e-115;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGCAACCTTTTGGCGATGTTCTTCTCCAGGCTTTGGCGCTGCAATTCAGTGTACCA 60  
DB 11 GGCAACCTTTTGGCGATGTTCTTCTCCAGGCTTTGGCGCTGCAATTCAGTGTACCA 70  
OY 61 GTGGAAGAAATCCAGCTGAACAACGCTCTCTCCCGAGTTATTTGTAATGAC 120  
DB 71 GTGGAAGAAATCCAGCTGAACAACGCTCTCTCTCCCGAGTTATTTGTAATGAC 130  
OY 121 GGTGAAGCTTCAGATGTTCTGAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180  
DB 131 GGTGAAGCTTCAGATGTTCTGAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 190  
OY 181 CCGCAAGTCTGTCATCATCAGGCGCTGTCATCGCTCGCGGGTACAGTCCCT 240  
DB 191 CCGCAAGTCTGTCATCATCAGGCGCTGTCATCGCTCGCGGGTACAGTCCCT 250  
OY 241 CTGCTCCCGAGGAAGTGAAGTCACTGTTGATCAGCTGCTGCAACCCCTTTGTAA 300  
DB 251 CTGCTCCCGAGGAAGTGAAGTCACTGTTGATCAGCTGCTGCAACCCCTTTGTAA 310  
OY 301 CGGGCCAAAG 310  
DB 311 CGGGCCAAAG 320  
RESULT 27  
ABL79431/c  
ID ABL79431 standard; CDNA: 349 BP.  
XX  
XX ABL79431;  
AC  
XX 17-MAY-2002 (first entry)  
DT  
XX Human ovarian cancer related CDNA clone SEQ ID NO:2409.  
DE  
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene: ss.  
KM  
XX Homo sapiens.  
OS  
XX WO200192581-A2.  
PN  
XX

PD 06-DEC-2001.  
XX  
XX 29-MAY-2001; 2001WO-US17756.  
PF  
XX  
XX 26-MAY-2000; 2000US-207484P.  
PR  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Algate PA, Harlocker SL, Jones R;  
PI  
XX MPI: 2002-122075/16.  
DR  
XX  
XX Composition for therapy and diagnosis of ovarian cancer comprising  
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
PT polypeptide -  
PT polypeptide  
PS Claim 1: SEQ ID 2409; 489pp; English.  
XX  
XX The present invention describes a composition (I) comprising: carriers  
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
CC polypeptide encoded by a polynucleotide (III) having a CDNA sequence  
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
CC population of (II), or antigen presenting cells that express (II).  
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
CC (S1) can be used for detecting ovarian cancer in a patient's biological  
CC sample preferably serum or ovarian tissue. The method comprises  
CC contacting a biological sample from a patient with (IV), detecting the  
CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
CC patient, where the amount of polynucleotide hybridising to (IV) is  
CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
CC specific for an ovarian tumour protein comprising contacting T cells  
CC with (III) or (II). (III) is useful in design and preparation of  
CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
CC and proteins in tumour cells; and to isolate a full length gene from a  
CC suitable library e.g., a tumour CDNA library using well known  
CC techniques.  
XX  
XX  
SQ Sequence 349 BP; 79 A; 84 C; 78 G; 108 T; 0 other:  
Query Match 19.0%; Score 307; DB 24; Length 349;  
Best Local Similarity 100.0%; Pred. No. 1.1e-113;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1292 CCATGATCCTCCGAAATCGTGGGCAATCCAGATACGGCCATGTCACAAATCAGCC 1351  
DB 310 CCATGATCCTCCGAAATCGTGGGCAATCCAGATACGGCCATGTCACAAATCAGCC 251  
OY 1352 CTGGGCAACAGCAG 1411  
DB 250 CTGGGCAACAGCAG 191  
OY 1412 GTAATGTAATAAACATTAATATTTAGCCCTCTGCTGCTTACTGCGCCAGGAA 1471  
DB 190 GTAATGTAATAAACATTAATATTTAGCCCTCTGCTGCTTACTGCGCCAGGAA 131  
OY 1472 TGGTACCAATTTTTCAGTGTGAGACTTCTTTTGCACAAAGAGAGAGAAAT 1531  
DB 130 TGGTACCAATTTTTCAGTGTGAGACTTCTTTTGCACAAAGAGAGAGAAAT 71  
OY 1532 TAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAGACATTAATGCTTTA 1591  
DB 70 TAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAGACATTAATGCTTTA 11  
OY 1592 GACAGTG 1598  
DB 10 GACAGTG 4  
RESULT 28

PS Claim 5: Page 119, 189pp; English.

XX  
CC The present invention provides a number of coding sequences and proteins,  
CC the over-expression of which is associated with ovarian carcinoma/cancer.  
CC These can be used in the diagnosis, treatment and prevention of ovarian  
CC cancer, optionally by gene therapy or in the form of a vaccine. The  
CC present sequence is an example of one of these sequences.

XX  
SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match 19.1%; Score 310; DB 22; Length 396;  
Best Local Similarity 100.0%; Pred. No. 6,7e-115;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACATTTTTCGGGATTTGTTCTTCTTCACAGCTTTGCGGCAAAATCCAGTGTACCA 60  
DB 11 GGCACATTTTTCGGGATTTGTTCTTCTTCACAGCTTTGCGGCAAAATCCAGTGTACCA 70  
QY 61 GTGTGAAGAATTCACAGCTGTGAACACGACTGCTCTCCCGAGTTCAATTGTGAATTCAC 120  
DB 71 GTGTGAAGAATTCACAGCTGTGAACACGACTGCTCTCCCGAGTTCAATTGTGAATTCAC 130  
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGTGAAGAGAACTGCGGGATCATGTA 180  
DB 131 GGTGAACGTTCAAGACATGTGTCAAGAAAGTGAAGAGAACTGCGGGATCATGTA 190  
QY 181 CCGCAAGTCTGTGTCATCATCAGCGGCTGTCTCATCGCTCTGCGGGATCATGTA 240  
DB 191 CCGCAAGTCTGTGTCATCATCAGCGGCTGTCTCATCGCTCTGCGGGATCATGTA 250  
QY 241 CTGCTCCCGAGGAAACGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 251 CTGCTCCCGAGGAAACGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 310  
QY 301 CGGGCCCAAG 310  
DB 311 CGGGCCCAAG 320

#### RESULT 25

ABT03085

ID ABT03085 standard; cDNA; 396 BP.

AC ABT03085;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 9.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001MO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR MPI; 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for

PT detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PT  
XX  
XX Example 1; Page 116, 197pp; English.

XX  
CC The present invention provides human ovarian cancer associated proteins  
CC and coding sequences. The sequences can be used in the diagnosis and  
CC treatment of ovarian cancers. The present sequence is a coding sequence  
CC of the invention.

XX  
SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match 19.1%; Score 310; DB 24; Length 396;  
Best Local Similarity 100.0%; Pred. No. 6,7e-115;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACATTTTTCGGGATTTGTTCTTCTTCACAGCTTTGCGGCAAAATCCAGTGTACCA 60  
DB 11 GGCACATTTTTCGGGATTTGTTCTTCTTCACAGCTTTGCGGCAAAATCCAGTGTACCA 70  
QY 61 GTGTGAAGAATTCACAGCTGTGAACACGACTGCTCTCCCGAGTTCAATTGTGAATTCAC 120  
DB 71 GTGTGAAGAATTCACAGCTGTGAACACGACTGCTCTCCCGAGTTCAATTGTGAATTCAC 130  
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGTGAAGAGAACTGCGGGATCATGTA 180  
DB 131 GGTGAACGTTCAAGACATGTGTCAAGAAAGTGAAGAGAACTGCGGGATCATGTA 190  
QY 181 CCGCAAGTCTGTGTCATCATCAGCGGCTGTCTCATCGCTCTGCGGGATCATGTA 240  
DB 191 CCGCAAGTCTGTGTCATCATCAGCGGCTGTCTCATCGCTCTGCGGGATCATGTA 250  
QY 241 CTGCTCCCGAGGAAACGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 251 CTGCTCCCGAGGAAACGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 310  
QY 301 CGGGCCCAAG 310  
DB 311 CGGGCCCAAG 320

#### RESULT 26

ABL48768

ID ABL48768 standard; cDNA; 396 BP.

AC ABL48768;

DT 18-JUN-2002 (first entry)

DE Ovarian carcinoma sequence isolate 21920.

XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KW ss.

OS Homo sapiens.

PN US200204491-A1.

PD 10-JAN-2002.

PF 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

PA (XUJ/) XU J.

PA (STOL/) STOLK J A.

PA (ALGA/) ALGATE P A.

PA (FLIN/) FLING S P.

PI Xu J, Stolk JA, Algate PA, Fling SP;



QY 330 CTGCTCGGCCCTCA 344  
 |||||||  
 DB 330 CTGCTCGGCCCTCA 344

## RESULT 21

ABT03274  
 ID ABL03274 standard; cDNA; 369 BP.

AC ABL03274;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 199.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KM cytosolic; gene; ss.

OS Homo sapiens.

OS WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;

DR WPI; 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for

PT detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

CC Example 1; Page 187; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins

CC and coding sequences. The sequences can be used in the diagnosis and

CC treatment of ovarian cancers. The present sequence is a coding sequence

CC of the invention.

CC Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

CC Query Match 19.5%; Score 315; DB 24; Length 369;

CC Best Local Similarity 100.0%; Pred. No. 6.6e-117;

CC Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTCAAAATCAGTGTACAGTGAAGAATTCAGGCAACAGCT 89

DB 30 CAGGCTTTGGCGTCAAAATCAGTGTACAGTGAAGAATTCAGGCAACAGCT 89

QY 90 GCTCCCTCCCGGAGTTCATTGTGAATTGACAGGTTCAAGCATGTGTCAAGAAG 149

DB 90 GCTCCCTCCCGGAGTTCATTGTGAATTGACAGGTTCAAGCATGTGTCAAGAAG 149

QY 150 AAGTGTATGAGCAAAATGCGGGGATGATACCGCAAGTCCGTGATCATCAGGCGCT 209

DB 150 AAGTGTATGAGCAAAATGCGGGGATGATACCGCAAGTCCGTGATCATCAGGCGCT 209

QY 210 GTCTCATGCGCTTCGCGGATACAGTCCCTTGTCCCGAAGAACTGAATCAGTTT 269

DB 210 GTCTCATGCGCTTCGCGGATACAGTCCCTTGTCCCGAAGAACTGAATCAGTTT 269

QY 270 GATATGAGTGTGCAACACCTCTTTTGAAGGGGCAAGGCCCAAGAAAGGGAGATT 329

DB 270 GATATGAGTGTGCAACACCTCTTTTGAAGGGGCAAGGCCCAAGAAAGGGAGATT 329

QY 330 CTGCTCGGCCCTCA 344  
 |||||||  
 DB 330 CTGCTCGGCCCTCA 344

## RESULT 22

ABL48956  
 ID ABL48956 standard; cDNA; 369 BP.

AC ABL48956;

DT 18-JUN-2002 (first entry)

DE Ovarian carcinoma sequence isolate 57887.

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KM ss.

OS Homo sapiens.

OS US2002004491-A1.

PD 10-JAN-2002.

PF 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

PA (XUJ/) XU J.

PA (STOL/) STOLK J A.

PA (ALGA/) ALGATE P A.

PA (FLIN/) FLING S P.

PI Xu J, Stolk JA, Algate PA, Fling SP;

DR WPI; 2002-171027/22.

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

PT prevention and/or treatment of cancer, especially ovarian cancer

PT Claim 1a; Page 116; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides

CC that may be utilised in cancer therapy, for example in a vaccine or

CC gene therapy. Polypeptides and polynucleotides of the invention are

CC useful for detecting a cancer in a patient, for stimulating and/or

CC developing T-cells specific for a tumour protein, and for inhibiting the

CC development of a cancer in a patient. They are also useful for

CC stimulating an immune response in a patient, and for treating a cancer in

CC a patient and for determining the presence of a cancer in a patient.

CC The isolated polynucleotides of the invention are useful for their

CC ability to selectively form duplex molecules with complementary stretches

CC of the entire desired gene or gene fragments, and for designing and

CC preparing ribozyme molecules for inhibiting expression of tumour

CC polypeptides in tumour cells. Polypeptides and polynucleotides of the

CC invention are also useful in recombinant DNA molecules to direct

CC expression of a polypeptide in appropriate host cells. The sequences

CC given in records ABL48760-ABL48956 represent polynucleotides encoding

CC ovarian carcinoma proteins.

CC Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

CC Query Match 19.5%; Score 315; DB 24; Length 369;

CC Best Local Similarity 100.0%; Pred. No. 6.6e-117;

CC Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTCAAAATCAGTGTACAGTGAAGAATTCAGGCAACAGCT 89

DB 30 CAGGCTTTGGCGTCAAAATCAGTGTACAGTGAAGAATTCAGGCAACAGCT 89

AAH50766/c  
 ID AAH50766 standard; cDNA: 444 BP.  
 AC  
 XX  
 XX  
 AAH50766;  
 DT 23-AUG-2001 (first entry)  
 DE Human tumour associated cDNA #95.  
 XX  
 XX  
 DE Human cancer specific gene expression; gene therapy;  
 XX  
 XX  
 KW age related differential expression; ss.  
 OS  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 PN WO200136685-A2.  
 XX  
 XX  
 PD 25-MAY-2001.  
 XX  
 XX  
 PF 17-NOV-2000; 2000WO-US31809.  
 XX  
 XX  
 PR 17-NOV-1999; 99US-0166056.  
 XX  
 PR 17-NOV-1999; 99US-0166106.  
 XX  
 XX  
 PA (NYXI-) NYXIS NEURO THERAPIES INC.  
 PI Kroes RA, Moskal JR, Yamamoto H;  
 DR  
 XX  
 XX  
 PI MPI; 2001-355647/37.  
 XX  
 PT Novel nucleic acid molecules differentially expressed in brain cancers,  
 PT useful for ascertaining propensity of cell for malignant phenotype or  
 PT ascertaining suitability of anti-neoplastic drug candidate -  
 PS  
 PS Claim 28; Page 50; 82pp; English.  
 XX  
 XX  
 CC The present invention provides the sequences of 184 cDNA fragments which  
 CC are differentially expressed in cancer cell depending on the age of the  
 CC patient. They can be used to diagnose and identify treatments for  
 CC cancers, particularly brain cancers such as haemangioblastoma, teratoma,  
 CC haemangioma, glioblastoma, schwannoma, osteoma and pinealoma. The  
 CC present sequence is a cancer-associated cDNA of the invention.  
 CC  
 XX  
 XX  
 SQ Sequence 444 BP; 95 A; 113 C; 94 G; 142 T; 0 other;  
 Query Match 22.5%; Score 364; DB 22; Length 444;  
 Best Local Similarity 99.8%; Pred. No. 1.3e-136;  
 Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1196 CCGAGCTGAGTGAAGAAACGCTCCGAGAGGAGAGATCATGTACGCCGGAAGT 1255  
 DB 431 CCGAGCTGAGTGAAGAAACGCTCCGAGAGGAGAGATCATGTACGCCGGAAGT 372  
 OY 1256 AGGACCTGCTCAGTGTGTTGGGTTGGCCGACCATGATCCCTCCCAATCTGTTGG 1315  
 DB 371 AGGACCTGCTCAGTGTGTTGGGTTGGCCGACCATGATCCCTCCCAATCTGTTGG 312  
 OY 1316 GCATCCAGCATGAGGCAATGTCACCAATCAGCCCTGGCGAGACAGGAGGAGGGA 1375  
 DB 311 GCATCCAGCATGAGGCAATGTCACCAATCAGCCCTGGCGAGACAGGAGGAGGGA 252  
 OY 1376 GAGACAGAGAAAGAAACACAGCATGAGACACAGTAATGAATTAATTAATTAATTA 1435  
 DB 251 GAGACAGAGAAAGAAACACAGCATGAGACACAGTAATGAATTAATTAATTAATTA 192  
 OY 1436 TTTAGCCCCCTGTGTGCTTACGTGGCAGGAAATGATCAATTTTCACTGTTGA 1495  
 DB 191 TTTAGCCCCCTGTGTGCTTACGTGGCAGGAAATGATCAATTTTCACTGTTGA 132  
 OY 1496 CTTGACAGCTTCTTTGGCACAAGCAGAGAGATTTTACACTGTTTCAACCCGGGGGA 1555  
 DB 131 CTTGACAGCTTCTTTGGCACAAGCAGAGAGATTTTACACTGTTTCAACCCGGGGGA 72  
 OY 1556 GTTGGCTGTGTTAAGAAAGACATTAAATGCTTTAGACAGTGTAAAAA 1610

DB 71 GTTGGCTGTGTTAAGAAAGACATTAAATGCTTTAGACAGTGTAAAAA 17  
 RESULT 20  
 AAF95007  
 ID AAF95007 standard; DNA: 369 BP.  
 AC  
 XX  
 XX  
 AAF95007;  
 DT 23-MAY-2001 (first entry)  
 DE Human ovarian cancer associated coding sequence SEQ ID NO: 199.  
 XX  
 XX  
 DE Human, ovarian cancer; vaccine; gene therapy; carcinoma; ds.  
 XX  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 PN WO200118046-A2.  
 XX  
 XX  
 PD 15-MAR-2001.  
 XX  
 XX  
 PF 08-SEP-2000; 2000WO-US24827.  
 XX  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 XX  
 XX  
 PA (CORI-) CORIXA CORP.  
 PI Xu J, Stolk JA;  
 DR  
 XX  
 XX  
 PI MPI; 2001-211395/21.  
 XX  
 XX  
 PT Isolated polypeptides associated with ovarian carcinomas, and the  
 PT nucleic acids that encode them, useful for the prevention diagnosis and  
 PT treatment of ovarian cancers -  
 PS  
 PS Claim 18; Page 189; 189pp; English.  
 XX  
 XX  
 CC The present invention provides a number of coding sequences and proteins,  
 CC the over-expression of which is associated with ovarian carcinoma/cancer.  
 CC These can be used in the diagnosis, treatment and prevention of ovarian  
 CC cancer, optionally by gene therapy or in the form of a vaccine. The  
 CC present sequence is an example of one of these sequences.  
 CC  
 XX  
 XX  
 SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;  
 Query Match 19.5%; Score 315; DB 22; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-117;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 30 CAGGCTTGGCGCAAAATCCATGCTACAGTGAAGATTTCCAGTGAACAGACT 89  
 DB 30 CAGGCTTGGCGCAAAATCCATGCTACAGTGAAGATTTCCAGTGAACAGACT 89  
 OY 90 GCTCTCTCCCGAGTTCATTTGTAATTGACGCTGAACGTTCAAGACATGTCTCAAAAG 149  
 DB 90 GCTCTCTCCCGAGTTCATTTGTAATTGACGCTGAACGTTCAAGACATGTCTCAAAAG 149  
 OY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGGGCT 209  
 DB 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGGGCT 209  
 OY 210 GTCTCATGCTCTGCGCGGTACAGTCTTCTGCTCCAGGGAATGAATCAGTTT 269  
 DB 210 GTCTCATGCTCTGCGCGGTACAGTCTTCTGCTCCAGGGAATGAATCAGTTT 269  
 OY 270 GCATCAGCTGCTGACACACCCCTCTTTTGAAGGCGCAAGGCCCAAGAAAGGGAAGTT 329  
 DB 270 GCATCAGCTGCTGACACACCCCTCTTTTGAAGGCGCAAGGCCCAAGAAAGGGAAGTT 329

CC preparing ribozyme molecules for inhibiting expression of tumour  
CC polypeptides in tumor cells. Polypeptides and polynucleotides of the  
CC invention are also useful in recombinant DNA molecules to direct  
CC expression of a polypeptide in appropriate host cells. The current  
CC sequence represents the ovarian carcinoma GPR39 cDNA.

XX Sequence 1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other;

Query Match 23.8%; Score 386; DB 24; Length 1362;

Best Local Similarity 99.8%; Pred. No. 1.7e-145;

Matches 506; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

QY 845 TCAAACTTCATGCTCTCTGCAAAACCAATTCCTCTGACAGCAATTTGGCTGTTCGGCCCTGA 904
DB 1362 TCAAACTTCATGCTCTCTGCAAAACCAATTCCTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1303
QY 905 GTTGGGCTCTGAGTCTGACAGCAATTCCTCTGACAGCAATTTGGCTGTTCGGCCCTGA 964
DB 1302 GTTGGGCTCTGAGTCTGACAGCAATTCCTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1243
QY 965 CTGAAAGTCTTAAAGAAATCTTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1024
DB 1242 CTGAAAGTCTTAAAGAAATCTTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1183
QY 1025 GAAGAGCAAGCGGCGCTGACAGCAATTTGGCTGTTCGGCCCTGA 1084
DB 1182 GAAGAGCAAGCGGCGCTGACAGCAATTTGGCTGTTCGGCCCTGA 1123
QY 1085 CAGGCGCTTCTGAGTCTGAGTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1144
DB 1122 CAGGCGCTTCTGAGTCTGAGTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1064
QY 1145 ACACCCCGCAAACTCTGAGTCTGAGTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1204
DB 1064 ACACCCCGCAAACTCTGAGTCTGAGTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1004
QY 1205 GGTGAAAAACGCTCTGAGTCTGAGTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1264
DB 1003 GGTGAAAAACGCTCTGAGTCTGAGTCTGACAGCAATTTGGCTGTTCGGCCCTGA 944
QY 1265 TCCAGTCTGCTTGGTCTGAGTCTGAGTCTGACAGCAATTTGGCTGTTCGGCCCTGA 1324
DB 943 TCCAGTCTGCTTGGTCTGAGTCTGAGTCTGACAGCAATTTGGCTGTTCGGCCCTGA 884
QY 1325 ATACGGCCATGTCACAAACATCAGCC 1351
DB 883 ATACGGCCATGTCACAAACATCAGCC 857

RESULT 18
AAF94186/c
ID AAF94186 standard; DNA; 587 BP.
XX
XX AAF94186;
AC
AC AAF94186;
XX
XX 23-MAY-2001 (first entry)
DT
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 620.
XX
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes; PCR primer; ss.
XX
XX Synthetic.
XX
XX EPI067182-A2.
PN
PD 10-JAN-2001.
XX
XX 07-JUL-2000; 2000EP-0114090.
PF
PR 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.

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XX (HELI-) HELIX RES INST.  
XX  
XX Oka T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
XX WPI; 2001-093989/11.  
XX

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
PT gene therapy or as candidate target molecules in drug development -  
XX  
XX Claim 5; SEQ ID 620; 609pp + CD ROM; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
XX which encode human secretory or membrane proteins represented by  
XX AAF88317 - AAF88419. Included in the invention are primers  
XX AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
XX cDNA sequences of the invention. The invention also includes methods for  
XX the production of antibodies directed against the proteins, and cDNA  
XX sequences, which can be used in vaccines. The polynucleotide sequences  
XX can be used in gene therapy. The polynucleotide sequences and the  
XX proteins they encode may be used in the prevention, treatment and  
XX diagnosis of diseases associated with inappropriate secretory  
XX protein/membrane protein expression. The nucleic acids and complementary  
XX sequences may also be used as DNA probes in diagnostic assays  
XX (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
XX presence of similar nucleic acid sequences in samples. They may also be  
XX used to study the expression and function of secretory proteins/membrane  
XX polypeptides and their role in metabolism. The polypeptides may be used  
XX as antigens in the production of antibodies against them and in assays to  
XX identify modulators (agonists and antagonists) of expression and  
XX activity. The antibodies and antagonists may also be used as therapeutic  
XX agents to down regulate expression and activity. The antibodies may also  
XX be used as diagnostic agents for detecting the presence of the  
XX (ELISA). Examples of diseases which may be treated include rheumatoid  
XX arthritis and diabetes.

XX Sequence 587 BP; 117 A; 162 C; 140 G; 162 T; 6 other;

Query Match 22.6%; Score 366; DB 22; Length 587;

Best Local Similarity 99.8%; Pred. No. 2e-137;

Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1183 AGCGGGTGTATGACGAGTGTAGAGAAACGCTCTCCGAGAGGAGAGATCATG 1242
DB 417 AGCGGGTGTATGACGAGTGTAGAGAAACGCTCTCCGAGAGGAGAGATCATG 358
QY 1243 TACGCCCGGAATAGACCTGCTCAGTCTGCTGGTGGTGGCCGAGCATGATCCTC 1302
DB 357 TACGCCCGGAATAGACCTGCTCAGTCTGCTGGTGGTGGCCGAGCATGATCCTC 298
QY 1303 CGAATCTGTTGGGATCAGCATACGCGCAATGTACACAAATCAGCCCTGGGACAGA 1362
DB 297 CGAATCTGTTGGGATCAGCATACGCGCAATGTACACAAATCAGCCCTGGGACAGA 238
QY 1363 CGAGCAGGAGGAGAGACAGAGAAAGAAACACAGCATAGAGAAACAGTAATGATA 1422
DB 237 CGAGCAGGAGGAGAGACAGAGAAAGAAACACAGCATAGAGAAACAGTAATGATA 178
QY 1423 AAACCATTAATATTTAGCCCTCTGCTGCTGCTTACTGCGCAGGAATGTCAAT 1482
DB 177 AAACCATTAATATTTAGCCCTCTGCTGCTGCTTACTGCGCAGGAATGTCAAT 118
QY 1483 TTTGAGTGTGAGTCTGACAGCTTCTTTGCGACAGCAAGAGAAATTAACACTGTT 1542
DB 117 TTTGAGTGTGAGTCTGACAGCTTCTTTGCGACAGCAAGAGAAATTAACACTGTT 58
QY 1543 CAACCCGCGGAGTGTGCTGTTAAAGAAAGCAATTAAGCTTAAAGCTGTG 1599
DB 57 CAACCCGCGGAGTGTGCTGTTAAAGAAAGCAATTAAGCTTAAAGCTGTG 1

RESULT 19

```









CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples. They may also be  
 CC used to study the expression and function of secretory proteins/membrane  
 CC polypeptides and their role in metabolism. The polypeptides may be used  
 CC as antigens in the production of antibodies against them and in assays to  
 CC identify modulators (agonists and antagonists) of expression and  
 CC activity. The antibodies (agonists and antagonists) may also be used as therapeutic  
 CC agents to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of the  
 CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay  
 CC (ELISA). Examples of diseases which may be treated include Rheumatoid  
 CC arthritis and diabetes.

XX Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other;

Query Match 62.6%; Score 1014; DB 22; Length 1890;

Best Local Similarity 99.6%; Pred. No. 0; Mismatches 2; Indels 4; Gaps 4;

Matches 1594; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

QY 1 GGCAACTTTTGGCGATTTGTTCTTCTTCAGAGGCTTTCGCTGCAAAATCGAGTCTACCA 60  
 DB 294 GGCAACTTTTGGCGATTTGTTCTTCTTCAGAGGCTTTCGCTGCAAAATCGAGTCTACCA 353  
 QY 61 GTGTAAATAATTCACGCTGAACAACGACTGCTCTCCCGAGTTTCAATTTGAAATTGCA 120  
 DB 354 GTGTAAATAATTCACGCTGAACAACGACTGCTCTCCCGAGTTTCAATTTGAAATTGCA 413  
 QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGTGAGCAAAAGTCCCGGATCATGTA 180  
 DB 414 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGTGAGCAAAAGTCCCGGATCATGTA 473  
 QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCTCCGGATACAGTCTT 240  
 DB 474 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCTCCGGATACAGTCTT 533  
 QY 241 CTGCTCCCGAGGAAATCGAATCTGATTCATGATGCTGTGCAACACCTCTTTTGTAA 300  
 DB 534 CTGCTCCCGAGGAAATCGAATCTGATTCATGATGCTGTGCAACACCTCTTTTGTAA 593  
 QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCGAGGCGAGGCTCCGAC 360  
 DB 594 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCGAGGCGAGGCTCCGAC 653  
 QY 361 CACCATCTGTCTCTCAAAATTAAGCCCTCTTCTGTGGCACTGCTGAAGCTGAAGAGATG 420  
 DB 654 CACCATCTGTCTCTCAAAATTAAGCCCTCTTCTGTGGCACTGCTGAAGCTGAAGAGATG 711  
 QY 421 CCACCCCTCTCTGATGTCTTCCAGCCCTCGGCCCAACCCGCCACCTCCCTGAGTGA 480  
 DB 712 CCACCCCTCTCTGATGTCTTCCAGCCCTCGGCCCAACCCGCCACCTCCCTGAGTGA 771  
 QY 481 GTTCTTCTGGGTGCTCTTTTATTTCTGGTAGGAGGCGGAGTCCGCTCTTTTGT 540  
 DB 772 GTTCTTCTGGGTGCTCTTTTATTTCTGGTAGGAGGCGGAGTCCGCTCTTTTGT 831  
 QY 541 CCGTGAATTAATGAAGAAGCTCGGTAAGCAATTCGAATTAATTCAGCTGAGTGAAT 600  
 DB 832 CCGTGAATTAATGAAGAAGCTCGGTAAGCAATTCGAATTAATTCAGCTGAGTGAAT 891  
 QY 601 TTTCAGTATGATGTGAAGAAGAGAGTGAAGTCAACCCCATGTCTGTGTAAAC 660  
 DB 892 TTTCAGTATGATGTGAAGAAGAGAGTGAAGTCAACCCCATGTCTGTGTAAAC 951  
 QY 661 CGGAGTCAAGGCCAGGCTGCGAGAGTCAATCTTGAAGTCACTGAGTGGGAGTCTGCC 720  
 DB 952 CGGAGTCAAGGCCAGGCTGCGAGAGTCAATCTTGAAGTCACTGAGTGGGAGTCTGCC 1011  
 QY 721 TTTTGAAGGCTTCCAGTGTCCATTCATCCCGATGGGGGCAATTTTGAAGTCTCAGA 780  
 DB 1012 TTTTGAAGGCTTCCAGTGTCCATTCATCCCGATGGGGGCAATTTTGAAGTCTCAGA 1071  
 QY 781 GTGAGAGTCACTTTTCTTAAAGGCTGAGGCGCAGTTCACACTCAAGGCTCCCTGCTTG 840  
 DB 1072 GTGAGAGTCACTTTTCTTAAAGGCTGAGGCGCAGTTCACACTCAAGGCTCCCTGCTTG 1131

DB 1072 GTGAGAGTCACTTTTCTTAAAGGCTGAGGCGCAGTTCACACTCAAGGCTCCCTGCTTG 1131  
 QY 841 ACATTCAAACTTCATGCTCTCGAANAACCATTTCTCGACAGAAATTTGGTTTCCGC 900  
 DB 1132 ACATTCAAACTTCATGCTCTCGAANAACCATTTCTCGACAGAAATTTGGTTTCCGC 1191  
 QY 901 CTGAGTGGGCTCTAAGTACTCGAGATCATCAATAGTGGACTTAAGTGGGCTCGGCT 960  
 DB 1192 CTGAGTGGGCTCTAAGTACTCGAGATCATCAATAGTGGACTTAAGTGGGCTCGGCT 1251  
 QY 961 CGCTCTGAAAAGTCTTAAGAAATCTTTCAGTTC-CTTCCAGAGGACCTGGCCCGG 1019  
 DB 1252 CGCTCTGAAAAGTCTTAAGAAATCTTTCAGTTC-CTTCCAGAGGACCTGGCCCGG 1311  
 QY 1020 GAGCGAAGAGCAAGCGGCGCTGCACAACCGGCGCTGTGGTGGTGAAGTCCGATG 1079  
 DB 1312 GAGCGAAGAGCAAGCGGCGCTGCACAACCGGCGCTGTGGTGGTGAAGTCCGATG 1371  
 QY 1080 ACGGCGAGGGGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1139  
 DB 1372 ACGGCGAGGGGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1430  
 QY 1140 CAGGAACCCCGCGCAAAAGTGTGCGAGACACGTTGACAGGAGGGGTTGATGACGA 1199  
 DB 1431 CAGGAACCCCGCGCAAAAGTGTGCGAGACACGTTGATGATGATGATGATGATGATG 1490  
 QY 1200 GCTGAGTGAAGAAAGCTCTCCGAGAAGGGAGAGAGATCATGTACCCCGGAATGAGA 1259  
 DB 1491 GCTGAGTGAAGAAAGCTCTCCGAGAAGGGAGAGAGATCATGTACCCCGGAATGAGA 1550  
 QY 1260 CTTGTCACATGCTGCTGGTGGGTTTGGCCGAGCATGATCTCCGAAATCTGGTGGGCT 1319  
 DB 1551 CTTGTCACATGCTGCTGGTGGGTTTGGCCGAGCATGATCTCCGAAATCTGGTGGGCT 1610  
 QY 1320 CCAAGATAGGCGCAATGTCAACAATCAAGCCCTGGGCGAGACAGAGAGGAGAGA 1379  
 DB 1611 CCAAGATAGGCGCAATGTCAACAATCAAGCCCTGGGCGAGACAGAGAGGAGAGA 1670  
 QY 1380 CAGAGAAAAGAAAACACAGCATGAGAACAGTAATTAATTAATTAATTAATTAAT 1439  
 DB 1671 CAGAGAAAAGAAAACACAGCATGAGAACAGTAATTAATTAATTAATTAATTAAT 1730  
 QY 1440 GCCCTCTGCTGCTGCTTACTGAGGAGCAATGATTTTCTGCTGCTGCTGCTGCTG 1499  
 DB 1731 GCCCTCTGCTGCTGCTTACTGAGGAGCAATGATTTTCTGCTGCTGCTGCTGCTG 1790  
 QY 1500 ACAAGTCTTTTGGCCACAAGAGAGATTTAAACACTGTTTCAAAACCCGGGAGTTG 1559  
 DB 1791 ACAAGTCTTTTGGCCACAAGAGAGATTTAAACACTGTTTCAAAACCCGGGAGTTG 1850  
 QY 1560 GCTGTTTAAAGAACCATTAATGCTTTTGAACAGTGT 1599  
 DB 1851 GCTGTTTAAAGAACCATTAATGCTTTTGAACAGTGT 1890

# RESULT 13

ABR03280  
 ID ABR03280 standard; cDNA; 625 BP.

XX ABR03280;

DF 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 210.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; Immunotherapy;

KM cytosolic; gene; ss.

OS Homo sapiens.

PN W020023985-h2.

XX 23-MAY-2002.



Db 1977 CATCAGCTGCTGCACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAAGGGGAAGTTC 1918  
 Qy 331 TGGCTGGGCGCTCAGGCGAGGGCTCCGCAACACATCCGTTCCAAATTAGCCCTCTT 390  
 Db 1917 TGGCTGGGCGCTCAGGCGAGGGCTCCGCAACACATCCGTTCCAAATTAGCCCTCTT 1858  
 Qy 391 CTGGGCACTGCTGAGAGTGAAGAGATGCAACCCCTCCTGCAATTTCTTCCAGCCC 450  
 Db 1857 CTGGGCACTGCTGAGAGTGAAGAGATGCAACCCCTCCTGCAATTTCTTCCAGCCC 1798  
 Qy 451 TGGCCCCCAACCCCACTCCCTGAGTAGTTCTTCTGGGTGTCTCTTTATCTGGGT 510  
 Db 1797 TGGCCCCCAACCCCACTCCCTGAGTAGTTCTTCTGGGTGTCTCTTTATCTGGGT 1738  
 Qy 511 AGGAGAGCGGAGTCCGTTCTCTTTCTCTGTCGCAATATGAAAGAGCTCGGTAA 570  
 Db 1737 AGGAGAGCGGAGTCCGTTCTCTTTCTCTGTCGCAATATGAAAGAGCTCGGTAA 1678  
 Qy 571 GCATTCTGATTAATTCACCTGACTGATTAATTTTCAGTATGATCTTGAAGAGAGAGTGG 630  
 Db 1677 GCATTCTGATTAATTCACCTGACTGATTAATTTTCAGTATGATCTTGAAGAGAGAGTGG 1618  
 Qy 631 AGTGAAGTTCAACCCCACTGCTGTGTAAACGAGTCAAGGCCAGCTGGCAGAGTCACT 690  
 Db 1617 AGTGAAGTTCAACCCCACTGCTGTGTAAACGAGTCAAGGCCAGCTGGCAGAGTCACT 1558  
 Qy 691 CCTTAGAGTCACTGAGTGGGCACTGCTCTTTGTAAAGCCCTCAGTGTCCATTCATC 750  
 Db 1557 CCTTAGAGTCACTGAGTGGGCACTGCTCTTTGTAAAGCCCTCAGTGTCCATTCATC 1498  
 Qy 751 CCTGATGGGGGCAATAGTTTGAAGACTGAGAGTGAAGTGTCTTTCTTAGGGCTGAGG 810  
 Db 1497 CCTGATGGGGGCAATAGTTTGAAGACTGAGAGTGAAGTGTCTTTCTTAGGGCTGAGG 1438  
 Qy 811 GCCAGTCCCACTCAAGGCTCCCTGCTGTGATTCATTAATTCATGCTCTGTAAGAACAT 870  
 Db 1437 GCCAGTCCCACTCAAGGCTCCCTGCTGTGATTCATTAATTCATGCTCTGTAAGAACAT 1378  
 Qy 871 TCTCTGACAGAAATGAGTGGTGGTTCGAGCTGAGTGGGCTCTGAGTACGTGAGACTCA 930  
 Db 1377 TCTCTGACAGAAATGAGTGGTGGTTCGAGCTGAGTGGGCTCTGAGTACGTGAGACTCA 1318  
 Qy 931 ATGACTGGGACTTGAAGTGGGCTCGGCTCGCTCTGAAAAGTGGTTAAGAAAATCTTCT 990  
 Db 1317 ATGACTGGGACTTGAAGTGGGCTCGGCTCGCTCTGAAAAGTGGTTAAGAAAATCTTCT 1258  
 Qy 991 CAGTCTCCTTGCAGAGGACTGGGCGCGGAGAGGCAAGAGCAAGGGCGCTGCACAAAGC 1050  
 Db 1257 CAGTCTCCTTGCAGAGGACTGGGCGCGGAGAGGCAAGAGCAAGGGCGCTGCACAAAGC 1198  
 Qy 1051 GGGCGCTGCTGGTGGTGGAGTGCAGATGAGCGAGGCGCTTCTGAGTGGTGGGCTGCT 1110  
 Db 1197 GGGCGCTGCTGGTGGTGGAGTGCAGATGAGCGAGGCGCTTCTGAGTGGTGGGCTGCT 1138  
 Qy 1111 GCAGCGACAGCGGAGCAGCAGACCTTGCACGAACACCCCGCAAGTGTGTCGAGAGAC 1170  
 Db 1137 GCAGCGACAGCGGAGCAGCAGACCTTGCACGAACACCCCGCAAGTGTGTCGAGAGAC 1079  
 Qy 1171 ACCGCTACAGAGGGGTTGATGACCGAGCTGAGAGTGAAGAAAAGCTCTCCGAGAGGG 1230  
 Db 1078 ACCGCTACAGAGGGGTTGATGACCGAGCTGAGAGTGAAGAAAAGCTCTCCGAGAGGG 1019  
 Qy 1231 AGGAGGATCATGACGCCCGGAGAGTGAAGACCTCGTCCAGTGTGTTGGGTTGGCCCA 1290  
 Db 1018 AGGAGGATCATGACGCCCGGAGAGTGAAGACCTCGTCCAGTGTGTTGGGTTGGCCCA 959  
 Qy 1291 GCCATGATCTCCGAATCTGTTGGGCAATCCAGCATACGCCCAATGTCAACAATCAGC 1350  
 Db 958 GCCATGATCTCCGAATCTGTTGGGCAATCCAGCATACGCCCAATGTCAACAATCAGC 899  
 Qy 1351 C 1351  
 Db 898 C 898

RESULT 11  
 AB054231  
 ID AB054231 standard; cDNA: 1608 BP.  
 XX  
 AC AB054231;  
 XX  
 DT 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.  
 DE  
 XX  
 KW Human: ovarian antigen; ovary: ovarian; breast: cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antineoplastic; gynecological; reproductive; chromosome 2q21-22;  
 KW gene; ss.  
 OS  
 XX Homo sapiens.  
 XX  
 EN MO200200677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US18569.  
 XX  
 PR 07-JUN-2000; 2000US-209467P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Birse CE, Rosen CA;  
 XX  
 DR WPI: 2002-147878/19.  
 XX P-PSDB: ABP41154.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
 PT ovarian cancer), immune disorders, cardiovascular disorders and  
 PT neurological diseases -  
 PS  
 PS Claim 1; SEQ ID NO 111; 2922pp; English.  
 CC  
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovarian and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present

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OY 781 GTGAGAGTACGTTTCTTCTAGGCTGGAGGCGCAGTTCCACATCAAGCTCCCTCGCTTG 840
    |||||||
DB 895 GTGAGAGAGAGTTTCTTCTAGGCTGGAGGCGCAGTTCCACATCAAGCTCCCTCGCTTG 836
OY 841 ACATTCAACTTTCATGCTCTCGTGAAGAACATTTCTCGACAGAAATTTGGCTTTGGCCG 900
    |||||||
DB 835 ACATTCAACTTTCATGCTCTCGTGAAGAACATTTCTCGACAGAAATTTGGCTTTGGCCG 776
OY 901 CTGATTTGGGCTCTAGTACTGAGACTCAATGACTGAGTACTGAGTACTGAGTACTGAGT 960
    |||||||
DB 775 CTGATTTGGGCTCTAGTACTGAGACTCAATGACTGAGTACTGAGTACTGAGTACTGAGT 716
OY 961 CGCTCTGAAAAGTCTCTAAGAAATCTTCTCAGTTCTCTTCTGACAGACTGGCGCCGG 1020
    |||||||
DB 715 CGCTCTGAAAAGTCTCTAAGAAATCTTCTCAGTTCTCTTCTGACAGACTGGCGCCGG 656
OY 1021 AGCGGAAGGCAACGGGGCGTGCACAAAGCGGGCGTGTGGTGGTGGAGTGGCGCATGTA 1080
    |||||||
DB 655 AGCGGAAGGCAACGGGGCGTGCACAAAGCGGGCGTGTGTGGTGGTGGAGTGGCGCATGTA 596
OY 1081 CGCGAGGCGCTTCTCTGTTGGCTGTGAGCAGACAGGCGGACAGACAGACCTTGC 1140
    |||||||
DB 595 CGCGAGGCGCTTCTCTGTTGGCTGTGAGCAGACAGGCGGACAGACAGACCTTGC 537
OY 1141 AGCAACACCCCGGCAACTGCTGCGAGCAGACACCTGTACAGAGCGGGTGTATGACCGAG 1200
    |||||||
DB 536 AGCAACACCCCGGCAACTGCTGCGAGCAGACACCTGTACAGAGCGGGTGTATGACCGAG 477
OY 1201 CTGAGGTAGAAAAGCTCTCCGAGAAAGGAGAGATCATGACGCCCGGAGAGTAGAGAC 1260
    |||||||
DB 476 CTGAGGTAGAAAAGCTCTCCGAGAAAGGAGAGATCATGAGTACGCCCGGAGAGTAGAGAC 417
OY 1261 CTGCTCACTGCTGCTTGGTGGTGGCGGACGATGATCTCCGATCTGTTGGGCATC 1320
    |||||||
DB 416 CTGCTCACTGCTGCTTGGTGGTGGCGGACGATGATCTCCGATCTGTTGGGCATC 357
OY 1321 CAGCATACGGCCCAATGTCACAAATCAGCCCTGGGAGACAGCAGAGAGAGAGAGAC 1380
    |||||||
DB 356 CAGCATACGGCCCAATGTCACAAATCAGCCCTGGGAGACAGCAGAGAGAGAGAGAC 297
OY 1381 AGAGAAAAGAAAACACAGCATGAGAACACAGTAAATGAATAAACATTAATATTTAG 1440
    |||||||
DB 296 AGAGAAAAGAAAACACAGCATGAGAACACAGTAAATGAATAAACATTAATATTTAG 237
OY 1441 CCCTCTGTTCTGTGCTTACTGCGCAGAAATGTATCAATTTTCAAGTGTGAGTGA 1500
    |||||||
DB 236 CCCTCTGTTCTGTGCTTACTGCGCAGAAATGTATCAATTTTCAAGTGTGAGTGA 1177
OY 1501 CAGCTTCTTTGGCACACAGCAAGAGAAATTTAACTGTTTCAAAACCCGGGGAGTTGG 1560
    |||||||
DB 176 CAGCTTCTTTGGCACACAGCAAGAGAAATTTAACTGTTTCAAAACCCGGGGAGTTGG 117
OY 1561 CTGTGTTAAAGAAAGACATTAAATGCTTTAGACAGTGA 1600
    |||||||
DB 116 CTGTGTTAAAGAAAGACATTAAATGCTTTAGACAGTGA 77

```

RESULT 10  
 AAD18690/c  
 ID AAD18690 standard; cdna; 2528 BP.

XX AAD18690;

XX 18-DEC-2001 (first entry)

DE Human G protein coupled receptor (GPCR) 4941 cdna.

XX Human; cardiovascular; tumorigenic disorder; aberrant angiogenesis;  
 KW gene therapy; aberrant vascularisation; arteriosclerosis; ovarian cancer;  
 KW ischaemia/reperfusion injury; hypertension; arterial inflammation;  
 KW psoriasis; endothelial cell disorder; diabetic retinopathy; restenosis;  
 KW myocardial infarction; grave's disease; G protein coupled receptor;

```

KW GPCR 4941: vasotropic; hypotensive; antiinflammatory; cytostatic;  

KW antidiabetic; antipsoriatic; Leukaemia; ss.  

XX Homo sapiens.  

XX Key Location/Qualifiers  

XX CDS 42..1403  

XX FT /*tag= a  

XX FT /product= "Human GPCR 4941"  

XX FT /note= "The CDS is specifically claimed in claim 1 of  

XX FT the specification"  

XX PN WO200181634-A2.  

XX PD 01-NOV-2001.  

XX PF 25-APR-2001; 2001WO-US13788.  

XX PR 26-APR-2000; 2000US-199908P.  

XX PR 09-AUG-2000; 2000US-0635521.  

XX PA (MILL-) MILLENNIUM PHARM INC.  

XX PI Galvin KA, Rudolph-owen LA;  

XX DR MPI: 2001-611743/70.  

XX DR P-PSDB; AME11751.  

XX PT Identifying nucleic acids for the diagnosis and treatment of  

XX PT cardiovascular and tumorigenic disorders, comprises identifying G  

XX PT protein coupled receptor (GPCR)-4941  

XX PS Example 1; Fig 1; 118pp; English.  

XX CC The present invention relates to a method for identifying a nucleic acid  

XX CC molecule (G protein coupled receptor gene, GPCR 4941) associated with a  

XX CC cardiovascular or tumorigenic disorder. The method comprising contacting  

XX CC a sample containing a nucleic acid molecule with a hybridisation probe or  

XX CC amplification primers and detecting the presence. The invention is used  

XX CC in gene therapy. The method of the invention is used for identifying  

XX CC nucleic acids or polypeptides associated with a cardiovascular or  

XX CC tumorigenic disorder such as aberrant angiogenesis, aberrant  

XX CC vascularisation, arteriosclerosis, or ovarian cancer, ischaemia/  

XX CC reperfusion injury, hypertension, restenosis, arterial inflammation,  

XX CC endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial  

XX CC infarction, grave's disease and leukaemia. The methods can also detect  

XX CC mRNA or genomic DNA in a sample. The present sequence is G protein  

XX CC coupled receptor (GPCR) 4941 cdna.  

XX SQ Sequence 2528 BP; 516 A; 766 C; 677 G; 567 T; 2 other:  

XX  

XX Query Match 71.0%; Score 1149; DB 22; Length 2528;  

XX Best Local Similarity 99.8%; Pred. No. 0;  

XX Matches 1319; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  

OY 31 AGGCTTGGCGCTGCAATCCAGTGTACAGTGTGAAGAAATTCAGCGAACAAGACTG 90  

    |||||||
DB 2217 AGGCTTGGCGCTGCAATCCAGTGTACAGTGTGAAGAAATTCAGCGAACAAGACTG 2158
OY 91 CTCTCCCGGAGTTCATGTGTAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAAGA 150
    |||||||
DB 2157 CTCTCCCGGAGTTCATGTGTAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAAGA 2098
OY 151 AGTATGAGACAAAGTCCGGGATCATGACCGAAGTCTGTGATCATCATCAGCGGCTG 210
    |||||||
DB 2097 AGTATGAGACAAAGTCCGGGATCATGACCGAAGTCTGTGATCATCATCAGCGGCTG 2038
OY 211 TCTATATGCGCTCTGCGGGGATGACAGTCTGTGCTCCCGAGGAAACTGAATCACTAGTTG 270
    |||||||
DB 2037 TCTATATGCGCTCTGCGGGGATGACAGTCTGTGCTCCCGAGGAAACTGAATCACTAGTTG 1978
OY 271 CATAGAGTGTGCAACACCCCTCTTTGTAAAGGCGCAAGGCCCAAGAAAAGGGAAGTTG 330
    |||||||

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One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -

Claim 2: Figure 15; 359pp: English.

The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor- $\alpha$  from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABR33536-ABR33657 represent human PRO protein coding sequences of the invention.

Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;

Query Match 78.1%; Score 1264; DB 24; Length 1524;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 1 GGCACATTTTGGCGATTTGTTCTTCTTCAGGCTTTGGCTGCAAAATTCAGTGTACCA 60
DB 141 GGCACATTTTGGCGATTTGTTCTTCTTCAGGCTTTGGCTGCAAAATTCAGTGTACCA 200
OY 61 GTGAGAAATTTCCAGCGAACAAGCACTGCTCTCCCGGAGTTCAATTTGATTTGAC 120
DB 201 GTGAGAAATTTCCAGCGAACAAGCACTGCTCTCCCGGAGTTCAATTTGATTTGAC 260
OY 121 GGTGAAGCTTCAAGACATGTGTCTCAGAAAGAGTGTAGAGCAAAAGTCCGGGATCATGTA 180
DB 261 GGTGAAGCTTCAAGACATGTGTCTCAGAAAGAGTGTAGAGCAAAAGTCCGGGATCATGTA 320
OY 181 CCGGAAGCTTCCGATCATCAGAGGCGCTGTCTATGCTCTGCGGGTACAGTCTT 240
DB 321 CCGGAAGCTTCCGATCATCAGAGGCGCTGTCTATGCTCTGCGGGTACAGTCTT 380
OY 241 CTGTCTCCCAAGGAACTGAATCAGTTTGCATCAGCTGCTGCAACACCCCTGTTTAA 300
DB 381 CTGTCTCCCAAGGAACTGAATCAGTTTGCATCAGCTGCTGCAACACCCCTGTTTAA 440
OY 301 CGGGCCAAAGGCGCAAGAAAGGGGAGTTGCTGCGGCCCTCAGGCCAGGCTCCGCAC 360
DB 441 CGGGCCAAAGGCGCAAGAAAGGGGAGTTGCTGCGGCCCTCAGGCCAGGCTCCGCAC 500
OY 361 CACCATCTGTCTCTCAAAATTTAGCCCTTCTGCGACATCTGTGAAGCTGAAGAGATG 420
DB 501 CACCATCTGTCTCTCAAAATTTAGCCCTTCTGCGACATCTGTGAAGCTGAAGAGATG 560
OY 421 CCAACCCCTCTGATGTTCTTCAAGCCCTGCGCCCAACCCCAACCCCTGAGTGA 480
DB 561 CCAACCCCTCTGATGTTCTTCAAGCCCTGCGCCCAACCCCAACCCCTGAGTGA 620
OY 481 GTTTCCTTCTGGGTCTCTTTTATTTGAGGAGCGGAGTCCGTTCTCTTCTTGT 540
DB 621 GTTTCCTTCTGGGTCTCTTTTATTTGAGGAGCGGAGTCCGTTCTCTTCTTGT 680
OY 541 CCGTGAAGTAAATGAAGAGCTCGTAAGAGCTTTGTAATTAATTCAGCTTACTGAAT 600
DB 681 CCGTGAAGTAAATGAAGAGCTCGTAAGAGCTTTGTAATTAATTCAGCTTACTGAAT 740
OY 601 TTTTCAGTATCTTGAAGAGAGGTGAGTGAAGTTCACCCCATGTCTGTGTAAC 660
DB 741 TTTTCAGTATCTTGAAGAGAGGTGAGTGAAGTTCACCCCATGTCTGTGTAAC 800

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OY 661 CGGAGTCAAGCCCAAGGCTGCGCAAGTCAATCTTTAGAGTCACTAGAGTGGCATCTGCC 720
DB 801 CGGAGTCAAGCCCAAGGCTGCGCAAGTCAATCTTTAGAGTCACTAGAGTGGCATCTGCC 860
OY 721 TTTTGTAAAGCTTCAGAGTGTCCATTCATCCCGATGGGGGCAATGATTTGAGATCGACA 780
DB 861 TTTTGTAAAGCTTCAGAGTGTCCATTCATCCCGATGGGGGCAATGATTTGAGATCGACA 920
OY 781 GTGAGAGTCAAGTCTTTCTTAAGGCTGAGGGCCAGTCTCCCACTCAAGGCTCCCTGCTTG 840
DB 921 GTGAGAGTCAAGTCTTTCTTAAGGCTGAGGGCCAGTCTCCCACTCAAGGCTCCCTGCTTG 980
OY 841 ACGTTCAACTTATGCTCTGTAAGAAACATCTCTCAGAGCAAGATGCTGTTTGGCC 900
DB 981 ACGTTCAACTTATGCTCTGTAAGAAACATCTCTCAGAGCAAGATGCTGTTTGGCC 1040
OY 901 CTGAGTTGGGCTCTAGAGTCAAGTCAATGACTGAGGCACTTGAAGTGGGCTGGGCT 960
DB 1041 CTGAGTTGGGCTCTAGAGTCAAGTCAATGACTGAGGCACTTGAAGTGGGCTGGGCT 1100
OY 961 CGCTCTGAAGAAAGTCTTGAAGAAATCTTCAATCTCTTCAAGAGCAAGTGGCCGG 1020
DB 1101 CGCTCTGAAGAAAGTCTTGAAGAAATCTTCAATCTCTTCAAGAGCAAGTGGCCGG 1160
OY 1021 ACGGGAAGCAAGCGGGCGCTGCAAAAGCGGCGCTGTCGCTGCTGAGTGCATGTA 1080
DB 1161 ACGGGAAGCAAGCGGGCGCTGCAAAAGCGGCGCTGTCGCTGCTGAGTGCATGTA 1220
OY 1081 CGGCGAGGCGCTCTCTGTGGTGGCGCTGTGAGAGCAAGCGGCGAGCACACACCTTGC 1140
DB 1221 CGGCGAGGCGCTCTCTGTGGTGGCGCTGTGAGAGCAAGCGGCGAGCACACACCTTGC 1279
OY 1141 ACGAACAACCCCGGAAGTCTGCGAGAGACACCGTGTACAGAGCGGGTGTGATGACCGAG 1200
DB 1280 ACGAACAACCCCGGAAGTCTGCGAGAGACACCGTGTGTACAGAGCGGGTGTGATGACCGAG 1339
OY 1201 CTGAGGTAGAAAACGTCCTCCGAAAGGGGAGAGATATATAGCCCGGGAAGTAAAGAG 1260
DB 1340 CTGAGGTAGAAAACGTCCTCCGAAAGGGGAGAGATATATAGCCCGGGAAGTAAAGAG 1399
OY 1261 CTGCTCAAGTCTGCTTGGGTTGGCGGAGGATGATCTCCGAATCTGTTGGGATC 1320
DB 1400 CTGCTCAAGTCTGCTTGGGTTGGCGGAGGATGATCTCCGAATCTGTTGGGATC 1459
OY 1321 CAGCATAGCGGCAATGTCAACAATCAGCCCTGGGAGACACGAGAGGAGAGAC 1380
DB 1460 CAGCATAGCGGCAATGTCAACAATCAGCCCTGGGAGACACGAGAGGAGAGAC 1519
OY 1381 AGAGA 1385
DB 1520 AGAGA 1524

```

RESULT 8  
AAE22400/c  
ID AAE22400 standard; cDNA; 1953 BP.

26-MAR-2001 (first entry)

Human secreted protein gene 28 spq ID NO:38.

Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
antirheumatic; antiproliferative; cytostatic; cardiant; vasodilator;  
cerebroprotective; neurotrophic; neuroprotective; antibacterial; virucide;  
fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;  
rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;  
cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;  
angiogenesis; nervous system disorder; Alzheimer's disease; infection;  
ocular disorder; corneal infection; wound healing; skin aging;  
food additive; preservative; ss.



Oy	241	CTGTGTCGCCAGGGGAAACTGAACCTACATTTTGACATCGAGCTGCTGCAACACACCCCTCTTTGGAA	300
Db	520	CTGTCTCCCCAGGGAAACTGAACCTACATTTTGACATCGAGCTGCTGCAACACCCCTCTTTGGTA	579
Oy	301	CGGGCCAGGCCCCAGAGAAAAGGGGAGTTCTCGCTCGGCCCTCAGGCCAGGGCTCCGCAC	360
Db	580	CGGGCCAGGCCCCAGAGAAAAGGGGAGTTCTCGCTCGGCCCTCAGGCCAGGGCTCCGCAC	639
Oy	361	CACCATCTCTGTTCCCTCAAAATTAGCCCTCTTTCGCGACACTGCTGAGCTGAGAGATG	420
Db	640	CACCATCTCTGTTCCCTCAAAATTAGCCCTCTTTCGCGACACTGCTGAAACTGAAGAGATG	699
Oy	421	CCACCCCCCTCTCGATTGTTCTTCCAGCCCCCTGGCCCCACACCCCCACCCTCCCTGAGTGA	480
Db	700	CCACCCCCCTCTCGATTGTTCTTCCAGCCCCCTGGCCCCACACCCCCACCCTCCCTGAGTGA	759
Oy	481	GTTCCTTCTGGAGTGCCTTTTATTTTCGGGAGGAGACGGAGTCCGTTGCTCTTTGTT	540
Db	760	GTTCCTTCTGGAGTGCCTTTTATTTTCGGGAGGAGACGGAGTCCGTTGTTCTTTTGT	819
Oy	541	CTGTGCAAAATTAATGAAGAAGCTCGGTAAAGCATTCGATTAATTAATTCAGCCTGACTGAT	600
Db	820	CTGTGCAAAATTAATGAAGAAGCTCGGTAAAGCATTCGATTAATTAATTCAGCTGACTGAT	879
Oy	601	TTTACGATGATGACTTGAAGAGAGAGGTGAGTGAAGAGTTCACCCCCCATGTCGTGTAAAC	660
Db	880	TTTACGATGATGACTTGAAGAGAGAGGTGAGTGAAGAGTTCACCCCCCATGTCGTGTAAAC	939
Oy	661	CGGAGTCAAGGCCAGGCTGCGCAGAGTCAAGTCCCTAGAAATCACTGAGGTGGGACTGTGCC	720
Db	940	CGGAGTCAAGGCCAGGCTGCGCAGAGTCAAGTCCCTAGAAATCACTGAGGTGGGACTGTGCC	999
Oy	721	TTTTGTAAAGCCTTCAGTGTCCATTCCTCATCCCTGATGGGGCATAGTTGAGACTGCAGA	780
Db	1000	TTTTGTAAAGCCTTCAGTGTCCATTCCTCATCCCTGATGGGGCATAGTTGAGACTGCAGA	1059
Oy	781	GTGAGAGGACGCTTTCTTGAAGGCTGAGAGGGCCAGTTCCTCACTCAAGGCTCCCTCGCTTG	840
Db	1060	GTGAGAGGACGCTTTCTTGAAGGCTGAGAGGGCCAGTTCCTCACTCAAGGCTCCCTCGCTTG	1119
Oy	841	ACATTCAAACTTCATGCTCCTGTGAAGAACCATTCCTCTGCACACAAATTTGGCTGTGTCGGC	900
Db	1120	ACATTCAAACTTCATGCTCCTGTGAAGAACCATTCCTCTGCACACAAATTTGGCTGTGTCGGC	1179
Oy	901	CTGAGTTGGGCTCTAGTGAAGTCAAGACTCAATGACTGGGACTTGAAGTGGGGCTCGGCT	960
Db	1180	CTGAGTTGGGCTCTAGTGAAGTCAAGACTCAATGACTGGGACTTGAAGTGGGGCTCGGCT	1239
Oy	961	CGCTCTGAAAAGTCTTAAAGAAATCTCTCAGATTTCTCTTGCAGAGAGTGTGGCGCGGG	1020
Db	1240	CGCTCTGAAAAGTCTTAAAGAAATCTCTCAGATTTCTCTTGCAGAGAGTGTGGCGCGGG	1299
Oy	1021	ACGCGAAGAGCAAGGGGCGCTGCACAAAGGGGGCGGTGTCGGGTGGAGTCCGATGTA	1080
Db	1300	ACGCGAAGAGCAAGGGGCGCTGCACAAAGGGGGCGGTGTCGGGTGGAGTCCGATGTA	1359
Oy	1081	CGCGAGGCGCTTCTCGTGTGTGGGCTGTGCAGCGACAGGGCGGACGACAGCACTTGTG	1140
Db	1360	CGCGAGGCGCTTCTCGTGTGTGGGCGTGTGCAGCGACAGGGCGGACGACAGCACTTGTG	1418
Oy	1141	ACGAAACACCCCGCAAACTGCTGCGAGAGACACCGTGTAAAGAGGGGGTGTATGACAG	1200
Db	1419	ACGAAACACCCCGCAAACTGCTGCGAGAGACACCGTGTAAAGAGGGGGTGTATGACAG	1478
Oy	1201	CTGAGGTGAAAAAAGCTCTCGAAGAGGGGAGAGATCATGACGCCCGAAGTAAAGAC	1260
Db	1479	CTGAGGTGAAAAAAGCTCTCGAAGAGGGGAGAGATCATGATACGCCCGAAGTAAAGAC	1538
Oy	1261	CTCGTCAAGTGTGCTTTGGGTTTTGGCCGACGCCATGATCCTCGAATCTGTTGGGCAATC	1320
Db	1539	CTCGTCAAGTGTGCTTTGGGTTTTGGCCGACGCCATGATCCTCGAATCTGTTGGGCAATC	1598
Oy	1321	CAGCATACGGCCATGTGCACACAATAGCCCTTGGCGAGACAGACGAGCGAGGAGAGAC	1380

Db	1599	CAGCATTCAGGCCAATGTCACAACAATCAGCCCTGGGTCAGACAGCAGCAGGAGGAGAC	1653
Qy	1381	AGAGAAAGAAAACACACGCACTGGAGACACACTGAATGAATAAACCATTAATATTAG	1444
Db	1659	AGAGAAAGAAAACACACGCACTGGAGACACACTGAATGAATAAACCATTAATATTAG	1717
Qy	1441	CCCTCTGTTCTGTGCTTACTGGCCAGGAATGCTACCAATTTTTCAGTGTGGACTTGA	1500
Db	1719	CCCTCTCTTCTGTGCTTACTGGCCAGGAATGCTACCAATTTTTCAGTGTGGACTTGA	1777
Qy	1501	CAGCTCTTTTGGCACAAGCAGAAGACATTTAACACTGTTTCAAAACCCGGGAGATTTG	1566
Db	1779	CAGCTCTTTTGGCACAAGCAGAAGACATTTAACACTGTTTCAAAACCCGGGAGATTTG	1833
Qy	1561	CTGCTTTAAAGAAAGACATTAATGCTTTGACAGCTTAAAAA	1619
Db	1839	CTGCTTTAAAGAAAGACATTAATGCTTTGACAGCTTAAAAA	1897

RESULT 7  
ABK33543

ID	ABK33543	standard;	CDNA;	1524	BP.
xx					

AA  
AC  
ABK33543;

XX	
DT	08-MAY-2002 (first entry)

xx CDNA encoding human PRO protein, Seq ID No 15  
DE

human: secreted protein; bD; tumour; lung cancer; colon cancer

KW breast cancer; prostate tumour; rectal tumour; liver tumour;

pericyte cell proliferation; chondrocyte cell proliferation;  
tumour necrosis factor-alpha; gene; ss.

XX  
05 Homo sapiens.

XX  
PN WO200208288-A1

XX 31 - TAN-0003

PD 31-JAN-2002.  
XX

PF 29-JUN-2001; 2001WO-US21066.  
XX

PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P

25-JUL-2000; 2000US-220605P.

PR 25-JUL-2000; 2000US-22060/P.  
PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.

PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P

28-JUL-2000; 2000WO-US20710.

PR 23-AUG-2000; 2000WO-US233522.  
PR 24-AUG-2000; 2000WO-US23328.

PR 15-SEP-2000; 2000US-0000000P,  
PR 10-NOV-2000; 2000WO-US30873.

PR	28-NOV-2000; 2000US-253646P
PR	01-DEC-2000; 2000WO-ITS32678

PR 20-DEC-2000; 2000US-0747259

PR 28-FEB-2001; 2001WO-US065520

PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.

XX  
PA (GETH ) GENENTECH INC.

Роберт ван Дорнебург

PI Baker AF, Desnoyers L, Gurney AL, Grimaldi JC, Gurney AL, Smith PI

XX  
DR WPI; 2002-172001/22.

DR P-PSDB; AAU83599.  
XX

Db 1000 TTTTGTAAAGCCCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGACTGCAGA 1059  
 QY 781 GTGAGAGTACGTTTCTTAGGGCTGAGGGGCACTTCCCACTCAAGGCTCCCTCGCTTG 840  
 Db 1060 GTGAGAGTACGTTTCTTAGGGCTGAGGGGCACTTCCCACTCAAGGCTCCCTCGCTTG 1119  
 QY 841 ACATTCAAACTTCATGCTCTGAAAAACCATTCCTGACAGCAGAAATTTGGCTTCCGGC 900  
 Db 1120 ACATTCAAACTTCATGCTCTGAAAAACCATTCCTGACAGCAGAAATTTGGCTTCCGGC 1179  
 QY 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGCTGGGCTCGGCT 960  
 Db 1180 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGCTGGGCTCGGCT 1239  
 QY 961 CGCTCTGAAAAAGTCTTAAAGAAATCTTCTAGTCTCTTGGCAGAGGACATGGGCGCGG 1020  
 Db 1240 CGCTCTGAAAAAGTCTTAAAGAAATCTTCTAGTCTCTTGGCAGAGGACATGGGCGCGG 1299  
 QY 1021 ACGCGAAGAGCAAGCGGGGCTGACACAAAGCGGGGCTGCTGGTGGTGGAGTGGCCATGTA 1080  
 Db 1300 ACGCGAAGAGCAAGCGGGGCTGACACAAAGCGGGGCTGCTGGTGGTGGAGTGGCCATGTA 1359  
 QY 1081 CGCGAGGCGCTCTCTGCTGCTGGTGGGCTGCTGACGACAGCGGCGACAGCACACCTTGC 1140  
 Db 1360 CGCGAGGCGCTCTCTGCTGCTGGTGGGCTGCTGACGACAGCGGCGACAGCACACCTTGC 1418  
 QY 1141 ACGAACCACCGCGGCAATGCTGCGAGGACACCGGTATCAGAGCGGGTGTATGACCGGAG 1200  
 Db 1419 ACGAACCACCGCGGCAATGCTGCGAGGACACCGGTATCAGAGCGGGTGTATGACCGGAG 1478  
 QY 1201 CTGAGGTAGAAAAACGCTCTCGAGAGAGGGGAGAGGATCATGTACGCCCGGAGTAGGAC 1260  
 Db 1479 CTGAGGTAGAAAAACGCTCTCGAGAGAGGGGAGAGGATCATGTACGCCCGGAGTAGGAC 1538  
 QY 1261 CTCGTCAGAGTGTGTGGTGGTGGGCTGGCCGACCATGATCTCCCAATCTGTTGGCATC 1320  
 Db 1539 CTCGTCAGAGTGTGTGGTGGTGGGCTGGCCGACCATGATCTCCCAATCTGTTGGCATC 1598  
 QY 1321 CAGCATAGGCGCAATGTCTACAAACATGACCCCTGGGCGACAGCAGGAGGAGGAGAC 1380  
 Db 1599 CAGCATAGGCGCAATGTCTACAAACATGACCCCTGGGCGACAGCAGGAGGAGGAGAC 1658  
 QY 1381 AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGAAATGAAATGAAATATTTAG 1440  
 Db 1659 AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGAAATGAAATGAAATATTTAG 1718  
 QY 1441 CCCCTCTGCTGTGCTTACTGGCCAGGAAATGTTACCAATTTTTCAGTGTGGACTTGA 1500  
 Db 1719 CCCCTCTGCTGTGCTTACTGGCCAGGAAATGTTACCAATTTTTCAGTGTGGACTTGA 1778  
 QY 1501 CAGCTTTCTTTTGGCACAAGCAGAGAGAAATTTAACACTGTTTCAAAACCCGGGAGTGG 1560  
 Db 1779 CAGCTTTCTTTTGGCACAAGCAGAGAGAAATTTAACACTGTTTCAAAACCCGGGAGTGG 1838  
 QY 1561 CTGCTTTAAGAAAGACCATTAATGCTTTAGACAGTGAATAAAAAAAAAAAAAA 1619  
 Db 1839 CTGCTTTAAGAAAGACCATTAATGCTTTAGACAGTGAATAAAAAAAAAAAAAA 1897

## RESULT 6

ABL40352 standard; cDNA; 1897 BP.  
 ID ABL40352  
 XX ABL40352;  
 AC  
 XX  
 DT 28-JUN-2002 (first entry)  
 DE Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.  
 XX  
 KM Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 XX ss.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 260..685  
 FT /\*tag= a  
 FT /product= "Ovarian carcinoma protein O1034C/O591S"  
 XX  
 PN US200204491-A1.  
 PD 10-JAN-2002.  
 XX  
 PE 03-APR-2001; 2001US-0825294.  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PA (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 PI  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 DR WPI: 2002-171027/22.  
 DR P-PSDB: ABB09417.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 PT prevention and/or treatment of cancer, especially ovarian cancer -  
 PS  
 PS Claim 1a: Page 127-128; 131pp; English.  
 XX  
 CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma O1034C/O591S consensus  
 CC nucleotide sequence.  
 CC  
 SO Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other:  
 Query Match 86.2%; Score 1396; DB 24; Length 1897;  
 Best local similarity 99.8%; Pred. No. 0;  
 Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 QY 1 GGCACCTTTTGGGATGTTGTTCTGCTTCCAGGCTTTGGCGTCAATTCAGTGTCTACA 60  
 Db 280 GGCACCTTTTGGGATGTTGTTCTGCTTCCAGGCTTTGGCGTCAATTCAGTGTCTACA 339  
 QY 61 GTGTGAAGATTCACCTCAACACAGCATGCTCCCTCCCGAGTTCATGTGAATTTGAC 120  
 Db 340 GTGTGAAGATTCACCTCAACACAGCATGCTCCCTCCCGAGTTCATGTGAATTTGAC 399  
 QY 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGAAGCAAGTGGCGGGATCATGTA 180  
 Db 400 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGAAGCAAGTGGCGGGATCATGTA 459  
 QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTGGCCGGGTACCACTCTT 240  
 Db 460 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTGGCCGGGTACCACTCTT 519

Db 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGAGACTTGAAGTGGGCTGCGCT 960  
 Qy 961 CGCTGAAAGAGTCTTAGAAATCTTCAATTCCTTGCAGAGAGATGCGCGGG 1020  
 Db 961 CGCTGAAAGAGTCTTAGAAATCTTCAATTCCTTGCAGAGAGATGCGCGGG 1020  
 Qy 1021 ACAGGAAAGCAACGCGGCTGACAAACGCGGCTGTCGCTGAGAGTGCAGATGA 1080  
 Db 1021 ACAGGAAAGCAACGCGGCTGACAAACGCGGCTGTCGCTGAGAGTGCAGATGA 1080  
 Qy 1081 CCGGACGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 Db 1081 CCGGACGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 Qy 1141 ACAGAACCCGCGGAAAGTCTGCGAGACACGCTGACAGAGGCGGCTGATGACCGAG 1200  
 Db 1141 ACAGAACCCGCGGAAAGTCTGCGAGACACGCTGACAGAGGCGGCTGATGACCGAG 1200  
 Qy 1201 CTGAGGTAGAAAACGCTCCGAGAGGAGAGGATCATGACGCGCGGAAATAGAGAC 1260  
 Db 1201 CTGAGGTAGAAAACGCTCCGAGAGGAGAGGATCATGACGCGCGGAAATAGAGAC 1260  
 Qy 1261 CTGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 Db 1261 CTGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 Qy 1321 CACGATACGCGCAATGCAACAAATCAGCGCTGGGAGACAGACAGAGAGAGAGAC 1380  
 Db 1321 CACGATACGCGCAATGCAACAAATCAGCGCTGGGAGACAGACAGAGAGAGAGAC 1380  
 Qy 1381 AGAGAAAGAAAAACAGACAGATGAGAAACAGTAATGATTAATTAATTTAG 1440  
 Db 1381 AGAGAAAGAAAAACAGACAGATGAGAAACAGTAATGATTAATTAATTTAG 1440  
 Qy 1441 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 Db 1441 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 Qy 1501 CACCTCTTCTTCCAGACAGAGAGAAATTTAACAATTTTCAACCCGCGGAGATGG 1560  
 Db 1501 CACCTCTTCTTCCAGACAGAGAGAAATTTAACAATTTTCAACCCGCGGAGATGG 1560  
 Qy 1561 CTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGTAAAAA 1619  
 Db 1561 CTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGTAAAAA 1619  
 RESULT 5  
 ABT03284  
 ID ABT03284 standard; cDNA; 1897 BP.  
 XX  
 AC ABT03284;  
 XX  
 DT 05-SEP-2002 (first entry)  
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.  
 XX  
 KM Human: ovarian cancer: ovarian carcinoma; gene therapy; immunotherapy;  
 XX cytosolic; gene; ss.  
 XX Homo sapiens.  
 OS  
 PN WO200239885-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PE 13-NOV-2001; 2001MO-US45395.  
 XX  
 PR 14-NOV-2000; 2000US-0713550.  
 PR 03-APR-2001; 2001US-0825294.  
 PR 02-OCT-2001; 2001US-0970966.  
 XX  
 PA (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;  
 PI WPI: 2002-500186/53.  
 DR  
 PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
 PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
 PS  
 PS Claim 2: Page 196; 197bp; English.  
 CC The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.  
 XX  
 SQ Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;  
 Query Match 86.2%; Score 1396; DB 24; Length 1897;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 Qy 1 GGCACATTTTGGCGATTTGCTTCTGCTCCAGGCTTGGCGTGCATAATCCAGTCTACCA 60  
 Db 280 GGCACATTTTGGCGATTTGCTTCTGCTCCAGGCTTGGCGTGCATAATCCAGTCTACCA 339  
 Qy 61 GTGTAAATAATCCAGCTGCAACAGACTGCTCTCCCGAGATTCATTTGAATTTGCAC 120  
 Db 340 GTGTAAATAATCCAGCTGCAACAGACTGCTCTCCCGAGATTCATTTGAATTTGCAC 399  
 Qy 121 GGTGAAGCTTCAAGCATGTGTCAAGAAAGAGTATGAGCAAGTCCGAGATCATGTA 180  
 Db 400 GGTGAAGCTTCAAGCATGTGTCAAGAAAGAGTATGAGCAAGTCCGAGATCATGTA 459  
 Qy 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTGATGCTCTGCGGGATACAGTCTT 240  
 Db 460 CCGCAAGTCTGTGATCATCAGCGGCTGTCTGATGCTCTGCGGGATACAGTCTT 519  
 Qy 241 CTGCTCCCGAGGAAACGAACTCATGCTGATCATGCTGCAACACCCCTTTTGA 300  
 Db 520 CTGCTCCCGAGGAAACGAACTCATGCTGATCATGCTGCAACACCCCTTTTGA 579  
 Qy 301 CCGGCAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCTCTCAAGGCGAGGCTCCGAC 360  
 Db 580 CCGGCAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCTCTCAAGGCGAGGCTCCGAC 639  
 Qy 361 CACCATCTGTTCTCAATTAAGCCCTCTCTGCGACATGCTGAAGCTGAAGAGATG 420  
 Db 640 CACCATCTGTTCTCAATTAAGCCCTCTCTGCGACATGCTGAAGCTGAAGAGATG 699  
 Qy 421 CCAGCCCTCCCGCATTTGCTTCCAGGCTCGCCGCCAACCCGCCACCTCCGAGAGA 480  
 Db 700 CCAGCCCTCCCGCATTTGCTTCCAGGCTCGCCGCCAACCCGCCACCTCCGAGAGA 759  
 Qy 481 GTTCTCTGAGGTGCTCTTTATTTCTGAGGAGAGCGAGTCCGATGCTCTTTTGT 540  
 Db 760 GTTCTCTGAGGTGCTCTTTATTTCTGAGGAGAGCGAGTCCGATGCTCTTTTGT 819  
 Qy 541 CCTGTCAATTAATGAAGAGCTGGTAAGCATTTGTAATTAATTCAGCTGACTGAAT 600  
 Db 820 CCTGTCAATTAATGAAGAGCTGGTAAGCATTTGTAATTAATTCAGCTGACTGAAT 879  
 Qy 601 TTTCAATTAATGAAGAGAGGAGGAGTGAAGTGAATTCACCCCACTGCTGTGAAC 660  
 Db 880 TTTCAATTAATGAAGAGAGGAGGAGTGAAGTGAATTCACCCCACTGCTGTGAAC 939  
 Qy 661 CGGAGTCAAGGCGAGCTGCGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 720  
 Db 940 CGGAGTCAAGGCGAGCTGCGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 999  
 Qy 721 TTTTGAAGGCTCCAGTGTCTCAATTCCTGATGAGGAGGAGTGTGAGACTGCAGA 780  
 Db 780 TTTTGAAGGCTCCAGTGTCTCAATTCCTGATGAGGAGGAGTGTGAGACTGCAGA



DE Ovarian carcinoma sequence isolate 57887 extended cDNA.  
XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
KM ss.  
XX Homo sapiens.  
OS US2002004491-A1.  
PN 10-JAN-2002.  
PD 03-APR-2001; 2001US-0852594.  
PE 10-SEP-1999; 9905-0394374.  
PR 01-MAY-2000; 2000US-0561778.  
PR 15-AUG-2000; 2000US-0640173.  
PR 07-SEP-2000; 2000US-0656668.  
PR 14-NOV-2000; 2000US-0713550.  
PA (XUJ/) XU J.  
PA (STOL/) STOLK J A.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PI Xu J, Stolk JA, Algate PA, Fling SP;  
PI WPI; 2002-171027/22.  
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
PT prevention and/or treatment of cancer, especially ovarian cancer -  
XX Claim 1a; Page 119-120; 131pp; English.  
XX The invention relates to ovarian tumour polynucleotides and polypeptides  
CC that may be utilized in cancer therapy, for example in a vaccine or  
CC gene therapy. Polypeptides and polynucleotides of the invention are  
CC useful for detecting a cancer in a patient, for stimulating and/or  
CC expanding T-cells specific for a tumour protein, and for inhibiting the  
CC development of a cancer in a patient. They are also useful for  
CC stimulating an immune response in a patient, and for treating a cancer in  
CC a patient and for determining the presence of a cancer in a patient.  
CC The isolated polynucleotides of the invention are useful for their  
CC ability to selectively form duplex molecules with complementary stretches  
CC of the entire desired gene or gene fragments, and for designing and  
CC preparing ribozyme molecules for inhibiting expression of tumour  
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
CC invention are also useful in recombinant DNA molecules to direct  
CC expression of a polypeptide in appropriate host cells. The current  
CC sequence represents the extended cDNA sequence of ovarian carcinoma  
CC isolate 57887 given in record ABL48956.  
XX  
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;  
Query Match 100.0%; Score 1619; DB 24; Length 1619;  
Best Local Similarity 100.0%; Freq. No. 0;  
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCGAAGTTTGGGAGATGTTCTTCTCCAGAGCTTGGCGTGCAGAAATCAGTGTACCA 60  
Db 1 GCGAAGTTTGGGAGATGTTCTTCTCCAGAGCTTGGCGTGCAGAAATCAGTGTACCA 60  
QY 61 GTGTGAAGAAATTCAGACTGAACAGACGTCTCTCCCGGAGTTGATTTGTAATTCAC 120  
Db 61 GTGTGAAGAAATTCAGACTGAACAGACGTCTCTCCCGGAGTTGATTTGTAATTCAC 120  
QY 121 GGTGAAGCTTCAAGACATGTGTAGAAAGAGTGTAGAGCAAGTCCGGGATCATGTA 180  
Db 121 GGTGAAGCTTCAAGACATGTGTAGAAAGAGTGTAGAGCAAGTCCGGGATCATGTA 180  
QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTCTGCGGGTACAGTCTT 240  
Db 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTCTGCGGGTACAGTCTT 240

QY 241 CTGCTCCCGAGGAAAGTAACTAGTGTGATCAGCTGCTGCAACACCCCTTTGTAA 300  
Db 241 CTGCTCCCGAGGAAAGTAACTAGTGTGATCAGCTGCTGCAACACCCCTTTGTAA 300  
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCTCTCAGGCGAGGCTCCGCAC 360  
Db 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCTCTCAGGCGAGGCTCCGCAC 360  
QY 361 CACCATCCTGTTCTCAATATAGCCCTCTTCTCGGCACTGCTGAAGCTGAAGAGATG 420  
Db 361 CACCATCCTGTTCTCAATATAGCCCTCTTCTCGGCACTGCTGAAGCTGAAGAGATG 420  
QY 421 CCACCCCTCTCGATTTGTTCTCCAGCCCTCGCCCAACCCCACTCCCTGATGA 480  
Db 421 CCACCCCTCTCGATTTGTTCTCCAGCCCTCGCCCAACCCCACTCCCTGATGA 480  
QY 481 GTTCTTCTGGGTGCTCTTTATTTCTGGGTAGGAGGCGGAGTCCGTTCTTTGTT 540  
Db 481 GTTCTTCTGGGTGCTCTTTATTTCTGGGTAGGAGGCGGAGTCCGTTCTTTGTT 540  
QY 541 CCGTGCAGAAATATGAAGAGCTCGGTAAAGCATTTGAAATTAATTCAGCTGATGAAT 600  
Db 541 CCGTGCAGAAATATGAAGAGCTCGGTAAAGCATTTGAAATTAATTCAGCTGATGAAT 600  
QY 601 TTTCAATATGATCTGAAGAGAGGTGAGTGAAGTTCAACCCCATGCTGTGTAA 660  
Db 601 TTTCAATATGATCTGAAGAGAGGTGAGTGAAGTTCAACCCCATGCTGTGTAA 660  
QY 661 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTCTTAAGAGTCACTGAGGTGGCATCTGCC 720  
Db 661 CGGAGTCAAGGCGCAGGCTGCGAGAGTCACTCTTAAGAGTCACTGAGGTGGCATCTGCC 720  
QY 721 TTTTGAAGGCTCCAGTCTCATTTCCATCCCTGATGGGGGATGATTTGATGATGAGA 780  
Db 721 TTTTGAAGGCTCCAGTCTCATTTCCATCCCTGATGGGGGATGATTTGATGATGAGA 780  
QY 781 GTGAGAGTGAAGTCTTCTTAAGGCTGAGGCGCACTTCCCACTCAAGCTCCCTGCTTG 840  
Db 781 GTGAGAGTGAAGTCTTCTTAAGGCTGAGGCGCACTTCCCACTCAAGCTCCCTGCTTG 840  
QY 841 ACATTCAGAACTTCAATGCTCTCGAAGAAACATTTCTGACAGCAAGTTGGTGTTCGCCG 900  
Db 841 ACATTCAGAACTTCAATGCTCTCGAAGAAACATTTCTGACAGCAAGTTGGTGTTCGCCG 900  
QY 901 CTGAGTGGGCTTACGTACCTGAGACATGATGATGAGTGGAGTGGGCTCGGCT 960  
Db 901 CTGAGTGGGCTTACGTACCTGAGACATGATGATGAGTGGAGTGGGCTCGGCT 960  
QY 961 CGCTCTGAAGAGTGTCTTAAGAAATCTTCTCAGTCTCTTGCAGAGAGTGGCGCGGG 1020  
Db 961 CGCTCTGAAGAGTGTCTTAAGAAATCTTCTCAGTCTCTTGCAGAGAGTGGCGCGGG 1020  
QY 1021 ACGCAAGAGCAAGGCGGCTGCAAAAGCGGCGCTGTGCTGTGTGATGGCATGTA 1080  
Db 1021 ACGCAAGAGCAAGGCGGCTGCAAAAGCGGCGCTGTGCTGTGTGATGGCATGTA 1080  
QY 1081 CGCGAGGCGCTTCTCGTGTGTTGGGCTGCTGACGAGAGGCGGCGACACGACTTGC 1140  
Db 1081 CGCGAGGCGCTTCTCGTGTGTTGGGCTGCTGACGAGAGGCGGCGACACGACTTGC 1140  
QY 1141 ACGAAGACCCCGAAGTGTGAGAGACACGCTGTACAGAGAGCGGCTGTATGATCCGAG 1200  
Db 1141 ACGAAGACCCCGAAGTGTGAGAGACACGCTGTACAGAGAGCGGCTGTATGATCCGAG 1200  
QY 1201 CTGAGGTGAAGAAAGCTTCCGAGAGGAGGAGATCATGTACGCCCGGAAGTACGAC 1260  
Db 1201 CTGAGGTGAAGAAAGCTTCCGAGAGGAGGAGATCATGTACGCCCGGAAGTACGAC 1260  
QY 1261 CTGCTCCAGTGTGCTGTTGGGTTGGCCGACGATGATCTCCGAAATCTGTTGGGATC 1320  
Db 1261 CTGCTCCAGTGTGCTGTTGGGTTGGCCGACGATGATCTCCGAAATCTGTTGGGATC 1320  
QY 1321 CAGCATAGGCGCAATGTCTCAACAATCAGCCCTGGGAGAGACAGGAGGAGAGAC 1380

XX 14-NOV-2000; 2000US-0713550.  
PR 03-APR-2001; 2001US-0825294.  
PR 02-OCT-2001; 2001US-0970966.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;  
XX WPI: 2002-500186/53.  
XX  
XX Novel ovarian cancer polypeptide and polynucleotide, useful for  
XX detecting the presence of ovarian cancer in a patient, and in  
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
XX  
XX  
PS Claim 2: Page 195; 197pp: English.  
XX  
XX The present invention provides human ovarian cancer associated proteins  
XX and coding sequences. The sequences can be used in the diagnosis and  
XX treatment of ovarian cancers. The present sequence is a coding sequence  
XX of the invention.  
SQ Sequence 1619 BP: 399 A; 415 C; 432 G; 373 T; 0 other:  
  
Query Match 100.0%; Score 1619; DB 24; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGCACATTTTGGCGATTTTCTTCTTCAGAGCTTTGGCTGCAAAATCCAGTCTACCA 60  
DB 1 GGCACATTTTGGCGATTTTCTTCTTCAGAGCTTTGGCTGCAAAATCCAGTCTACCA 60  
QY 61 GTGTGAAGATTCACGCTGACACAGACGCTGCTCCCGGATCATTTGTAATGAC 120  
DB 61 GTGTGAAGATTCACGCTGACACAGACGCTGCTCCCGGATCATTTGTAATGAC 120  
QY 121 GGTGAAGCTTCAAGACATGCTCAGAAAGATGATGAGCAAAATGCGGAGTATGTA 180  
DB 121 GGTGAAGCTTCAAGACATGCTCAGAAAGATGATGAGCAAAATGCGGAGTATGTA 180  
QY 181 CGGCAAGTCTGCTGATCATCAGCGGCTGCTCATCGGCTCTGCGGGTACCACTCTT 240  
DB 181 CGGCAAGTCTGCTGATCATCAGCGGCTGCTCATCGGCTCTGCGGGTACCACTCTT 240  
QY 241 GTGTCTCCCGAGGAAACGTAAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
DB 241 GTGTCTCCCGAGGAAACGTAAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
QY 301 CGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTGCGGCTCAGGCGAGGCTCCGAC 360  
DB 301 CGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTGCGGCTCAGGCGAGGCTCCGAC 360  
QY 361 CACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
DB 361 CACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 421 CCACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
DB 421 CCACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 GTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
DB 481 GTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
QY 541 CCTGTGCAATATGAAGAGCTCGGTAAAGCATTTCTGATTAATTCAGCCGATGAT 600  
DB 541 CCTGTGCAATATGAAGAGCTCGGTAAAGCATTTCTGATTAATTCAGCCGATGAT 600  
QY 601 TTTTCAATATGCTGTAAGAGAGGAGTGAAGTCAACCCCAATGCTGTGTAC 660  
DB 601 TTTTCAATATGCTGTAAGAGAGGAGTGAAGTCAACCCCAATGCTGTGTAC 660

QY 661 CGGAGTCAAGGCGAGGCTGCGAGATGCTTCTTGAAGTCACTGAGTGGCATCTGCC 720  
DB 661 CGGAGTCAAGGCGAGGCTGCGAGATGCTTCTTGAAGTCACTGAGTGGCATCTGCC 720  
QY 721 TTTTGTAAAGCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
DB 721 TTTTGTAAAGCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
QY 781 GTGAGAGTGAAGTCTTCTTGAAGGAGGAGTTCACCACTCAAGGCTCCGCTG 840  
DB 781 GTGAGAGTGAAGTCTTCTTGAAGGAGGAGTTCACCACTCAAGGCTCCGCTG 840  
QY 841 ACATTCAAACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
DB 841 ACATTCAAACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
QY 901 CTGAGTTGGCTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
DB 901 CTGAGTTGGCTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
QY 961 CGCTGTGAAGGCTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
DB 961 CGCTGTGAAGGCTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
QY 1021 ACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080  
DB 1021 ACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080  
QY 1081 CGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
DB 1081 CGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
QY 1141 ACAGAACCCCGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
DB 1141 ACAGAACCCCGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
QY 1201 CTGAGTGAAGAAAGCTCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260  
DB 1201 CTGAGTGAAGAAAGCTCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260  
QY 1261 CTGCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
DB 1261 CTGCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
QY 1321 CAGCATACGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
DB 1321 CAGCATACGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
QY 1381 AGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1440  
DB 1381 AGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1440  
QY 1441 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
DB 1441 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
QY 1501 CAGCTCTTTTGGCAAG 1560  
DB 1501 CAGCTCTTTTGGCAAG 1560  
QY 1561 CTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAGAGAGAGAGAG 1619  
DB 1561 CTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAGAGAGAGAGAG 1619  
  
RESULT 3  
ABLA0345  
ID ABLA0345 standard; cDNA; 1619 BP.  
XX  
XX ABLA0345;  
AC  
XX  
XX 28-JUN-2002 (first entry)  
XX

PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
 PT  
 XX  
 PS Claim 2: Page 189-190; 197pp; English.

XX The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 100.0%; Score 1619; DB 24; Length 1619;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATGTTCTTCTGCTCCAGGCTTGGCTGCAAAATCCAGTGTACCA 60  
 DB 1 GGCACCTTTTGGGATGTTCTTCTGCTCCAGGCTTGGCTGCAAAATCCAGTGTACCA 60  
 QY 61 GTGTGAAGATTCACAGCTGACAGACCTGCTCCCGGAGTTCAATGTAATTTGCAC 120  
 DB 61 GTGTGAAGATTCACAGCTGACAGACCTGCTCCCGGAGTTCAATGTAATTTGCAC 120  
 QY 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180  
 DB 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180  
 QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTTCCCGGGATACAGTCTT 240  
 DB 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTTCCCGGGATACAGTCTT 240  
 QY 241 CTGCTCCCGAGGAAACATGACATGTTGATGATGCTGCTCAACACCCCTTTGTA 300  
 DB 241 CTGCTCCCGAGGAAACATGACATGTTGATGATGCTGCTCAACACCCCTTTGTA 300  
 QY 301 CCGGCGCAAGGCCCAAGAAAGGGGAAATTCGCTCGGCGCTCAGGCGCAAGGCTCCGAC 360  
 DB 301 CCGGCGCAAGGCCCAAGAAAGGGGAAATTCGCTCGGCGCTCAGGCGCAAGGCTCCGAC 360  
 QY 361 CACCAATCCCTGCTCTCAAAATTAAGCCCTCTTCGCGCACACTGCTGAAGTGAAGAGATG 420  
 DB 361 CACCAATCCCTGCTCTCAAAATTAAGCCCTCTTCGCGCACACTGCTGAAGTGAAGAGATG 420  
 QY 421 CCACCCCTCTGCAATGTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTAGATGA 480  
 DB 421 CCACCCCTCTGCAATGTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTAGATGA 480  
 QY 481 GTTCTTCTGGGTGTCCTTTATTCGAGTGAAGGAGCGGAGTCCGTTCTTTGTT 540  
 DB 481 GTTCTTCTGGGTGTCCTTTATTCGAGTGAAGGAGCGGAGTCCGTTCTTTGTT 540  
 QY 541 CCGTGCAAAATATGAAGAGAGCTCGGTAAAGCATCTGTAATTAATTCAGCTGACTGAAT 600  
 DB 541 CCGTGCAAAATATGAAGAGAGCTCGGTAAAGCATCTGTAATTAATTCAGCTGACTGAAT 600  
 QY 601 TTTCAGTATGATTAAGAGAGAGAGTGAAGTCAACCCCACTGCTGTGTAC 660  
 DB 601 TTTCAGTATGATTAAGAGAGAGAGTGAAGTCAACCCCACTGCTGTGTAC 660  
 QY 661 CCGAGTCAAGGCCAGGCTGGCAGAGTCACTCTTGAAGTCACTAGGTGGGCTATGCC 720  
 DB 661 CCGAGTCAAGGCCAGGCTGGCAGAGTCACTCTTGAAGTCACTAGGTGGGCTATGCC 720  
 QY 721 TTTTGAAGCCCTCAGCTGCTCATTCACCTGATGGGGGATAGTTTGAAGTGCAGA 780  
 DB 721 TTTTGAAGCCCTCAGCTGCTCATTCACCTGATGGGGGATAGTTTGAAGTGCAGA 780  
 QY 781 GTGAGAGTACGTTTCTTAGGGCTGAGAGGCCACTTCCACTCAAGGCTCCCTGCTTG 840  
 DB 781 GTGAGAGTACGTTTCTTAGGGCTGAGAGGCCACTTCCACTCAAGGCTCCCTGCTTG 840

QY 841 ACATTCAACTTCAATGCTCCTGAAGAACCATTCCTGACAGAGAAATGGCTGTTGCGCC 900  
 DB 841 ACATTCAACTTCAATGCTCCTGAAGAACCATTCCTGACAGAGAAATGGCTGTTGCGCC 900  
 QY 901 CTGATTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCT 960  
 DB 901 CTGATTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCT 960  
 QY 961 CGCTCTGAAAAGTCTTGAAGAAATCTTCTCAGTTCCTTTCAGAGAGACTGGCGCGG 1020  
 DB 961 CGCTCTGAAAAGTCTTGAAGAAATCTTCTCAGTTCCTTTCAGAGAGACTGGCGCGG 1020  
 QY 1021 ACAGCAAGACAG 1080  
 DB 1021 ACAGCAAGACAG 1080  
 QY 1081 CGCGAGGCGCTTCTGTTGTTGGCTGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
 DB 1081 CGCGAGGCGCTTCTGTTGTTGGCTGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
 QY 1141 ACAGCAAGACAG 1200  
 DB 1141 ACAGCAAGACAG 1200  
 QY 1201 CTGAGGTGAAGAAAGTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
 DB 1201 CTGAGGTGAAGAAAGTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
 QY 1261 CTGCTCAGTGTGCTGTTGGGTTGGCGCAGACCATGATCTCCGAATCTGTTGGGATC 1320  
 DB 1261 CTGCTCAGTGTGCTGTTGGGTTGGCGCAGACCATGATCTCCGAATCTGTTGGGATC 1320  
 QY 1321 CAGCATACGCGCAATGTCACACAAATACAGCCCTGCGAGACAGAGAGAGAGAGAGAG 1380  
 DB 1321 CAGCATACGCGCAATGTCACACAAATACAGCCCTGCGAGACAGAGAGAGAGAGAGAG 1380  
 QY 1381 AGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1440  
 DB 1381 AGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1440  
 QY 1441 CCCCTCTGTTCTGCTTACTGAGGCAAGAAATGATCAATTTTTCAGTGTGACTTGA 1500  
 DB 1441 CCCCTCTGTTCTGCTTACTGAGGCAAGAAATGATCAATTTTTCAGTGTGACTTGA 1500  
 QY 1501 CAGCTCTTTTGGCAAG 1560  
 DB 1501 CAGCTCTTTTGGCAAG 1560  
 QY 1561 CTGCTTGAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAGAGAGAGAGAG 1619  
 DB 1561 CTGCTTGAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAGAGAGAGAGAG 1619

# RESULT 2

ABT03281  
 ID ABT03281 standard; cDNA; 1619 BP.

XX AC ABT03281;

XX 05-SEP-2002 (first entry)

XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

XX cytosolic; gene; ss.

XX Homo sapiens.

XX MO200239885-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US45395.

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 15:03:08 ; Search time 318.774 Seconds

11437.514 Million cell updates/sec

Title: US-09-970-966-2111

Sequence: 1 ggcaacttttcgcatgt.....aaaaaaaaaaaaaa 1619

Scoring table: OLIGO\_NUC

Searched: 2185239 seqs, 1125999159 residues

word size :

Total number of hits satisfying chosen parameters: 1309984

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Minimum DB seq length: 0
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Maximum DB seq length: 200000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

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24:	/SDS2/gcgdata/genseq/genseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1619	100.0	1619	24	ABT03277	Human ovarian cancer
2	1619	100.0	1619	24	ABT03381	Human ovarian cancer
3	1619	100.0	1619	24	ABL40345	Ovarian carcinoma
4	1619	100.0	1619	24	ABL40349	Ovarian carcinoma
5	1396	86.2	1897	24	ABT03284	Human ovarian cancer
6	1396	86.2	1897	24	ABL40352	Ovarian carcinoma
7	1264	78.1	1524	24	AKR33543	cdNA encoding human
8	1205	74.4	1953	21	AAE22400	Human secreted protein
9	1205	74.4	1956	22	AAE64188	Human secreted protein

C	10	1149	71.0	2528	22	AAD184260	Human G protein cou
C	11	1030	63.6	1608	24	ABO544331	Human ovarian anti
C	12	1014	62.6	1890	22	AAF93845	Human CDNA encodin
C	13	486	30.0	625	24	ABT03280	Human ovarian carc
C	14	486	30.0	625	24	ABL40348	Ovarian carcinoma
C	15	486	30.0	625	24	ABL87898	Human ovarian carc
C	16	386	23.8	1362	24	ABT03279	Human ovarian carc
C	17	386	23.8	1362	24	ABL40347	Ovarian carcinoma
C	18	366	22.6	587	22	AAF94186	Primer specific for
C	19	364	22.5	444	22	AAF50766	Human tumour assoc
C	20	315	19.5	369	22	AAF95007	Human ovarian carc
C	21	315	19.5	369	24	ABT03274	Human ovarian carc
C	22	315	19.5	369	24	ABL48956	Ovarian carcinoma
C	23	315	19.5	373	24	ABL78538	Human ovarian carc
C	24	310	19.1	396	22	AAF94818	Human ovarian carc
C	25	310	19.1	396	24	ABT03085	Human ovarian carc
C	26	310	19.1	396	24	ABL48768	Ovarian carcinoma
C	27	307	19.0	349	24	ABL79431	Human ovarian carc
C	28	271	16.7	1010	24	ABT03282	Human ovarian carc
C	29	271	16.7	1010	24	ABL40350	Ovarian carcinoma
C	30	264	16.3	409	24	ABL81262	Human ovarian carc
C	31	250	15.4	591	22	AAF94044	Primer specific for
C	32	166	10.3	201	24	ABL85916	Human ovarian carc
C	33	154	9.5	390	24	ABL78554	Human ovarian carc
C	34	146	9.0	480	24	ABT03283	Human ovarian carc
C	35	146	9.0	480	24	ABL40351	Ovarian carcinoma
C	36	125	7.7	381	24	ABL84848	Human ovarian carc
C	37	120	7.4	430	24	ABL81273	Human ovarian carc
C	38	112	6.9	558	24	ABL79397	Human ovarian carc
C	39	60	3.7	60	24	ABN41927	Human spliced tran
C	40	27	1.7	1368	22	AA560824	Human cancer agent
C	41	26	1.6	50	22	AAL33984	Human SNP oligonuc
C	42	26	1.6	50	22	AAL33985	Human SNP oligonuc
C	43	26	1.6	50	22	AAL33986	Human SNP oligonuc
C	44	25	1.6	2481	22	AA084571	Soybean magnesium
C	45	25	1.5	51	22	AAL27277	Human SNP oligonuc

## ALIGNMENTS

## RESULT 1

ID ABT03277 standard; cDNA; 1619 BP.

AC ABT03277

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

**KW** cytostatic; gene; ss.

OS Homo sapiens

PN W0200239885-A2

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stoilk JA, Algate PA, Fling SP, Molesh DA;

DR WPI; 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for



264

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repeat_region      9096. .9246      /rpt_family="MIR"
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1594 CAGGTGTAATAAAAAAAAAAAAAAAAAAAAA 1619
Db 83484 CAGGTGTAATAAAAAAAAAAAAAAAAAAAAA 83459
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Search completed: November 7, 2002, 23:01:52  
Job time : 6567.22 secs





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REFERENCE 1 (bases 1 to 1409)
AUTHORS Eshel,D., Prusky,D. and Dimor,A.
TITLE Exoglucanase of Alternaria alternata
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1409)
AUTHORS Eshel,D., Prusky,D. and Dimor,A.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1999) Postharvest Sciences, Volcani Center, POB
6, Bet-Dagan 50250, Israel
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1..1409
Location/Qualifiers
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CDACCPRLKRTKINGENYEGKRPSSNDNAGVGGHSCCAEMDIWANSSTAVTPHS
CTTEQSKCDSDGGGTTISADRTAGVCDPCDGNSTRMGVKDFYGGKTVDSKRTF
VTFPTGTGDAMEIKRFYVQNGKTIADPASVAPGVENSTTTKCDQOKAVFGDTYF
KDKGMMAMAKALANGVLMVSLMDHDHYSNLMIDSTYPTDKNPDITDLGTRGECETS
SGVPADVESQHADATVYVSNINIKFGLNPTG"
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Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1594 CAGGTGTAATAAAAAAAAAAAAAA 1619
DB 1383 CAGGTGTAATAAAAAAAAAAAAAA 1408

RESULT 41
LOCUS AX056994 2481 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 11 from Patent WO0075340.
ACCESSION AX056994
VERSION AX056994.1 GI:12309857
KEYWORDS
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 2481)
REFERENCE Butler,K.H., Farnodu,O.O., Gutteridge,S. and Maxwell,C.A.
AUTHORS Magnesium chelate
TITLE Patent: WO 0075340-A 11 14-DEC-2000;
JOURNAL E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
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1..2481
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1594 CAGGTGTAATAAAAAAAAAAAAAA 1619
DB 2424 CAGGTGTAATAAAAAAAAAAAAAA 2449

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RESULT 42
LOCUS AF514845
DEFINITION Rana catesbeiana epithelial sodium channel ENac beta subunit mRNA,
complete cds.
ACCESSION AF514845
VERSION AF514845.1 GI:21435743
KEYWORDS
SOURCE bullfrog.
ORGANISM Rana catesbeiana
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
Aquarana.
REFERENCE 1 (bases 1 to 2745)
AUTHORS Jensik,P.J., Holbird,D. and Cox,T.
TITLE Cloning and partial characterization of an amiloride-sensitive
sodium channel (fEnac) from adult bullfrog skin
JOURNAL J. Comp. Physiol. B, Biochem. Syst. Environ. Physiol. (2002) In
press
2 (bases 1 to 2745)
REFERENCE Jensik,P.J., Holbird,D. and Cox,T.
AUTHORS Direct Submission
TITLE Submitted (22-MAY-2002) Physiology, Southern Illinois University,
JOURNAL 1135 Lincoln Drive, Carbondale, IL 62901, USA
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168..2135
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ELCTNRTQCSYENFTSGAQAIRKDWYLQFNSTFSTIPEEVKKGXQAEMLILCMF
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BASE COUNT 853 a 381 c 545 g 766 t
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Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1594 CAGGTGTAATAAAAAAAAAAAAAA 1619
DB 2719 CAGGTGTAATAAAAAAAAAAAAAA 2744

RESULT 43
LOCUS BC034500
DEFINITION Homo sapiens, similar to RIKEN CDNA 0610013117 gene, clone
MGC:26926 IMAGE:4838423, mRNA, complete cds.
ACCESSION BC034500
VERSION BC034500.1 GI:21759790
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3889)

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repeat_region      24716..25027
                    /note="AluXs repeat: matches 1..312 of consensus"
repeat_region      25028..25409
                    /note="L1Mc repeat: matches 743..1115 of consensus"
repeat_region      27260..27378
                    /note="L1M2 repeat: matches 5391..5471 of consensus"
repeat_region      27379..27683
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repeat_region      27684..27829
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repeat_region      27830..27938
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misc_feature       complement(27918..28199)
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gene              join(27994..28372,28928..29009)
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                    29660..29707
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                    29662..29705
                    /note="11 copies 4 mer caca 90% conserved"
                    30354..30466
                    /note="L2 repeat: matches 2634..2746 of consensus"
                    30874..30954
                    /note="MIR repeat: matches 160..250 of consensus"
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                    /note="MIR repeat: matches 52..207 of consensus"

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DEFINITION	Zea mays homocysteine S-methyltransferase-1 mRNA, complete cds.		
ACCESSION	AF297044		
VERSION	AF297044.1 GI:10732784		
KEYWORDS	.		
SOURCE	Zea mays.		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.		
REFERENCE	Li,C. and Tarczyński,M. Direct Submission Submitted (18-AUG-2000) RefSeq, Pioneer Hi-Bred International Inc., 7300 NW 62nd Ave., Johnston, IA 50131, USA		
AUTHORS			
TITLE			
JOURNAL			
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BASE COUNT	341 a 301 c 356 g 277 t		
ORIGIN			
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	Best Local Similarity	100.0%; Pred. No. 0.0039;	
	Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1594	CAGTGTAATAAAAAAAAAAAAAA 1619	
	Db	1196 CAGTGTAATAAAAAAAAAAAAAA 1221	
RESULT 40			
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DEFINITION	Alternaria alternata exoglucanase (cl) mRNA, complete cds.		
ACCESSION	AF176571		
VERSION	AF176571.1 GI:6179688		
KEYWORDS	.		
SOURCE	Alternaria alternata.		
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria; Alternaria alternata group.		

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 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1593 ACAGTGTAAAAAAAAAAAAAAAAAAAA 1619  
 Db 80773 ACAGTGTAAAAAAAAAAAAAAAAAAAA 80799

RESULT 38  
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 LOCUS  
 DEFINITION Human DNA sequence from clone RP11-446H13 on chromosome 10.  
 Contains the 3' end of the gene for a novel protein similar to KIAA1059 (ortholog of mouse VPS10 domain receptor protein SORCS), an RPL23A (60S ribosomal protein 23A) pseudogene, ESTs, STS and GSSs, complete sequence.  
 AL133395  
 VERSION AL133395.21 GI:10045255  
 KEYWORDS HTG; KIAA1059; RPL23A; SORCS; VPS10 domain.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 217929)  
 Bird.C.  
 Direct Submission  
 Submitted (11-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequests@sanger.ac.uk  
 On Sep 9, 2000 this sequence version replaced gi:9943953.  
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone configs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr10  
 This sequence is the entire insert of clone RP11-446H13. The true left end of clone RP11-699H2 is at 128287 in this sequence. The true right end of clone RP11-41D21 is at 75932 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unSURE' feature key. RP11-446H13 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see  
 http://www.horl.org/bacpac/home.htm  
 VECTOR: pBACE3.6.

FEATURES  
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 Location/Qualifiers  
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 /chromosome="10"  
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 /clone\_lib="RPCI-11.2"  
 1157..1438  
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 1652..1703  
 /note="Charlie3 repeat: matches 802..850 of consensus"  
 1889..2188  
 /note="AluY repeat: matches 9..308 of consensus"  
 2471..2531  
 /note="L1BP1 repeat: matches 5922..5979 of consensus"  
 2532..2624  
 /note="L1BP1 repeat: matches 6059..6151 of consensus"  
 2628..2689  
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 3591..4071  
 /note="match: GSS: Em:AQ215368"  
 3764..3816  
 /note="L2 repeat: matches 2656..2708 of consensus"  
 complement(4214..4593)  
 /note="match: GSS: Em:AQ516952"  
 4344..4687  
 /note="MSRD repeat: matches 1..394 of consensus"  
 4694..6438  
 /note="MSRD-internal repeat: matches 7..1651 of consensus"  
 6382..6771  
 /note="MSRD repeat: matches 204..394 of consensus"  
 8471..8598  
 /note="2 copies 64 mer 85% conserved"  
 9137..9438  
 /note="AluY repeat: matches 1..302 of consensus"  
 11951..12152  
 /note="MIR repeat: matches 16..205 of consensus"  
 12027..12332  
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 13042..13203  
 /note="MIR repeat: matches 93..260 of consensus"  
 13204..13680  
 /note="L1R22 repeat: matches 5..509 of consensus"  
 13681..13741  
 /note="MIR repeat: matches 34..93 of consensus"  
 16416..16730  
 /note="AluSx repeat: matches 5..310 of consensus"  
 17322..17384  
 /note="AluS repeat: matches 15..77 of consensus"  
 17855..17931  
 /note="MIR repeat: matches 47..113 of consensus"  
 17932..18227  
 /note="AluYb repeat: matches 5..309 of consensus"  
 18228..18321  
 /note="MIR repeat: matches 113..239 of consensus"  
 18961..19248  
 /note="AluSx repeat: matches 5..292 of consensus"  
 complement(19592..20040)  
 /note="match: GSS: Em:AQ359125"  
 20092..20223  
 /note="FLM-C repeat: matches 1..131 of consensus"  
 20286..20341  
 /note="28 copies 2 mer ac 85% conserved"  
 20300..20343  
 /note="11 copies 4 mer acac 95% conserved"  
 21326..21831  
 /note="match: GSS: Em:AQ560506"  
 21616..22005  
 /note="match: GSS: Em:AQ191866"  
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 /note="AluY repeat: matches 1..307 of consensus"  
 22747..23126  
 /note="L1 repeat: matches 4745..5127 of consensus"

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misc_feature      47492..59604
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misc_feature      59705..74258
                  /note="assembly_fragment"
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Query Match      1.7%; Score 27; DB 2; Length 212690;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1593 ACAGGTGTAACAAAAA 1619
    |||||||
Db 42174 ACAGGTGTAACAAAAA 42200

RESULT 37
AC069297      214411 bp DNA linear HTG 25-MAY-2000
LOCUS      Mus musculus chromosome 12 clone RP23-2N7 strain C57BL6/J, WORKING
DEFINITION
AC069297      AC069297.1 GI:8072378
VERSION      AC069297.1 GI:8072378
KEYWORDS
SOURCE      Mus musculus.
ORGANISM      Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      1 (bases 1 to 214411)
                Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
                Bouffard,G.G., Dietrich,N.L., Eagle,W.O., Gupta,J., Ho,S.-L.,
                Huang,M.C., Idol,J., Lee-Lin,S.-O., Maduro,Q.L., Maduro,V.B.,
                Mastrian,S.D., McCloskey,J.C., Morse,E., Ojodu,M.A., Pearson,R.,
                Stantitop,S., Summers,T.J., Thomas,J.W., Thomas,P.J.,
                Tingson,E.E., Touchman,J.W., Tran,J.T., Vogt,J.L., Walker,M.A.,
                Wechtery,K.D. and Green,E.D.
TITLE      NISC Mouse Sequencing Initiative
JOURNAL
REFERENCE      Unpublished
AUTHORS      2 (bases 1 to 214411)
                Green,E.D.
TITLE      Direct Submission
JOURNAL
REFERENCE      Submitted (25-MAY-2000) NIH Intramural Sequencing Center, 8717
AUTHORS      Grovmont Circle, Gaithersburg, MD 20877, USA
TITLE      Genome Center
JOURNAL
REFERENCE      -----
AUTHORS      Center: NIH Intramural Sequencing Center
                Center code: NISC
                Web site: http://www.nisc.nih.gov
                Contact: nisc.mouse@nhgri.nih.gov
                ----- Project Information
                Center project name: us
                Center clone name: 002N07
                ----- Summary Statistics
                Sequencing vector: plasmid; n/a; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.990319
                Consensus quality: 204922 bases at least Q40
                Consensus quality: 207590 bases at least Q30
                Consensus quality: 209017 bases at least Q20
                Insert size: 205000; agarose-tp
                Insert size: 248000; pulse-field-gel
                Insert size: 212611; sum-of-ctrls
                Quality coverage: 5.40x in Q20 bases; agarose-tp
                Quality coverage: 4.46x in Q20 bases; pulse-field-gel
                Quality coverage: 5.20x in Q20 bases; sum-of-ctrls
                -----
                * NOTE: This is a 'working draft' sequence. It currently
                * consists of 19 contigs. The true order of the pieces
                * is not known and their order in this sequence record is
                * arbitrary. Gaps between the contigs are represented as
                * runs of N, but the exact sizes of the gaps are unknown.
                * This record will be updated with the finished sequence
                * as soon as it is available and the accession number will
                * be preserved.

```

```

1
* 2372 2371: contig of 2371 bp in length
* 2472 2471: gap of unknown length
* 7037 7036: contig of 4565 bp in length
* 7137 7136: gap of unknown length
* 11837 11837: contig of 4701 bp in length
* 11938 11937: gap of unknown length
* 11938 16456: contig of 4519 bp in length
* 16457 16556: gap of unknown length
* 16557 24064: contig of 7508 bp in length
* 24065 24164: gap of unknown length
* 24165 30372: contig of 6208 bp in length
* 30373 30472: gap of unknown length
* 30473 38478: contig of 8006 bp in length
* 38479 38579: gap of unknown length
* 38579 47748: contig of 9170 bp in length
* 47749 47848: gap of unknown length
* 47849 56374: contig of 8526 bp in length
* 56375 56474: gap of unknown length
* 56475 68247: contig of 11773 bp in length
* 68248 68347: gap of unknown length
* 68348 78809: contig of 10462 bp in length
* 78810 78909: gap of unknown length
* 78910 89212: contig of 10303 bp in length
* 89213 89312: gap of unknown length
* 89313 99267: contig of 9955 bp in length
* 99268 99367: gap of unknown length
* 99368 110419: contig of 11052 bp in length
* 110420 110519: gap of unknown length
* 110520 124151: contig of 13632 bp in length
* 124152 124251: gap of unknown length
* 124252 141079: contig of 16828 bp in length
* 141080 141179: gap of unknown length
* 141180 160980: contig of 19801 bp in length
* 160981 161080: gap of unknown length
* 161081 185614: contig of 24534 bp in length
* 185615 214411: contig of 28697 bp in length.
* 185715

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        /strain="C57BL6/J"
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        /chromosome="12"
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        /clone_1b="RPCT mouse BAC library 23"
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```



TITLE  
JOURNAL  
COMMENT

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lepocky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strassman, N., Subramanian, A., Talmas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (15-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 15, 2002 this sequence version replaced g1:20531892.  
All repeats were identified using RepeatMasker:  
Smith, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information  
Center project name: L22352  
Center clone name: 67\_H-24

----- Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 203101 bases at least Q40  
Consensus quality: 204725 bases at least Q30  
Consensus quality: 205415 bases at least Q20  
Insert size: 210000; agarose-fp  
Quality coverage: 14.3 in Q20 bases; sum-of-coverage  
Quality coverage: 14.3 in Q20 bases; sum-of-coverage

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 26 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

1 618: contig of 618 bp in length  
\* 619 718: gap of 100 bp  
\* 719 1375: contig of 657 bp in length  
\* 1376 1475: gap of 100 bp  
\* 1476 2114: contig of 639 bp in length  
\* 2115 2214: gap of 100 bp  
\* 2215 2843: contig of 629 bp in length  
\* 2844 2943: gap of 100 bp  
\* 2944 3067: contig of 124 bp in length  
\* 3068 3167: gap of 100 bp  
\* 3168 3352: contig of 185 bp in length  
\* 3353 3452: gap of 100 bp  
\* 3453 4030: contig of 578 bp in length  
\* 4031 4130: gap of 100 bp  
\* 4131 4757: contig of 627 bp in length  
\* 4758 4857: gap of 100 bp  
\* 4858 5064: contig of 207 bp in length  
\* 5065 5164: gap of 100 bp  
\* 5165 6283: contig of 1119 bp in length  
\* 6284 6383: gap of 100 bp  
\* 6384 7505: contig of 1122 bp in length  
\* 7506 7605: gap of 100 bp

## FEATURES

## source

\* 7606 8326: contig of 721 bp in length  
\* 8327 8426: gap of 100 bp  
\* 8427 9838: contig of 1412 bp in length  
\* 9839 9938: gap of 100 bp  
\* 9939 11695: contig of 1757 bp in length  
\* 11696 11795: gap of 100 bp  
\* 11796 15821: contig of 4026 bp in length  
\* 15822 15921: gap of 100 bp  
\* 15922 20158: contig of 4237 bp in length  
\* 20159 20258: gap of 100 bp  
\* 20259 26711: contig of 6453 bp in length  
\* 26712 26811: gap of 100 bp  
\* 26812 35760: contig of 8949 bp in length  
\* 35761 35860: gap of 100 bp  
\* 35861 47391: contig of 11531 bp in length  
\* 47392 47491: gap of 100 bp  
\* 47492 59604: contig of 12113 bp in length  
\* 59605 59704: gap of 100 bp  
\* 59705 74258: contig of 14554 bp in length  
\* 74259 74358: gap of 100 bp  
\* 74359 93680: contig of 19322 bp in length  
\* 93681 93780: gap of 100 bp  
\* 93781 113564: contig of 19784 bp in length  
\* 113565 113664: gap of 100 bp  
\* 113665 134201: contig of 20537 bp in length  
\* 134202 134301: gap of 100 bp  
\* 134302 159668: contig of 25367 bp in length  
\* 159669 159768: gap of 100 bp  
\* 159769 212690: contig of 52922 bp in length.

Location/Qualifiers  
1. 212690  
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/db\_xref="taxon:10090"  
/clone="RP23-67H24"  
/clone\_lib="RP23 Female Mouse BAC"  
1. 618  
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719. 1375  
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1476. 2114  
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2215. 2843  
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2944. 3067  
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3168. 3352  
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3453. 4030  
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11796. 15821  
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15922. 20158  
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* 4202 4301: gap of 100 bp
* 4302 4985: contig of 684 bp in length
* 4986 5085: gap of 100 bp
* 5086 5675: contig of 594 bp in length
* 5680 5779: gap of 100 bp
* 5780 6465: contig of 687 bp in length
* 6467 6566: gap of 100 bp
* 6567 7975: contig of 1409 bp in length
* 7976 8075: gap of 100 bp
* 8076 9524: contig of 1445 bp in length
* 9525 9624: gap of 100 bp
* 9625 11091: contig of 1467 bp in length
* 11092 11191: gap of 100 bp
* 11192 12839: contig of 1648 bp in length
* 12840 12939: gap of 100 bp
* 12940 16045: contig of 3110 bp in length
* 16050 16149: gap of 100 bp
* 16150 19066: contig of 2917 bp in length
* 19067 19166: gap of 100 bp
* 19167 26753: contig of 7587 bp in length
* 26754 26853: gap of 100 bp
* 26854 35082: contig of 8225 bp in length
* 35083 35182: gap of 100 bp
* 35183 79627: contig of 44445 bp in length
* 79628 79727: gap of 100 bp
* 79728 97908: contig of 18181 bp in length
* 97909 98008: gap of 100 bp
* 98009 119320: contig of 21312 bp in length
* 119321 119420: gap of 100 bp
* 119421 142295: contig of 22875 bp in length
* 142296 142395: gap of 100 bp
* 142396 166770: contig of 24275 bp in length
* 166771 167770: gap of 100 bp
* 167771 197264: contig of 30494 bp in length
* 197265 197364: gap of 100 bp
* 197365 209572: contig of 12208 bp in length.

```

## FEATURES

```

source

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misc_feature
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Query Match 1.7% Score 27; DB 2; Length 209572;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1593 ACAGTGTAAAAA 1619
DB 204291 ACAGTGTAAAAA 204317

```

```

RESULT 36
AC110232
LOCUS
DEFINITION
  Mus musculus clone RP23-67H24, WORKING DRAFT SEQUENCE, 26 ordered
  pieces.
AC110232
VERSION
  AC110232.4 GI:20800203
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
  Mus musculus.
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
  1 (bases 1 to 212690)
  Birren, B., Linton, L., Nusbaum, C. and Lander, E.
  Mus musculus, clone RP23-67H24
  Unpublished
  2 (bases 1 to 212690)
  Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
  Anderson, S., Baran, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,
  Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B.,
  Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
  Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
  Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Galdyna, S.,
  Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
  Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
  Kamat, A., Karatas, A., Kelle, C., LaRoque, K., Lamazares, R.,
  Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
  MacDonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M.,
  McKean, P., McKernan, K., Meldrum, J., Menus, L., Milnova, T.,
  Milenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
  Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
  Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
  Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
  Roselli, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S.,
  Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
  Strauss, N., Subramanian, A., Talamas, J., Teste, S., Theodore, J.,
  Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
  Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
  Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

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```

TITLE
  Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  3 (bases 1 to 212690)
JOURNAL
  Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
  Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J.,
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  Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
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  Kamat, A., Karatas, A., Kelle, C., LaRoque, K., Lamazares, R.,
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  Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
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  Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
  Strauss, N., Subramanian, A., Talamas, J., Teste, S., Theodore, J.,
  Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
  Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
  Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

```

```

REFERENCE
  Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  3 (bases 1 to 212690)
AUTHORS
  Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
  Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J.,
  Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
  Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
  Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Galdyna, S.,
  Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
  Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
  Kamat, A., Karatas, A., Kelle, C., LaRoque, K., Lamazares, R.,
  Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
  MacDonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M.,
  McKean, P., McKernan, K., Meldrum, J., Menus, L., Milnova, T.,
  Milenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
  Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
  Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
  Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
  Roselli, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S.,
  Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
  Strauss, N., Subramanian, A., Talamas, J., Teste, S., Theodore, J.,
  Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
  Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
  Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

```

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misc_feature      /rpt_family="L2"
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6652..6934
/rpt_family="L2"
repeat_region    /rpt_family="L2"
7091..7404
/rpt_family="Alu"
repeat_region    /rpt_family="Alu"
7375..7426
/rpt_family="(A)n"
repeat_region    /rpt_family="(A)n"
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/rpt_family="Alu"
repeat_region    /rpt_family="Alu"
7650..7671
/rpt_family="AT-rich"
repeat_region    /rpt_family="Alu"
7816..8125
/rpt_family="Alu"
repeat_region    /rpt_family="(TAA)n"
8100..8151
/rpt_family="ERV1"
8144..8534
/rpt_family="ERV1"
8535..8804
/rpt_family="Alu"
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(NID:910797985)"
misc_feature      8811..8830
/Note="similar to Homo sapiens EST BG940653
(NID:914340025)"
misc_feature      8874..9366
/Note="similar to Homo sapiens EST AL545950
(NID:912878612)"
misc_feature      8877..9753
/Note="similar to Homo sapiens EST AL539591
(NID:912868947)"
misc_feature      8877..9633
/Note="similar to Homo sapiens EST B1857420
(NID:915998167)"
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/Note="similar to Homo sapiens EST B1222665
(NID:914676109)"
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/Note="similar to Homo sapiens EST BE552470
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/Note="similar to Homo sapiens EST C04272
(NID:91467523)"
misc_feature      8962..9144
/Note="similar to Homo sapiens EST B1831665
(NID:915943215)"
misc_feature      8973..9366
/Note="similar to Homo sapiens EST BM153036
(NID:917177822)"
misc_feature      8976..9411
/Note="similar to Homo sapiens EST AA449551
(NID:92163301)
zx08b07.r1"
misc_feature      8982..9519
/Note="similar to Homo sapiens EST AW303542
(NID:96713231)
xv20605.x1"

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Query Match      1.7%; Score 27; DB 9; Length 195782;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1593 ACAGTGTAAAAA 1619
DB 55644 ACAGTGTAAAAA 55670

```

RESULT 35

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AC099615          209572 bp   DNA   linear   HTG 16-NOV-2001
LOCUS             Mus musculus clone RP23-41263, WORKING DRAFT SEQUENCE, 19 unordered
DEFINITION        pieces
AC099615          AC099615.1 GI:16946996
VERSION           HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS           Mus musculus.
SOURCE            Mus musculus
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE          1 (bases 1 to 209572)
AUTHORS           Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE             Mus musculus clone RP23-41263
JOURNAL            Unpublished
REFERENCE          2 (bases 1 to 209572)
AUTHORS           Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
                  Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B.,
                  Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
                  Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
                  Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
                  Ginde,S., Gord,S., Goyette,W., Graham,L., Grand-Pierre,N.,
                  Hages,B., Hearford,A., Horton,L., Hulme,W., Illiev,I., Johnson,R.,
                  Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K.,
                  Lamazares,R., Landers,T., Lehoczeky,J., Levine,R., Liu,G.,
                  Maclean,C., MacDonald,P., Major,J., Margus,N., Matthews,C.,
                  McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,
                  Meunus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
                  Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
                  Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
                  Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
                  Roman,J., Roselli,M., Roy,A., Santos,R., Schauer,N., Schupack,R.,
                  Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
                  Straus,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
                  Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,G.,
                  Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
                  Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
DIRECT SUBMISSION Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```

TITLE            JOURNAL
COMMENT           Center: Whitehead Institute/ MIT Center for Genome Research
                  Web site: http://www-seq.wi.mit.edu
                  Contact: sequence_submissions@genome.wi.mit.edu
                  Project Information
                  Center project name: L17310
                  Center clone name: 412.G.3

```

```

----- Summary Statistics -----
Sequencing Vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 204261 bases at least Q40
Consensus quality: 206670 bases at least Q30
Consensus quality: 207399 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 207772; sum-of-ctrls
Quality coverage: 8.2 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-ctrls

```

```

----- NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 4201: contig of 4201 bp in length

```

OY 1593 ACAGTGTAAAAA 1619  
 Db 166939 ACAGTGTAAAAA 166965

RESULT 34  
 AC074389 195782 bp DNA linear PRI 10-JAN-2002  
 LOCUS Homo sapiens BAC clone RP11-510K8 from 7, complete sequence.  
 DEFINITION AC074389  
 VERSION AC074389.8 GI:18042461  
 KEYWORDS HTG.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 AUTHORS Sulston, J.E. and Waterston, R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 MEDLINE 99053792  
 PUBMED 9847074

REFERENCE  
 AUTHORS Cordes, M., Doebber, A., Hawkins, M. and Kozlowski, A.  
 TITLE The sequence of Homo sapiens BAC clone RP11-510K8  
 JOURNAL Unpublished (2002)  
 REFERENCE  
 AUTHORS 3 (bases 1 to 195782)  
 TITLE Waterston, R.H.  
 JOURNAL Direct Submission  
 Submitted (30-JUL-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

REFERENCE  
 AUTHORS 4 (bases 1 to 195782)  
 TITLE Waterston, R.H.  
 JOURNAL Direct Submission  
 Submitted (03-JAN-2002) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

REFERENCE  
 AUTHORS 5 (bases 1 to 195782)  
 TITLE Waterston, R.  
 JOURNAL Direct Submission  
 Submitted (10-JAN-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Jan 3, 2002 this sequence version replaced gl:14209801.

----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [saplens@wustl.edu](mailto:saplens@wustl.edu)  
 ----- Summary Statistics  
 Center project name: H\_NH0510K08

NOTICE: This sequence may not represent the entire insert of this  
 clone. It may be shorter because we only sequence overlapping  
 clone sections once, or longer because we provide a small overlap  
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

MAPPING INFORMATION:  
 The sequence of this clone was established as part of a mapping and  
 sequencing collaboration between the NHGRI Chromosome 7 Mapping  
 Project (Eric D. Green, Director), John D. McPherson in the  
 Department of Genetics (Washington University), and the Washington  
 University Genome Sequencing Center. For additional information

about the map position of this sequence, see  
<http://www.nhgri.nih.gov/DIR/CTB/CHR7>, send  
<mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
 The RPCI-11 human BAC library was made from the blood of one male  
 donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,  
 Tatenio, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved  
 approach for construction of bacterial artificial chromosome  
 libraries. Genomics 51:1-8. The clone may be obtained either from  
 Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong  
 and coworkers at the Roswell Park Cancer Institute  
 (<http://pacpac.med.buffalo.edu>)  
 VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RP11-16P10, 2000 bp overlap.  
 Actual start of this clone is at base position 112086 of  
 RP11-16P10; actual end is at base position 195782 of RP11-510K8.

Data from AC093734 was used to finish this clone, AC074389. There  
 is single M13 clone coverage from 64639 to 64773.

## FEATURES

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 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /chromosome="7"  
 /map="7"  
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 /clone\_id="RPCI-11"  
 3..269  
 /rpl\_family="L1"  
 repeat\_region  
 304..372  
 /rpl\_family="MIR"  
 558..736  
 /rpl\_family="Alu"  
 807..844  
 /rpl\_family="(TTCA)n"  
 946..1126  
 /rpl\_family="C-rich"  
 1099..1278  
 /rpl\_family="CT-rich"  
 1417..1585  
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 1621..1647  
 /rpl\_family="(CA)n"  
 2190..2265  
 /rpl\_family="(GGCTG)n"  
 2261..2383  
 /rpl\_family="MIR"  
 2804..3125  
 /rpl\_family="L2"  
 3175..3277  
 /rpl\_family="MALR"  
 3599..3761  
 /rpl\_family="L2"  
 3762..4059  
 /rpl\_family="Alu"  
 4030..4073  
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 4060..4157  
 /rpl\_family="L2"  
 4173..4432  
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 5572..5740  
 /rpl\_family="MIR"  
 5736..6038  
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 6036..6588  
 /note="match to EST BG924902 (NID:g14319425)"  
 6222..6225  
 /note="similar to Homo sapiens EST BM153036  
 (NID:g17177822)"  
 6506..6560  
 repeat\_region

ACCESSION AC074245  
 VERSION AC074245.3 GI:9887809  
 HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 179364)  
 AUTHORS Waterston, R.H.  
 TITLE The sequence of Homo sapiens clone  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 179364)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-JUL-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 On Aug 24, 2000 this sequence version replaced gi:965207.

----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 ----- Project Information -----  
 Center project name: H\_NH0341F08  
 ----- Summary Statistics -----  
 Sequencing vector: MJ3; 100%  
 Chemistry: Dye-terminator Big Dye; 0% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 167601 bases at least Q40  
 Consensus quality: 170488 bases at least Q30  
 Consensus quality: 171954 bases at least Q20  
 Insert size: 179000; agarose-fp  
 Insert size: 177364; sum-of-contigs  
 Quality coverage: 4.14 in Q20 bases; agarose-fp  
 Quality coverage: 4.29 in Q20 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 21 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 \* 1 1477: contig of 1477 bp in length  
 \* 1478 1577: gap of unknown length  
 \* 1578 3799: contig of 2222 bp in length  
 \* 3800 3899: gap of unknown length  
 \* 3900 6403: contig of 2504 bp in length  
 \* 6404 6503: gap of unknown length  
 \* 6504 10328: contig of 3825 bp in length  
 \* 10329 10428: gap of unknown length  
 \* 10429 13400: contig of 2972 bp in length  
 \* 13401 13500: gap of unknown length  
 \* 13501 18872: contig of 5372 bp in length  
 \* 18873 18972: gap of unknown length  
 \* 18973 25292: contig of 6320 bp in length  
 \* 25293 25392: gap of unknown length  
 \* 25393 30836: contig of 5444 bp in length  
 \* 30837 30936: gap of unknown length  
 \* 30937 36567: contig of 5631 bp in length  
 \* 36568 36667: gap of unknown length  
 \* 36668 45390: contig of 8623 bp in length  
 \* 45391 45391: gap of unknown length  
 \* 45391 55146: contig of 9756 bp in length  
 \* 55147 55246: gap of unknown length  
 \* 55247 66342: contig of 11096 bp in length  
 \* 66343 66442: gap of unknown length  
 \* 66443 76462: contig of 10020 bp in length  
 \* 76463 76562: gap of unknown length

FEATURES  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="2"  
 /clone="RP11-341F8"  
 1..1477  
 /note="assembly\_name:Contig10  
 clone\_end:17  
 vector\_side:left"  
 1578..3799  
 /note="assembly\_name:Contig11"  
 3900..6403  
 /note="assembly\_name:Contig12"  
 6504..10328  
 /note="assembly\_name:Contig13"  
 10429..13400  
 /note="assembly\_name:Contig14"  
 13501..18872  
 /note="assembly\_name:Contig15"  
 18973..25292  
 /note="assembly\_name:Contig16"  
 25393..30836  
 /note="assembly\_name:Contig17"  
 30937..36567  
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 36668..45290  
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 45391..55146  
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 55247..66342  
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 66443..76462  
 /note="assembly\_name:Contig22"  
 76563..89099  
 /note="assembly\_name:Contig23"  
 89200..102001  
 /note="assembly\_name:Contig24"  
 102102..119488  
 /note="assembly\_name:Contig25"  
 119589..135844  
 /note="assembly\_name:Contig26  
 clone\_end:SP6  
 vector\_side:left"  
 135945..153641  
 /note="assembly\_name:Contig27"  
 153742..175739  
 /note="assembly\_name:Contig28"  
 175840..177387  
 /note="assembly\_name:Contig29"  
 177488..179364  
 /note="assembly\_name:Contig29"  
 misc\_feature  
 56993 a 32967 c 33013 g 54383 t 2008 others  
 ORIGIN  
 Query Match 1.7%: Score 27; DB 2; Length 179364;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	Matches	27;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1593	ACACGCTAAAAAAAAAAAAA	1619							
Db	31571	ACACGTAAAAAAAAAAAAAA	31545							

FEATURES

82417 84866: contig of 2450 bp in length  
\* 84867 84966: gap of unknown length  
\* 84967 87959: contig of 2993 bp in length  
\* 87960 88059: gap of unknown length  
\* 88060 92874: contig of 4815 bp in length.  
Location/Qualifiers  
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/organism="Rattus norvegicus"  
/db\_xref="taxon:10116"  
/clone="CH230-286021"

BASE COUNT 23927 a 19653 c 20425 g 23828 t 5041 others

ORIGIN

Query Match 1.7%; Score 27; DB 2; Length 92874;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 GAGAGGAGGAGGATCATGTACGCC 1248  
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DB 75643 GAGAGGAGGAGGATCATGTACGCC 75669

RESULT 29

AL807806/c 127524 bp DNA linear HTG 17-AUG-2002  
LOCUS Mus musculus chromosome X clone RP23-67K19, \*\*\* SEQUENCING IN  
DEFINITION PROGRESS \*\*\*, 2 unordered pieces.  
ACCESSION AL807806  
VERSION AL807806.4 GI:22416117  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 127524)  
Whitehead, S.  
Direct Submission  
Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Aug 21, 2002 this sequence version replaced gi:21694507.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: bm67K19  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 127311 bases at least Q40  
Consensus quality: 127389 bases at least Q30  
Consensus quality: 127413 bases at least Q20  
Insert size: 127424; sum-of-contigs  
Insert size: 142249; 4.2% error; agarose-fp  
Quality coverage: 8.11x in Q20 bases; sum-of-contigs Quality  
coverage: 7.35x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 24018: contig of 24018 bp in length  
\* 24019 24118: gap of 100 bp  
\* 24119 127524: contig of 103406 bp in length.  
Location/Qualifiers  
1..127524  
/organism="Mus musculus"

FEATURES

source

/db\_xref="taxon:10090"  
/chromosome="X"  
/clone="RP23-67K19"  
/clone\_1lb="RP23-23"  
1..24018  
/note="assembly-fragment:00530"  
24119..127524  
/note="assembly-fragment:00777.0"

BASE COUNT 37921 a 23572 c 23357 g 42574 t 100 others

ORIGIN

Query Match 1.7%; Score 27; DB 2; Length 127524;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 ACAGGCTAAAAA 1619  
|||||  
DB 87560 ACAGGCTAAAAA 87534

RESULT 30

AL645938/c 138851 bp DNA linear ROD 11-APR-2002  
LOCUS Mouse DNA sequence from clone RP23-15E24 on chromosome 1, complete  
DEFINITION sequence.  
ACCESSION AL645938  
VERSION AL645938.9 GI:20145949  
KEYWORDS HTG.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Corby, N.  
Direct Submission  
Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Apr 12, 2002 this sequence version replaced gi:20135756.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em: EMBL; Sw:  
SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP  
database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)  
from the RPI-23 Mouse PAC library  
constructed by the group of Pieter de Jong.  
For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pBac3.6.  
Location/Qualifiers  
1..138851  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/chromosome="1"  
/clone="RP23-15E24"  
/clone\_1lb="RP23-23"

BASE COUNT 40695 a 25907 c 27333 g 44916 t

ORIGIN

Query Match 1.7%; Score 27; DB 10; Length 138851;  
Best Local Similarity 100.0%; Pred. No. 0.001;

Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,  
 Rivers, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G.,  
 Scherer, S., Scott, G., Shen, H., Shoochari, N., Sisson, I.,  
 Sodergren, E., Soneike, T., Sparks, A., Stanley, H., Stone, H.,  
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,  
 Tansey, J., Taylor, C., Taylor, T., Telirod, B., Thomas, N., Thomas, S.,  
 Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,  
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,  
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,  
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Nelson, D.,  
 Weinstein, G. and Gibbs, R.

Direct Submission  
 Unpublished  
 2 (bases 1 to 92874)  
 Worley, K.C.

Direct Submission  
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 92874)  
 Worley, K.C.

Direct Submission  
 Submitted (17-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 13, 2002 this sequence version replaced gi:20303189.

----- Genome Center -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
 ----- Project Information -----  
 Center project name: GRJD  
 Center clone name: CH230-286021  
 ----- Summary Statistics -----  
 Sequencing vector: Plasmid:  
 Chemistry: Dye-terminator Big Dye: 100% of reads  
 Assembly program: Phrap: version 0.990329  
 Consensus quality: 32512 bases at least Q40  
 Consensus quality: 34515 bases at least Q30  
 Consensus quality: 35930 bases at least Q20  
 -----

\* NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 50 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1	1057: contig of 1057 bp in length	*	14585	14684: gap of unknown length	*
1058	1157: gap of unknown length	*	14685	14604: contig of 1720 bp in length	*
1158	2410: contig of 1253 bp in length	*	16405	16504: gap of unknown length	*
2411	2510: gap of unknown length	*	16505	17655: contig of 1151 bp in length	*
2511	3571: contig of 1061 bp in length	*	17656	17755: gap of unknown length	*
3572	3671: gap of unknown length	*	17756	19240: contig of 1485 bp in length	*
3672	5259: contig of 1588 bp in length	*	19241	19340: gap of unknown length	*
5260	5359: gap of unknown length	*	19341	20647: contig of 1307 bp in length	*
5360	6436: contig of 1077 bp in length	*	20648	20747: gap of unknown length	*
6437	6536: gap of unknown length	*	20748	22171: contig of 1424 bp in length	*
6537	7705: contig of 1169 bp in length	*	22172	22271: gap of unknown length	*
7706	7805: gap of unknown length	*	22272	23762: contig of 1491 bp in length	*
7806	8811: contig of 1106 bp in length	*	23763	23862: gap of unknown length	*
8812	9011: gap of unknown length	*	23863	25556: contig of 1694 bp in length	*
9012	10370: contig of 1359 bp in length	*	25557	26711: contig of 1055 bp in length	*
10371	10470: gap of unknown length	*	26712	26811: gap of unknown length	*
10471	11914: contig of 1444 bp in length	*	26812	28747: contig of 1936 bp in length	*
11915	12014: gap of unknown length	*	28748	30564: gap of unknown length	*
12015	13145: contig of 1131 bp in length	*	30565	30664: gap of unknown length	*
13146	13245: gap of unknown length	*	30665	32045: contig of 1382 bp in length	*
13246	14584: contig of 1339 bp in length	*	32046	32146: gap of unknown length	*
			32147	33729: contig of 1583 bp in length	*
			33730	33829: gap of unknown length	*
			33830	35524: contig of 1695 bp in length	*
			35525	35624: gap of unknown length	*
			35625	37292: contig of 1668 bp in length	*
			37293	37392: gap of unknown length	*
			37393	38486: contig of 1094 bp in length	*
			38487	38586: gap of unknown length	*
			38587	40145: contig of 1559 bp in length	*
			40146	40245: gap of unknown length	*
			40246	41925: contig of 1680 bp in length	*
			41926	42025: gap of unknown length	*
			42026	43669: contig of 1644 bp in length	*
			43670	43769: gap of unknown length	*
			43770	45713: contig of 1944 bp in length	*
			45714	45813: gap of unknown length	*
			45814	47315: contig of 1502 bp in length	*
			47316	47415: gap of unknown length	*
			47416	48852: contig of 1437 bp in length	*
			48853	48952: gap of unknown length	*
			48953	50511: contig of 1559 bp in length	*
			50512	50611: gap of unknown length	*
			50612	52672: contig of 2061 bp in length	*
			52673	52772: gap of unknown length	*
			52773	54274: contig of 1502 bp in length	*
			54275	54374: gap of unknown length	*
			54375	55993: contig of 2619 bp in length	*
			55994	57093: gap of unknown length	*
			57094	59515: contig of 2422 bp in length	*
			59516	59615: gap of unknown length	*
			59616	61878: contig of 2263 bp in length	*
			61879	61978: gap of unknown length	*
			61979	64520: contig of 2542 bp in length	*
			64521	64620: gap of unknown length	*
			64621	67430: contig of 2810 bp in length	*
			67431	67530: gap of unknown length	*
			67531	68852: contig of 1322 bp in length	*
			68853	68952: gap of unknown length	*
			68953	70700: contig of 1748 bp in length	*
			70701	72350: gap of unknown length	*
			72351	72450: contig of 1550 bp in length	*
			72451	74628: gap of unknown length	*
			74629	74728: contig of 2178 bp in length	*
			74729	76922: gap of unknown length	*
			76923	77022: contig of 2194 bp in length	*
			77023	79345: gap of unknown length	*
			79346	79445: contig of 2323 bp in length	*
			79446	82316: gap of unknown length	*
			82317	82416: contig of 2871 bp in length	*



CDS

/db\_xref="FlyBase:FBgn0022772"  
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 VANGDIHTPTPKSKKEPLESAATEQTPSTRRSILKSASTRALAECPRSIHSNIV  
 EQRFEDDEITSTPRGRSKTVDNEDDTPSKSVCKTPTRTSRSTTKATTSK  
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 YALRVEEVMV"

BASE COUNT 847 a 864 c 821 g 623 t

ORIGIN

Query Match 1.7% Score 27; DB 3; Length 3155;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1593 ACAGTGTAAAAA 1619  
 |||||||||||||||||||  
 DB 3127 ACAGTGTAAAAA 3153

RESULT 27  
 AL645986 48206 bp DNA linear ROD 19-JUL-2002  
 LOCUS Mouse DNA sequence from clone DN-35368 on chromosome 1, complete  
 DEFINITION  
 ACCESSION AL645986  
 VERSION AL645986.6 GI:18855238  
 KEYWORDS HTG;  
 SOURCE Mus musculus.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 48206)  
 Kimberley A.  
 Direct Submission  
 Submitted (18-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humqueres@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Feb 21, 2002 this sequence version replaced gi:11529535.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found they are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em, EMBL; SW,  
 SWISSPROT; Tr, TrEMBL; Wp, WormPeP; Information on the WormPeP

database can be found at  
<http://www.sanger.ac.uk/Projects/C.elegans/wormpep> -----  
 Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: humqueres@sanger.ac.uk  
 -----  
 DN-35368 is from a DIL (Diabetes and Inflammation Laboratory) NOD  
 Mouse BAC library  
 VECTOR: pBAC3.6.  
 Location/Qualifiers  
 1..48206  
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 /db\_xref="taxon:10090"  
 /chromosome="1"  
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 /clone\_lib="NOD mouse library"

BASE COUNT 14007 a 8876 c 9129 g 16194 t

ORIGIN

Query Match 1.7% Score 27; DB 10; Length 48206;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1593 ACAGTGTAAAAA 1619  
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 DB 33779 ACAGTGTAAAAA 33753

RESULT 28  
 AC112072 92874 bp DNA linear HTG 17-JUL-2002  
 LOCUS Rattus norvegicus clone CH230-286021, \*\*\* SEQUENCING IN PROGRESS  
 DEFINITION  
 ACCESSION AC112072.3 GI:21744373  
 VERSION AC112072.3  
 KEYWORDS HTG; HTGS\_PHASE1.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 92874)  
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
 Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,  
 Barberia,J., Benton,J., Bimarge,K., Blankenburg,K., Bonnin,D.,  
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,  
 Buhaey,C., Burch,P., Burkett,C., Butrell,K.L., Byrd,N.C.,  
 Carion,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
 Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,  
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,  
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,T., Dinh,H.H.,  
 Douthwaite,K.J., Drepper,H., Dugan-Rocha,S., Durbin,K.J.,  
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,  
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,  
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
 Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K.,  
 Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,  
 Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,  
 Homs,I.F., Howard,S., Huber,J., Huiyk,S., Hume,J., Jackson,L.E.,  
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,  
 Karlsson,E., Kelly,S., Khan,U., Kling,L., Korvah,J., Kovar,C.,  
 Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loussenge,H.,  
 Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,  
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,B.,  
 Massey,E., Mawliny,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,  
 Miner,G., Miner,Z., Mitchell,T., Mohabhat,K., Morgan,M., Morris,S.,  
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,  
 Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogun,M., Okwuonu,G.,  
 Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,

TITLE  
JOURNAL

Direct Submission  
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure Analysis, Human  
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,  
Japan (E-mail:cdnaletms.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
Fax:81-3-5449-5416)

## COMMENT

NEO human cDNA sequencing project supported by Ministry of  
International Trade and Industry of Japan; CDNA full insert  
sequencing: Research Association for Biotechnology; CDNA library  
construction, 5'- & 3'-end one pass sequencing: Department of  
Virology and Human Genome Center, Institute of Medical Science,  
University of Tokyo (partly supported by Science and Technology  
Agency).

FEATURES  
source

Location/Qualifiers  
1. 1614  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="KAT02340"  
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/cell\_type="signet-ring cell carcinoma"  
/clone\_lib="KAT"  
/note="cloning vector pME18SFL3"

## misc-feature

1. 1614  
/note="highly similar to HUMTSLIC Homo sapiens  
transcription factor SL1 mRNA"

BASE COUNT  
ORIGIN

557 a 296 c 337 g 424 t

Query Match 1.7%; Score 27; DB 9; Length 1614;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGTGTAACAAAAA 1619  
DB 1581 ACAGTGTAACAAAAA 1607

RESULT 25  
LOCUS

BC028978 2625 bp mRNA linear PRI 16-MAY-2002

## DEFINITION

Homo sapiens, clone IMAGE:3919084, mRNA.

ACCESSION  
VERSION

BC028978.1 GI:20810049

KEYWORDS  
SOURCE

Homo sapiens.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 2625)  
Strausberg, R.

TITLE  
JOURNAL

Direct Submission  
Submitted (01-MAY-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC/DCMP/DMP

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amgdbcm.tmc.edu](mailto:amgdbcm.tmc.edu)

Gunnarone, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 42 Row: b Column: 17.

FEATURES  
source

Location/Qualifiers  
1. 2625  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3919084"  
/tissue\_type="Skin, melanotic melanoma."  
/clone\_lib="NIH\_MGC\_72"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORE6"

BASE COUNT  
ORIGIN

860 a 538 c 502 g 725 t

Query Match 1.7%; Score 27; DB 9; Length 2625;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGTGTAACAAAAA 1619  
DB 2567 ACAGTGTAACAAAAA 2593

## RESULT 26

AY094780 3155 bp mRNA linear INV 15-APR-2002

## LOCUS

Drosophila melanogaster LD11626 full insert cDNA.

## DEFINITION

AY094780

ACCESSION  
VERSION

AY094780.1 GI:20151546

KEYWORDS  
SOURCE

FLI-CDNA.

Drosophila melanogaster.

## ORGANISM

Drosophila melanogaster

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 3155)  
Stapleton, M., Brooks, P., Hong, L., Agdayani, A., Carlson, J.,  
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,  
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,  
Miranda, A., Mungall, C.J., Munoz, J., Paclob, J., Paragas, V., Park, S.,  
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.  
and Celniker, S.

Direct Submission  
Submitted (03-APR-2002) Berkeley Drosophila Genome Project,  
Lawrence Berkeley National Laboratory, One Cyclotron Road,  
Berkeley, CA 94720, USA

## COMMENT

Sequence submitted by:

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to  
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,  
Science 2000). The sequence has been subjected to integrity checks  
for sequence accuracy. Presence of a polyA tail and contiguity  
within 100 kb in the genome. Thus we believe the sequence to  
reflect accurately this particular cDNA clone. However, there are  
artifacts associated with the generation of cDNA clones that may  
have not been detected in our initial analyses such as internal  
priming, priming from contaminating genomic DNA, retained introns  
due to reverse transcription of unspliced precursor RNAs, and  
reverse transcriptase errors that result in single base changes.  
For further information about this sequence, including its location  
and relationship to other sequences, please visit our web site  
(<http://fruitfly.berkeley.edu>) or send email to  
[cdna@fruitfly.berkeley.edu](mailto:cdna@fruitfly.berkeley.edu).

FEATURES  
source

Location/Qualifiers  
1. 3155  
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/strain="Y; cn bw sp"

/db\_xref="taxon:7227"

/map="43D3-43D3"

1. 3155  
/gene="Orcl1"

/note="alignment with genomic scaffold AE003840 and gene  
has no introns and polyA tail is encoded in the genomic"

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IGRPVYSLPAEGAGVRKVLQMLRDEFELTMALSCRSRLKETTSHITADMDTPRVN  
PRAIPRL"

BASE COUNT 332 a 199 c 249 g 306 t  
ORIGIN

Query Match 1.7%; Score 27; DB 8; Length 1086;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGGTGTAACAAAAA 1619  
Db 1053 ACAGGTGTAACAAAAA 1079

RESULT 22  
AY118558 1114 bp mRNA linear INV 15-JUN-2002  
LOCUS Drosophila melanogaster LD37258 full insert cDNA.  
ACCESSION AY118558  
VERSION AY118558.1 GI:21428533  
KEYWORDS FLI\_CDNA.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1114)  
Stapleton, M., Brockslein, P., Hong, L., Agbayan, A., Carlson, J.,  
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,  
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,  
Miranda, A., Mungall, C. J., Nuno, J., Paclob, J., Paragas, V., Park, S.,  
Patel, S., Phoumenavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M.,  
and Celisner, S.  
Direct Submission  
Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,  
Lawrence Berkeley National Laboratory, One Cyclotron Road,  
Berkeley, CA 94720, USA  
Sequence submitted by:  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
This clone was sequenced as part of a high-throughput process to  
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,  
Science 2000). The sequence has been subjected to integrity checks  
for sequence accuracy, presence of a polyA tail and contiguity  
within 100 kb in the genome. Thus we believe the sequence to  
reflect accurately this particular cDNA clone. However, there are  
artifacts associated with the generation of cDNA clones that may  
have not been detected in our initial analyses such as internal  
priming, priming from contaminating genomic DNA, retained introns  
due to reverse transcription of unspliced precursor RNAs, and  
reverse transcriptase errors that result in single base changes.  
For further information about this sequence, including its location  
(http://fruitfly.berkeley.edu) or send email to  
cdna@fruitfly.berkeley.edu

FEATURES  
source location/Qualifiers

1..1114  
/organism="Drosophila melanogaster"  
/strain="y: cn bw sp"  
/db\_xref="taxon:7227"  
1..1114  
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48..815  
/note="Longest ORF"  
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CDS

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SROTIEKKNELAOSKEMELTNMLENFRERDDAOIRETRVLADLDSNIFRW  
KEPIORVPEFDDTPDQASANPKPKFBSLDLPDQGMARALHFLDTQIFVDGRNRKA  
KERLQHLDEVAQVLEOSTGEAVTVASSLPKRAVL"

BASE COUNT 334 a 259 c 278 g 243 t  
ORIGIN

Query Match 1.7%; Score 27; DB 3; Length 1114;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGGTGTAACAAAAA 1619  
Db 1066 ACAGGTGTAACAAAAA 1092

RESULT 23  
AX285020 1368 bp DNA linear PAT 20-NOV-2001  
LOCUS AX285020  
DEFINITION Sequence 825 from Patent WO0179556.  
ACCESSION AX285020  
VERSION AX285020.1 GI:17045708  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Lillie, J., Brown, J. L., Bolt, A. and van Hufel, C.  
Novel genes, compositions and methods for the identification,  
assessment, prevention, and therapy of human cancers  
Patent: WO 0179556-A 825 25-OCT-2001;  
Millennium Predictive Medicine, Inc. (US)  
Location/Qualifiers  
1..1368  
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BASE COUNT 517 a 312 c 321 g 213 t 5 others  
ORIGIN

Query Match 1.7%; Score 27; DB 6; Length 1368;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1593 ACAGGTGTAACAAAAA 1619  
Db 459 ACAGGTGTAACAAAAA 485

RESULT 24  
AK026521 1614 bp mRNA linear PRI 29-SEP-2000  
LOCUS AK026521  
DEFINITION Homo sapiens cDNA: FLJ22868 fis, clone KAT02340, highly similar to  
HUTPFLC1 Homo sapiens transcription factor SL1 mRNA.  
ACCESSION AK026521  
VERSION AK026521.1 GI:10439398  
KEYWORDS  
SOURCE Homo sapiens  
Homo sapiens clone\_11b:KAT clone:KAT02340.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Matanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H.,  
Nakamura, Y., Isogai, T., and Sugano, S.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1614)  
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,  
Shibahara, T., Tanaka, T. and Nakamura, T.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Matanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H.,  
Nakamura, Y., Isogai, T., and Sugano, S.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1614)  
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,  
Shibahara, T., Tanaka, T. and Nakamura, T.

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* 46727 47819: contig of 1093 bp in length
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* 47920 49621: contig of 1702 bp in length
* 49622 49721: gap of unknown length
* 49722 51446: contig of 1725 bp in length
* 51447 53382: gap of unknown length
* 53383 53482: gap of unknown length
* 53483 55863: contig of 2381 bp in length
* 55864 55963: gap of unknown length
* 55964 58498: contig of 2435 bp in length
* 58499 61923: gap of unknown length
* 61924 62023: gap of unknown length
* 62024 65252: contig of 3229 bp in length
* 65253 65352: gap of unknown length
* 65353 67262: contig of 1910 bp in length
* 67263 67362: gap of unknown length
* 67363 69710: contig of 2348 bp in length
* 69711 69810: gap of unknown length
* 69811 73439: contig of 3629 bp in length
* 73440 73539: gap of unknown length
* 73540 76475: contig of 2936 bp in length
* 76476 76575: gap of unknown length
* 76576 80568: contig of 3993 bp in length
* 80569 80668: gap of unknown length
* 80669 84177: gap of unknown length
* 84178 84277: gap of unknown length
* 84278 89159: contig of 4882 bp in length
* 89160 89259: gap of unknown length
* 89260 92924: contig of 3665 bp in length
* 92925 93024: gap of unknown length
* 93025 96972: contig of 3948 bp in length
* 96973 97072: gap of unknown length
* 97073 100972: contig of 3900 bp in length
* 100973 101072: gap of unknown length
* 101073 107076: contig of 6004 bp in length
* 107077 107176: gap of unknown length
* 107177 113525: contig of 6349 bp in length
* 113526 113625: gap of unknown length
* 113626 119430: contig of 5805 bp in length
* 119431 119530: gap of unknown length
* 119531 125703: contig of 6173 bp in length.

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OY 1590 TAGACAGTGTAAAAA 1619
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DB 37842 TAGACAGTGTAAAAA 37813

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RESULT 20
AF150733 487 bp mRNA linear PRI 04-MAY-2000
LOCUS Homo sapiens AD-014 protein mRNA, complete cds.
DEFINITION AF150733
ACCESSION AF150733
VERSION AF150733.1 GI:7688664
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

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REFERENCE 1 (bases 1 to 487)
AUTHORS Fu, S., Gu, Y., Li, Y., Peng, Y., Gu, J., Zhang, L., Jiang, C., Yu, Y.,
TITLE Fu, G., Wang, Y., Chen, Z., and Han, Z.
JOURNAL A novel gene expressed in human adrenal gland
REFERENCE 2 (bases 1 to 487)
AUTHORS Fu, S., Gu, Y., Li, Y., Peng, Y., Gu, J., Zhang, L., Jiang, C., Yu, Y.,
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1998) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, P. R. China
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BASE COUNT 135 a 101 c 128 g 122 t 1 others
ORIGIN

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Query Match      1.7%; Score 27; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1593 ACAGTGTAAAAA 1619
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DB 452 ACAGTGTAAAAA 478

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RESULT 21
AF082874 1086 bp mRNA linear PLN 20-AUG-1998
LOCUS Medicago sativa glycolate oxidase mRNA, partial cds.
DEFINITION AF082874
ACCESSION AF082874
VERSION AF082874.1 GI:3435305
KEYWORDS Medicago sativa.
SOURCE Medicago sativa.
ORGANISM Medicago sativa;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.

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REFERENCE 1 (bases 1 to 1086)
AUTHORS Stout, J.M. and McKersie, B.D.
TITLE Gene expression in alfalfa
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1086)
AUTHORS Stout, J.M. and McKersie, B.D.
TITLE Direct Submission
JOURNAL Submitted (07-AUG-1998) Plant Biotechnology Division, Dept of Plant
Agriculture, University of Guelph, Crop science Building, Guelph,
Ont N1G 2W1, Canada
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ACCESSION \*\*\* 52 unordered pieces.  
 AC123338  
 VERSION AC123338.2 GI:21671554  
 HTG: HTGS.PHASE1.  
 KEYWORDS  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 125703)

REFERENCE  
 AUTHORS Muzny D.M., Adams C., Adio-Oduola B., Alt-Osman F.R., Allen C., Alsbrooks S.L., Amaralunga H.C., Are J.R., Ayala M., Banks T., Barabara U., Benton J., Blum K., Blankenburg K., Bonin D., Bouck J., Bowle S., Brileva M., Brown E., Brown M., Bryant N.P., Burch C., Burch P., Burkett C., Burrell K.L., Byrd N.C., Carron T.F., Carter M., Cavazos S.R., Chacko J., Chavez D., Chen G., Chen R., Chen Z., Chowdhry I., Christopoulos C., Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R., Davila M.L., Davis C., Davy Carroll L., Dederich D.A., Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinh H.H., Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J., Earhart C., Edgar D., Edwards C.C., Elhaj C., Escoto M., Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frantz P., Gabisi A., Gao J., Garcia A., Garner T., Garza N., Gill R., Gorrell J.H., Guevara W., Gunaratne P., Hale S., Hamilton K., Harris C., Harris K., Hart M., Havlak P., Hawes A., Hernandez J., Hernandez O., Hodgson A., Hognes M., Holloway C., Hollins B., Homsl F., Howard S., Huber J., Hulik S., Hume J., Jackson L.E., Jacobson B., Jia Y., Johnson R., Jollivet S., Joudh S., Karlsson E., Kelly S., Khan U., King L., Korvah J., Kovar C., Kratoch J., Kuresh A., Landy N., Leal B., Lewis L.C., Lewis L., Li J., Li Z., Lichtarge O., Lieu C., Liu J., Liu W., Louised H., Lozado R.J., Lu X., Lucier A., Lucier R., Luna R., Ma J., Maheshwari M., Mapua P., Martin R., Marindale A., Martinez E., Massey E., Mawhney E., McLeod M.P., Meador M., Mel G., Metzker M., Miner G., Miner Z., Mitchell T., Mohabat K., Morgan M., Morris S., Moser N., Neal D., Newton J., Newton N., Nguyen A., Nguyen N., Nguyen N., Nickerson E., Nwokwkw S., Ogun M., Okunolu G., Ogunye N., Oviedo R., Pace A., Payton B., Peery J., Perez L., Peters L., Pickens R., Primus E., Pu L., Quides M., Ren Y., Rives M., Rojas A., Rojokokan I., Rolfe M., Ruiz S., Savary G., Scherer S., Scott G., Shen H., Shoostari N., Sisson I., Sodergren E., Sotolake T., Sparks A., Stanley H., Stone H., Sutton A., Swatek A., Taber P., Tameris A., Tameris K., Tang H., Tansley J., Taylor C., Taylor T., Teitord B., Thomas N., Thomas S., Umanal K., Vasquez U., Vera V., Villalón D., Vinson R., Wang Q., Wang S., Ward-Moore S., Warren R., Washington C., Watlington S., Williams G., Williamson A., Wlarczyk R., Wooden S., Worley K., Wu C., Wu Y., Wu Y.F., Zhou J., Zorilla S., Nelson D., Weinstock G. and Gibbs R.

TITLE  
 JOURNAL Direct Submission  
 REFERENCE 2 (bases 1 to 125703)  
 AUTHORS Worley K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 125703)  
 REFERENCE  
 AUTHORS Worley K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Jul 2, 2002 this sequence version replaced gi:21240186.  
 COMMENT  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc.help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GUSG  
 Center clone name: CH230-71J19

## ----- Summary Statistics

Sequencing vector: Plasmid.  
 Chemistry: Dye-terminator Big Dye 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 82161 bases at least Q40  
 Consensus quality: 88014 bases at least Q30  
 Consensus quality: 92229 bases at least Q20

NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 NOTE: This is a "working draft" sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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*	7595:	contig of 1648 bp in length
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*	8847:	contig of 1151 bp in length
*	8946:	gap of unknown length
*	10063:	contig of 1117 bp in length
*	10647:	gap of unknown length
*	10664:	gap of unknown length
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*	11482:	gap of unknown length
*	11581:	gap of unknown length
*	11582:	contig of 1071 bp in length
*	12652:	gap of unknown length
*	12752:	gap of unknown length
*	13756:	contig of 1004 bp in length
*	13856:	gap of unknown length
*	14899:	contig of 1043 bp in length
*	14900:	gap of unknown length
*	15000:	contig of 1179 bp in length
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*	16278:	gap of unknown length
*	16279:	contig of 1436 bp in length
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*	17815:	contig of 1691 bp in length
*	19505:	gap of unknown length
*	21884:	contig of 2279 bp in length
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*	28501:	contig of 1578 bp in length
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*	29631:	contig of 1030 bp in length
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*	30814:	gap of unknown length
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*	32629:	contig of 1716 bp in length
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*	33902:	contig of 1173 bp in length
*	34002:	gap of unknown length
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*	37117:	contig of 1651 bp in length
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*	38825:	contig of 1608 bp in length
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*	41573:	contig of 2648 bp in length
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15184..15321
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15184..15321
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15184..15320
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19407..19710
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19498..19795
/note="similar to Bos taurus EST BE682268 (NID:g10067956)"
19873..20090
misc_feature      /note="match to EST BG200485 (NID:g13722172)"
19926..20089
misc_feature      /note="similar to Homo sapiens EST BE963800
(NID:g1167217)"

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Query Match      8.8% Score 142; DB 9; Length 147131;
Best Local Similarity 100.0%; Pred. No. 1,1e-71;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTGCAGAAATCCAGTCTACAGTGCAGAAATTCAGTGAACAACGACT 89
DB 15324 CAGGCTTGGCGTGCAGAAATCCAGTCTACAGTGCAGAAATTCAGTGAACAACGACT 15265

QY 90 GCTCCTCCCGCAGATTCATTCGTAATTCACAGGTGACAGTTCAGACATCTGTGCAAGA 149
DB 15264 GCTCCTCCCGCAGATTCATTCGTAATTCACAGGTGACAGTTCAGACATCTGTGCAAGA 15205

QY 150 AAGTGATGAGCAAGTGCAGG 171
DB 15204 AAGTGATGAGCAAGTGCAGG 15183

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RESULT 17
AC124493/C 209885 bp DNA linear HTG 05-JUL-2002
LOCUS Mus musculus chromosome UNK clone RP23-462P13, WORKING DRAFT
DEFINITION AC124493
ACCESSION AC124493
VERSION AC124493.2 GI:21699722
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 209885)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 209885)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
REFERENCE 3 (bases 1 to 209885)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission

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AX136556      AX136556      591 bp      DNA      linear      PAT 30-MAY-2001
LOCUS
DEFINITION   Sequence 478 from Patent EP1067182.
ACCESSION   AX136556
VERSION     AX136556.1 GI:14727960
KEYWORDS
SOURCE      human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 591)
AUTHORS     Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
            Hayashil, K.
TITLE       Secretory protein or membrane protein
JOURNAL     Patent: EP 1067182-A 478 10-JAN-2001;
            Helix Research Institute (JP)
FEATURES
source      1..591
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT   108 a 198 c 173 g 109 t 3 others
ORIGIN
Query Match      15.4% Score 250; DB 6; Length 591;
Best Local Similarity 100.0%; Pred. No. 1,6e-135;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCACCTTTTGGCGGATTTCTTCTTCCAGGCTTTGCGTGCAGAAATCCAGTGTACCA 60
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DB 294 GGCACCTTTTGGCGGATTTCTTCTTCCAGGCTTTGCGTGCAGAAATCCAGTGTACCA 353
OY 61 GTTGAGAGATTTCCAGTGAACAGACTGCTCTCCCGGAGTTCATTGTGATTCAC 120
    |||||||
DB 354 GTTGAGAGATTTCCAGTGAACAGACTGCTCTCCCGGAGTTCATTGTGATTCAC 413
OY 121 GGTGAACCTTCAGACATGTGTCTTCCAGAAAGATGAGAGCAAGTCCGGGATCATGTA 180
    |||||||
DB 414 GGTGAACCTTCAGACATGTGTCTTCCAGAAAGATGAGAGCAAGTCCGGGATCATGTA 473
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCTCTCCGGGATCCAGTCTT 240
    |||||||
DB 474 CCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCTCTCCGGGATCCAGTCTT 533
OY 241 CTGCTCCCA 250
DB 534 CTGCTCCCA 543

RESULT 16
AC010974/c      147131 bp      DNA      linear      PRI 01-MAR-2002
LOCUS
DEFINITION   Homo sapiens BAC clone RP11-159N20 from 2, complete sequence.
ACCESSION   AC010974
VERSION     AC010974.9 GI:19033964
KEYWORDS
SOURCE      HTG.
ORGANISM     Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 147131)
AUTHORS     Sulston, J.E. and Waterston, R.
TITLE       Toward a complete human genome sequence
JOURNAL     Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE     99063792
PUBMED     9847074
REFERENCE   2 (bases 1 to 147131)
AUTHORS     Vanbrunt, A. and Stromwater, C.
TITLE       The sequence of Homo sapiens BAC clone RP11-159N20
JOURNAL     Unpublished (2001)
REFERENCE   3 (bases 1 to 147131)
AUTHORS     Waterston, R.H.
TITLE       Direct Submission
JOURNAL     Submitted (28-SEP-1999) Genome Sequencing Center, Washington
            Submitted (28-SEP-1999) Genome Sequencing Center, Washington

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REFERENCE
AUTHORS     Waterston, R.H.
TITLE       Direct Submission
JOURNAL     Submitted (23-MAR-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5 (bases 1 to 147131)
AUTHORS     Waterston, R.
TITLE       Direct Submission
JOURNAL     Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
            On Mar 1, 2002 this sequence version replaced gi:13435273.
            ----- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc
            Contact: saplens@wustl.wustl.edu
            ----- Summary Statistics
            Center project name: H_NH0159N20
            -----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osogawa, K., Moon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.choil.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-458A7, 200 bp overlap; the
clone sequenced to the right is RP11-258B17. Actual start of this
clone is at base position 1 of RP11-159N20; actual end is at base
position 147131 of RP11-159N20.

There are polymorphic base differences in the overlap between the
clone RP11-159N20 and RP11-258B17.

FEATURES
source      1..147131
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="2"
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            . 1013
            /rpt_family="L1"
            984..1176
            misc_feature

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BASE COUNT      95 a /db_xref="taxon:9606" 142 t
ORIGIN
Query Match      22.5%; Score 364; DB 6; Length 444;
Best Local Similarity 99.8%; Pred. No. 6.9e-203;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1196 CCGAGTGAAGTGAAGAAAGCTCTCCGAGAGAGGAGAGATCATGTAACCGCGGAAGT 1255
DB 431 CCGAGCTGAGTGAAGAAAGCTCTCCGAGAGAGGAGAGATCATGTAACCGCGGAAGT 372
QY 1256 AGGACCTGCTCCAGTGTCTGTTGGTGGCCGAGCCATGATCTCCGAATCTGTTGG 1315
DB 371 AGGACCTGCTCCAGTGTCTGTTGGTGGCCGAGCCATGATCTCCGAATCTGTTGG 312
QY 1316 GCATCCAGCATAGCGGCAATGTACACAAATCAGCCCTGGGCAACAGCAGAGAGGGA 1375
DB 311 GCATCCAGCATAGCGGCAATGTACACAAATCAGCCCTGGGCAACAGCAGAGAGGGA 252
QY 1376 GAGACAGAGAAAGAAACACAGCATGAGAAACAGTAATGAATAAACCATTAATA 1435
DB 251 GAGACAGAGAAAGAAACACAGCATGAGAAACAGTAATGAATAAACCATTAATA 192
QY 1436 TTTAGCCCCCTGTTCTGTGCTTACTGGCCAGGAAATGTTCAAGTGTGGA 1495
DB 191 TTTAGCCCCCTGTTCTGTGCTTACTGGCCAGGAAATGTTCAAGTGTGGA 132
QY 1496 CTTCACACTCTTCTTGGCCACAGCAAGAGAAATTAACACTGTTCAACCCGGGGA 1555
DB 131 CTTCACACTCTTCTTGGCCACAGCAAGAGAAATTAACACTGTTCAACCCGGGGA 72
QY 1556 GTTGCTGTGTTAAAGAAAGCACTTAATGCTTTTACAGCTGTAACAAAAA 1610
DB 71 GTTGCTGTGTTAAAGAAAGCACTTAATGCTTTTACAGCTGTAACAAAAA 17

RESULT 13
AX093381 369 bp DNA linear PAT 30-MAR-2001
LOCUS
DEFINITION Sequence 199 from Patent WO0118046.
ACCESSION AX093381
VERSION AX093381.1 GI:13509629
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS Xu,J. and Stolk,J.A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A 199 15-MAR-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. 369
Location/Qualifiers
misc_feature
1..369
/db_xref="taxon:9606"
"/note="n = A,T,C or G"
BASE COUNT 82 a 109 c 90 g 86 t 2 others
ORIGIN
Query Match 19.5%; Score 315; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.3e-174;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGCTGCAAAATCCAGTGTCTACAGTGTGAAGATTCAGCTGAACAAGACT 89
DB 30 CAGGCTTTCGCTGCAAAATCCAGTGTCTACAGTGTGAAGATTCAGCTGAACAAGACT 89
QY 90 GCTCTCCCGCCAGTTCATGTAATTCAGAGTGAAGCTTCAAGACATGTGTCAAGAA 149
DB 90 GCTCTCCCGCCAGTTCATGTAATTCAGAGTGAAGCTTCAAGACATGTGTCAAGAA 149

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QY 150 AAGTATGAGCAAGATGGCGGATCATGTATACCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 150 AAGTATGAGCAAGATGGCGGATCATGTATACCGCAAGTCTGTGCATCATCAGCGGCT 209
QY 210 GTCTCATGCGCTTTCGCGGGGTACAGTCTCTGCTCCCGAGGAAATCAATCACTGTT 269
DB 210 GTCTCATGCGCTTTCGCGGGGTACAGTCTCTGCTCCCGAGGAAATCAATCACTGTT 269
QY 270 GCATCAGCTGTGCAACACCCCTTTTGTACGGGCAAGGCCCAAGAAAGGGAAGTT 329
DB 270 GCATCAGCTGTGCAACACCCCTTTTGTACGGGCAAGGCCCAAGAAAGGGAAGTT 329
QY 330 CTGCTCTGGCGCTCA 344
DB 330 CTGCTCTGGCGCTCA 344

RESULT 14
AX093191 396 bp DNA linear PAT 30-MAR-2001
LOCUS
DEFINITION Sequence 9 from Patent WO0118046.
ACCESSION AX093191
VERSION AX093191.1 GI:13509640
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS Xu,J. and Stolk,J.A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A 9 15-MAR-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. 396
Location/Qualifiers
misc_feature
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/db_xref="taxon:9606"
"/note="n = A,T,C or G"
BASE COUNT 90 a 117 c 95 g 92 t 2 others
ORIGIN
Query Match 19.1%; Score 310; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.6e-171;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATGTTCTTCTCCAGGCTTGGCGTGAATCCAGTGTACCA 60
DB 11 GGCACCTTTTGGCGATGTTCTTCTCCAGGCTTGGCGTGAATCCAGTGTACCA 70
QY 61 GTGTGAAGATTCACAGTGTACAGACAGTGTCTCCCGGAGTTCAATGTAATTCGAC 120
DB 71 GTGTGAAGATTCACAGTGTACAGACAGTGTCTCCCGGAGTTCAATGTAATTCGAC 130
QY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGTGTGAGCAAAAGTGGCGGATCATGTA 180
DB 131 GGTGAAGCTTCAAGACATGTGTCAAGAAAGTGTGAGCAAAAGTGGCGGATCATGTA 190
QY 181 CCGCAGTCTCTGTCATCATGCAAGCGGCTGTCTATGCGCTCTCCGAGTACAGTCTT 240
DB 191 CCGCAGTCTCTGTCATCATGCAAGCGGCTGTCTATGCGCTCTCCGAGTACAGTCTT 250
QY 241 CTGCTCCCGAGGAAATCAAGTCAAGTGTGATGAGTGTGCAACAGCCCTCTTTGTA 300
DB 251 CTGCTCCCGAGGAAATCAAGTCAAGTGTGATGAGTGTGCAACAGCCCTCTTTGTA 310
QY 301 CCGGCCAAG 310
DB 311 CCGGCCAAG 320

RESULT 15

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source	1.. 1362	/organism="Homo sapiens"
gene	1.. 1362	/db_xref="taxon:9606"
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	1.. 1362	/codon_start=1
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BASE COUNT	263 a 435 c 362 g 302 t	
ORIGIN		
Query Match	23.8%; Score 386; DB 9; Length 1362;	
Best Local Similarity	99.8%; Pred. No. 6, 9e-216;	
Matches	506; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
QY	845 TCAAACCTTCATGCTCTGCGAAACCATTCCTCTGACGACGAGAATGGCTGGCTTCGGCCCTGA	904
Db	1362 TCAAACCTTCATGCTCTCTGAAACCATTCCTCTGACGACGAGAATGGCTGGCTTCGGCCCTGA	1303
QY	905 GTTGGGCTCTAGTGCATGACGACATCAATGACTGGGACTTGAAGTGGGCTCGGCTCGCT	964
Db	1302 GTTGGGCTCTAGTGCATGACGACATCAATGACTGGGACTTGAAGTGGGCTCGGCTCGCT	1243
QY	965 CTGAAAAAGTCTTAAGAAAAATCTTCTCAGTTCTCTTCGTGCAAGAGACTGGCGCCGGAGCG	1024
Db	1242 CTGAAAAAGTCTTAAGAAAAATCTTCTCAGTTCTCTTCGTGCAAGAGACTGGCGCCGGAGCG	1183
QY	1025 GAAGACCAACGGGGCGCTGCACAAACGGGGCGCTGCGTGGTGGATGGCATGTACGGG	1084
Db	1182 GAAGACCAACGGGGCGCTGCACAAACGGGGCGCTGCGTGGTGGATGGCATGTACGGG	1123
QY	1085 CAGGCGCTTCGTGCTGGTTGGCGTGTGCTGACGACGACGGCGGACGACGACCTTTGCAGA	1144
Db	1122 CAGGCGCTTCGTGCTGGTTGGCGTGTGCTGACGACGACGGCGGACGACGACCTTTGCAGA	1064
QY	1145 ACACCGCCGGAACATCTCTCCGAGGACACCGTGTACAGGAGGGGGTGTATGACCGAGCTGA	1204
Db	1063 ACACCGCCGGAACATCTCTCCGAGGACACCGTGTACAGGAGGGGGTGTATGACCGAGCTGA	1004
QY	1205 GGTGAAAAACGCTCTCCGAGAGGGGAGAGATCATGTACGCCGGAAGTAGACCTCG	1264
Db	1003 GGTGAAAAACGCTCTCCGAGAGGGGAGAGATCATGTACGCCGGAAGTAGACCTCG	944
QY	1265 TCCAGTCTGCTGGCTTTGGCTGGCGGACGACCATGATCTCTCCGAATGTGGTTGGGACCTCAGC	1324
Db	943 TCCAGTCTGCTGGCTTTGGCTGGCGGACGACCATGATCTCTCCGAATGTGGTTGGGACCTCAGC	884
QY	1325 ATACGGCCAATGTCCAAACAATCAGCC	1351
Db	883 ATACGGCCAATGTCCAAACAATCAGCC	857
LOCUS	AX136698	587 bp DNA linear
LOCUS	AX136698	587 bp DNA linear

DEFINITION	Sequence 620 from Patent EP1067182.
ACCESSION	AX136698
VERSION	AX136698.1 GI:14273102
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 587)
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE	Secretory protein or membrane protein
JOURNAL	Patent: EP 1067182-A 620 10-JAN-2001;
FEATURES	Helix Research Institute (JF)
source	location/Qualifiers
	1..587
BASE COUNT	/organism="Homo sapiens"
ORIGIN	/db_xref="taxon:9606"
	117 a 162 c 140 g 162 t 6 others
Query Match	22.6%; Score 366; DB 6; Length 587;
Best Local Similarity	99.8%; Pred. No. 4,5e-204;
Matches 416; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1183 AGCGGTTATGATACCGACTGAGTAGAAGAAAACGCTCCGAGAAAGGGAGGAGGATCATG 1242
Db	417 AGCGGGTTGATGACCGAGCTGAGTAGAAGAAACGCTCCGAGAAAGGGAGGAGGATCATG 358
OY	1243 TAGCGCCGGAAGTAGAGACCTCGTCCAGTGCCTTGGGTTGGCCGACGATATCTC 1302
Db	357 TAGGCCGGAAAGTAGAGACCTCGTCCAGTGCCTTGGGTTGGCCGACGATATCTC 298
OY	1303 CGAATCTGTTGGGCATCCAGCATACGGCCATGTCACAAATCAGCCCTGGCGACACA 1362
Db	297 CGAATCTGTTGGGCATCCAGCATAGCGCAATGTCACAAATAGCCCTGGCGACACA 238
OY	1363 CGAGCAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAAACACAGTAAATGAATA 1422
Db	237 CGAGCAGAGGAGAGAGACAGAAAAAGAAAAACACAGCATGAGAAACACAGTAAATGAATA 178
OY	1423 AAACCATTAATTTTAAAGCCCTCTGTTCTGTCGTCTACAGTGGCCAGGAAATGTTACCAATT 1482
Db	177 AAACCATTAATTTTAAAGCCCTCTGTTCTGTCGTCTACAGTGGCCAGGAAATGTTACCAATT 118
OY	1483 TTTCAGTGTGGAATGACAGCTTCTTTTGGCCACAAGACAGAGAGATTTAAACACTGTTT 1542
Db	117 TTTCAGTGTGGAATGACAGCTTCTTTTGGCCACAAGACAGAGATTTAAACACTGTTT 58
OY	1543 CAACCCGGGGAGTGGCTGTGTTAAAGAAACCATTAATTAAGCTTTAGACAGTGT 1599
Db	57 CAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAATTAAGCTTTAGACAGTGT 1
RESULT 12	
AX150120/c	444 bp DNA linear PAT 08-JUN-2001
LOCUS	AX150120
DEFINITION	Sequence 95 from Patent WO0136685.
ACCESSION	AX150120
VERSION	AX150120.1 GI:14348148
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 444)
AUTHORS	Kroes,R.A., Moskal,J.R. and Yamamoto,H.
TITLE	Differential gene expression in cancer
JOURNAL	Patent: WO 0136685-A 95 25-MAY-2001;
FEATURES	NXIS Neurotherapies, Inc. (US)
source	location/Qualifiers
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	/organism="Homo sapiens"

Db	225	AGAGCAAGGGGCGCTGCACAAAGCGGGCGCTGTCGGTGGTGGAGTGGGCATGTACGGCGCA	294
Qy	1087	GGGGCTTCTCGTGGTGGGCTGCTGCAAGCAGCAGCGGGCAGCACAGCACTTGCAGAAC	1146
Db	285	GGGGCTTCTCGTGGTGGGCTGCTGCAAGCAGCAGCGGGCAGCACAGCACTTGCAGAAC	343
Qy	1147	ACCGCGCAAACTGCTGCGAGCAGCAGCGTGTACAGAGCGGGTGTGATGACCGAGCTGAG	1206
Db	344	ACCGCGCAAACTGCTGCGAGCAGCAGCGTGTACAGAGCGGGTGTGATGACCGAGCTGAG	403
Qy	1207	TAGAAAAAGCTCTCCGAGAAAGGAGAGGATCATGTACGCCCGGAGATAGAGACTTCGTC	1266
Db	404	TAGAAAAAGCTCTCCGAGAAAGGAGAGGATCATGTACGCCCGGAGATAGAGACTTCGTC	463
Qy	1267	CAGTCTGCTGGGTTTGGGCGGAGGCATGATCTTCGGAATCTGTGGTGGCATTCAGCAT	1326
Db	464	CAGTCTGCTGGGTTTGGGCGGAGGCATGATCTTCGGAATCTGTGGTGGCATTCAGCAT	523
Qy	1327	ACGGCCAAATGTCACAACAATTCAGCCCTGGGCGAGACAGCAGAGAGGAGAGACAGAA	1386
Db	524	ACGGCCAAATGTCACAACAATTCAGCCCTGGGCGAGACAGCAGAGAGGAGAGACAGAA	583
Qy	1387	AAGAAACACACAGCATGAGACACACACTTAATGAAATGAATAAACATTAATATTAGCCCTTC	1446
Db	584	AAGAAACACACAGCATGAGACACACACTTAATGAAATGAATAAACATTAATATTAGCCCTTC	643
Qy	1447	TGTTCTGCTCTTACTGGCCAGGAATGTATACCAATTTTTCAGTGTGACCTTGACACGTT	1506
Db	644	TGTTCTGCTCTTACTGGCCAGGAATGTATACCAATTTTTCAGTGTGACCTTGACACGTT	703
Qy	1507	CTTTTGGCCACAGCAGACAGAAATTTAAACAGCTTTCACAAACCCGGGGAGTTGGCTGT	1566
Db	704	CTTTTGGCCACAGCAGACAGAAATTTAAACAGCTTTCACAAACCCGGGGAGTTGGCTGT	763
Qy	1567	TAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAAA 1619	
Db	764	TAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAAA 816	
RESULT 9			
LOCUS	AXJ19942	1362 bp	DNA linear PAT 14-DEC-2001
DEFINITION	Sequence 1 from Patent WO0181634.		
ACCESSION	AXJ19942		
VERSION	AXJ19942.1	GI:17901489	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1		
JOURNAL	Galvin, K.A. and Rudolph-Owen, L.A.		
FEATURES	Methods and compositions for the diagnosis and treatment of		
source	cardiovascular and tumorigenic disease using 4941		
	Patent: WO 0181634-A 1 01-NOV-2001;		
	Millennium Pharmaceuticals, Inc. (US)		
	Location/Qualifiers		
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	/db_xref="GI:17901490"		
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	LLGSAITRTVOYLQKGYLQKEVTDHMSLACSDILVFLGPMFEYSIIWNLTTIS		
	SYTSLCLHFLFEACSYATLHLVLTLSFERYIACHPFRKAVSGCOVYLIGFWW		
	VTSALVALPLFLFAMGTEYPLVNVMSHRLGICNRSSTHDEPSSNMSICNLSSRW		
	VFSOSIGAEVYLVLLVLSVAFKMMNMVYLKMSKSLAGSTRPOLRSESESTPT		
	ARQRTIFLRILIVTLAVCMNPDIIRCRILMAAKRKHMWTSYPAVYVILDFSTFPY		
	LSSYINELTVTSQSDRFVYVQVIRISLQAHNHEKRLRYAHNHTDTSARVQRL		
	LFSARRSASARTKILFTSPQSAEPQSSQSLTSLSELSGAKPANSVAENGFOE		

BASE COUNT	263 a	435 c	362 g	302 t
HEV"				
ORIGIN				
Query Match	23.8%	Score 386;	DB 6;	Length 1362;
Best Local Similarity	99.8%	Pred. No. 6,9e-216;		
Matches 506;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1
QY 845	TCAACCTTCATGCTCCGTGAAACACCATTCCTCTGAGACAGAAATTCGCTGGCTGGCTGA	904		
Db 1362	TCAACCTTCATGCTCCGTGAAACACCATTCCTCTGAGACAGAAATTCGCTGGCTGGCTGA	1303		
QY 905	GTTGGGCTCTAGTACTCGAGACTCAATGACTGGAATTAGACTGGGGCTCGGCTCGGT	964		
Db 1302	GTTGGGCTCTAGTACTCGAGACTCAATGACTGGAATTAGACTGGGGCTCGGCTCGGT	1243		
QY 965	CTGAAGAAGTCTTAAAGAAATCTTCACATGTCCTGATTCGATTCGAGAGAGACTGGCGCGGAGCC	1024		
Db 1242	CTGAAGAAGTCTTAAAGAAATCTTCACATGTCCTGATTCGATTCGAGAGAGACTGGCGCGGAGCC	1183		
QY 1025	GAAGACCAACGGGCGCTGCAACAAGCGGGCGCTGCTGGTGTGAGTCCGCATGTACGG	1084		
Db 1182	GAAGACCAACGGGCGCTGCAACAAGCGGGCGCTGCTGGTGTGAGTCCGCATGTACGG	1123		
QY 1085	CAGGCGCTTCTCGTGGTTGGCGCTGCAAGCGACGACGAGCGGCGACACAGACCTTGCACGA	1144		
Db 1122	CAGGCGCTTCTCGTGGTTGGCGCTGCAAGCGACGACGAGCGGCGACACAGACCTTGCACGA	1064		
QY 1145	ACAACCGCGGAAATCTGCTCGAGACACCGTGTACAGAGACGGGTTGATGACCGAGCTGA	1204		
Db 1063	ACAACCGCGGAAATCTGCTCGAGACACCGTGTACAGAGACGGGTTGATGACCGAGCTGA	1004		
QY 1205	GGTAGAAAAACGTCCTCGAAGGGAGGAGAGATCATGTACGCCCGGGAAGTAGACTTCG	1264		
Db 1003	GGTAGAAAAACGTCCTCGAAGGGAGGAGAGATCATGTACGCCCGGGAAGTAGACTTCG	944		
QY 1265	TCCAGTCGTGCTTGGTTGGCGCGACGCATATCCTCCGAATTCGTGGTGGGCATTCAGC	1324		
Db 943	TCCAGTCGTGCTTGGTTGGCGCGACGCATATCCTCCGAATTCGTGGTGGGCATTCAGC	884		
QY 1325	ATACGGCCCAATGTCAACACATCAGCC 1351			
Db 883	ATACGGCCCAATGTCAACACATCAGCC 857			
RESULT 10				
AF034633/c				
LOCUS	AF034633	1362 bp	mRNA	linear PRI 13-JUL-1998
DEFINITION	Homo sapiens orphan G protein-coupled receptor (GPR39) mRNA,			
ACCESSION	AF034633			
VERSION	AF034633.1	GI:2654160		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens.			
	Homo sapiens.			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1362)			
AUTHORS	McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feilghner,S.D.,			
	Hreniuk,D.L., Smith,R.G., Howard,A.D. and Van der Ploeg,L.H.			
TITLE	Cloning and characterization of two human G protein-coupled			
	receptor genes (GPR38 and GPR39) related to the growth hormone			
JOURNAL	secretagogue and neurotensin receptors			
MEDLINE	Genomics 46 (3), 426-434 (1997)			
PUBMED	98110578			
REFERENCE	9441746			
AUTHORS	2 (bases 1 to 1362)			
	McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feilghner,S.D.,			
TITLE	Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howard,A.D.			
JOURNAL	Direct Submission			
	Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.,			
TEATRRES	Inc., PO Box 2000, Rahway, NJ 07065, USA			
	Location/Qualifiers			

contact: nisc\_mgc@nhl.nih.gov  
 Shevchenko, Y., Wehrt, K.D., Beckstrom-Sternberg, S.M.,  
 Benjamini, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,  
 Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Snyder, B., Stanciu, S., Thomas, P.J.,  
 Tlionson, E.E., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,  
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 39 Row: b Column: 19  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis. Similarity but not identity to protein.

## FEATURES

## source

1. 946  
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 /db\_xref="taxon:9606"  
 /clone="MGC:29643 IMAGE:3641660"  
 /tissue\_type="Pancreas, adenocarcinoma"  
 /clone\_lib="NIH\_MGC\_39"  
 /lab\_host="DH10B-R"  
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## CDS

## BASE COUNT

197 a 292 c 261 g 196 t

## ORIGIN

Query Match 40.0%; Score 648; DB 9; Length 946;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCACCTTTTGGCGATTTCTTCTCCAGGCTTTGGCTGCAATCCAGTCTTCCA 60  
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 281 GGCACCTTTTGGCGATTTCTTCTCCAGGCTTTGGCTGCAATCCAGTCTTCCA 340  
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 61 GTGTGAAGAATTCACAGTGAACAAGACTGCTCCGCCAGTTCATTGTGAATTGCAC 120  
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 341 GTGTGAAGAATTCACAGTGAACAAGACTGCTCCGCCAGTTCATTGTGAATTGCAC 400  
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 121 GGTGAAGCTTCAAGCATGTGTGAGAAAGATGAGCAAAAGTCCGGGATCATGTA 180  
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 401 GGTGAAGCTTCAAGCATGTGTGAGAAAGATGAGCAAAAGTCCGGGATCATGTA 460  
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 181 CCGCAAGTCTGTCATATGAGGGGCTGTCTCATGCTCTGCGGGGTACAGTCTT 240  
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 461 CCGCAAGTCTGTCATATGAGGGGCTGTCTCATGCTCTGCGGGGTACAGTCTT 520  
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 241 CTGCTCTCCAGGAAATGAACTGATTGATCAGTGTGCAACACCCCTCTTTGTA 300  
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 521 CTGCTCTCCAGGAAATGAACTGATTGATCAGTGTGCAACACCCCTCTTTGTA 580  
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 301 CCGGCAAGGCCCCAAGAAAGGGAATTTGCTCTGCGGCTCAGGCCAAGGCTCCGAC 360  
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 581 CCGGCAAGGCCCCAAGAAAGGGAATTTGCTCTGCGGCTCAGGCCAAGGCTCCGAC 640  
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 361 CACCATCTGTCCTCAATTTAGCCCTCTGTCGCGACACTGCTGAAGTGAAGAGATG 420  
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 641 CACCATCTGTCCTCAATTTAGCCCTCTGTCGCGACACTGCTGAAGTGAAGAGATG 700  
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 421 CCACCCCTCTCTGATTTGTTTTCAGGCTTGCCCCCAACCCCTCCTCTGAGTGA 480  
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 701 CCACCCCTCTCTGATTTGTTTTCAGGCTTGCCCCCAACCCCTCCTCTGAGTGA 760  
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 481 GTTCTCTCTGAGTCTCTTTTATTTCTGGGTAGGAGCGGAGTCCGTCTCTTTGTT 540  
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Db 761 GTTCTCTCTGAGTCTCTTTTATTTCTGGGTAGGAGCGGAGTCCGTCTCTTTGTT 820  
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 QY 541 CCTGTCCAAATATGAAAGCTCGGTAAAGCATTTCAATTAATTCAGCTGACTGAT 600  
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 Db 821 CCTGTCCAAATATGAAAGCTCGGTAAAGCATTTCAATTAATTCAGCTGACTGAT 880  
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 Db 881 TTTCACTATGTTGTAAGAGAGAGTGTGAGTGAAGTTCACCCCA 928  
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RESULT 8  
 BC011449 826 bp mRNA linear PRI 22-AUG-2001  
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 DEFINITION  
 BC011449 Homo sapiens, clone IMAGE:4026092, mRNA.  
 VERSION  
 BC011449.1 GI:15277472  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 826)  
 Strausberg, R.  
 Direct Submission  
 Submitted (25-JUL-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

## REFERENCE

1 (bases 1 to 826)  
 Strausberg, R.  
 Direct Submission  
 Submitted (25-JUL-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: ATCC/DC/DP  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Institute for Systems Biology  
 http://www.systemsbio.org  
 Contact: amadan@systemsbiology.org  
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia  
 Greene, Mark Kettelman and Anuradha Madan

## REMARK

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 25 Row: n Column: 18  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis.

## FEATURES

Location/Qualifiers  
 1. 826  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4026092"  
 /tissue\_type="Skin, melanotic melanoma."  
 /clone\_lib="NIH\_MGC\_20"  
 /lab\_host="DH10B-R"  
 /note="Vector: pOT87"

## BASE COUNT

237 a 197 c 228 g 164 t

## ORIGIN

Query Match 33.4%; Score 541; DB 9; Length 826;  
 Best Local Similarity 99.7%; Pred. No. 1; 7e-307;  
 Matches 711; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

907 TGGGCTCTAGTACTCAGACTCAATGAGTGGACTTGAAGTGGGCTGCGCTGCT 966  
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 105 TGGGCTCTAGTACTCAGACTCAATGAGTGGACTTGAAGTGGGCTGCGCTGCT 164  
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 QY 967 GAAAGTCTTAAGAAATCTTCTCACTTCTCTTGAAGAGACTGGCGCGGAGAGCCA 1026  
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 Db 165 GAAAGTCTTAAGAAATCTTCTCACTTCTCTTGAAGAGACTGGCGCGGAGAGCCA 224  
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 QY 1027 AGAGCAAGGCGGTGCAAAAGCGGCGGTGCGGTGAGGAGTGTACCGCA 1086  
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TP10NGBRPRKRSASSALRPGRLTTLILFKLASRHTAEKEMPPPALFQPSPT  
 PHLEP  
 BASE COUNT 419 a 528 c 533 g 410 t  
 ORIGIN

Query Match 62.6% Score 1014; DB 6; Length 1890;  
 Best Local Similarity 99.6% Pred. No. 0;  
 Matches 1594; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

1 GGCACATTTTGGCGATGTTCTTGTCTCCAGGCTTTGGCGTGAATTCAGTCTACCA 60  
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 294 GGCACATTTTGGCGATGTTCTTCTTCCAGGCTTTGGCGTGAATTCAGTCTACCA 353  
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 61 GTTGAAAGATTTCCAGCTGGAACAACGACTGCTCTCCCGAGTTCAATTTGAAATTCAC 120  
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 354 GTTGAAAGATTTCCAGCTGGAACAACGACTGCTCTCCCGAGTTCAATTTGAAATTCAC 413  
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 121 GGTGAAGTTTCAACATATGCTGCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180  
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 414 GTTGAAGTTTCAACATATGCTGCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 473  
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 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTGCGGGATACAGTCTT 240  
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 474 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTGCGGGATACAGTCTT 533  
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 241 CTGCTCCCCAGGGAAGTGAATCAGTTTGCATCAGCTGCTGCAACACCCCTTTGTA 300  
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 534 CTGCTCCCCAGGGAAGTGAATCAGTTTGCATCAGCTGCTGCAACACCCCTTTGTA 593  
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 361 CACCATCTCTTCTCTCAATTAATTAAGCCCTCTCTGCGCACACTGCTGAAGCTGAAGAGATG 420  
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 541 CCTGTCAAAATTAAGAAAGAGCTGGTAAAGCATTTCTGAATTAATTCAGCTGATGAAT 600  
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 601 TTTTCAATGATGATTAAGAAAGAGGAGTGAAGTTCACCCCATGCTGCTGATAC 660  
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 781 GTGAGAGTACGTTTCTTAAGGCTGAGAGGCGCAGTTCCACTCAAGGCTCCCTGCTTG 840  
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 841 ACATTTAAATTCATGCTCCCTGAAAAACATTTCTGCGACAGAAATTTGGTGTTCGCGC 900  
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 1192 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGAGCTTAGACTGGGGCTGGGCT 1251  
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QY 961 CGCTCTGAAAAGTGTCTTAAAGAAATCTTCTCACTTCT -CCTTGACAGAGACTGGGCGCG 1019  
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RESULT 7  
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 LOCUS  
 DEFINITION Homo sapiens, clone MGC:29643 IMAGE:3641660, mRNA, complete cds.  
 VERSION BC017318  
 KEYWORDS MGC.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 946)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK  
 COMMENT  
 Contact: MGC help desk  
 Email: gcaps-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>

FEATURES  
source  
CDS

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ARRQTIIFLRILVITLVAVCMNPQIRIIMAAKPKHDMRSTFRVYMLLPSEFFY  
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HEV"

BASE COUNT 516 a 766 c 677 g 567 t 2 others  
ORIGIN

Query Match 71.0%; Score 1149; DB 6; Length 2528;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1319; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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91 CTCCTCCCGAGTTCATTGTGATTCACAGTGTGAAGTTCAGTGTGAACAGCAGT 150  
2157 CTCCTCCCGAGTTCATTGTGATTCACAGTGTGAAGTTCAGTGTGAACAGCAGT 2098  
151 AGTATGAGCAAGATGCGCGGATCATGTACCGCAATCTGTGCATCATCAGCGCTG 210  
2097 AGTATGAGCAAGATGCGCGGATCATGTACCGCAATCTGTGCATCATCAGCGCTG 2038  
211 TCTATATGCGCTGCGGGATACAGTGTCTGTCCCGAGGGAATGAACTAGTTTG 270  
2037 TCTATATGCGCTGCGGGATACAGTGTCTGTCCCGAGGGAATGAACTAGTTTG 1978  
271 CATCAGCTGTGCAACACCCCTTTGTAAAGGGGCAAGGCCCAAGAAAGGGAGTTTC 330  
1977 CATCAGCTGTGCAACACCCCTTTGTAAAGGGGCAAGGCCCAAGAAAGGGAGTTTC 1918  
331 TGCCTCGGCGCTCAAGGCGAGGCTCCGACACCATCTGTCTCTCAATTAAGCCCTCT 390  
1917 TGCCTCGGCGCTCAAGGCGAGGCTCCGACACCATCTGTCTCTCAATTAAGCCCTCT 1858  
391 CTCGGACACATGCTGAAGCTGAAGAGATGACACCCCTCTGATTTCTTCCAGCCC 450  
1857 CTCGGACACATGCTGAAGCTGAAGAGATGACACCCCTCTGATTTCTTCCAGCCC 1798  
451 TCGCCCGACACCCCTCTGATTTCTTCTGTGGGTCTCTTTATTTCTGGGT 510  
1797 TCGCCCGACACCCCTCTGATTTCTTCTGTGGGTCTCTTTATTTCTGGGT 1738  
511 AGGAGGGGAGTCCGTTCTCTTTTCTGCTGCAAAATGAAGAGCTGGTAA 570  
1737 AGGAGGGGAGTCCGTTCTCTTTTCTGCTGCAAAATGAAGAGCTGGTAA 1678  
571 GCATTCTGAATTAATTCAGCTGATGATTTCTAGTATGATTTGAAGAGAGGTGG 630  
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631 AGTGAAGTTCACCCCATGTCTGTGTAAACCGAGATCAAGGCCAGGCTGAGTCACT 690  
1617 AGTGAAGTTCACCCCATGTCTGTGTAAACCGAGATCAAGGCCAGGCTGAGTCACT 1558  
691 CCTTGAAGTTCAGTGAAGGAGCATCTCTTTTGTAAAGGCTCCAGTGTCCATTTCCATC 750  
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751 CCGATGGGGGCAATAGTTTGAAGTGCAGAGTGAAGTGAAGTTCCTTGAAGGCTGGAG 810  
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811 GCCAGTTCACACTCAAGGCTCCCTGCTTGAACATTCATTCATCTCTGAAACCAT 870  
1437 GCCAGTTCACACTCAAGGCTCCCTGCTTGAACATTCATTCATTCATCTCTGAAACCAT 1378  
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1257 CAGTTCTCTTGCAGAGACTGGCGCGCGGAGCGCAAGAGAGAGGCGCTGCAACAAAC 1198  
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1111 GCAGCGACAGCGGCGAGCAGCAGCAGCTTGCAGAAACACCCCGAATCTGTCGAGAGAC 1170  
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1351 C 1351  
898 C 898

RESULT 6  
AX136281  
LOCUS  
DEFINITION  
SEQUENCE  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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Sequence 203 from Patent EP1067182.  
AX136281  
AX136281.1 GI:14272687  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1890)  
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and  
Hayashi,K.  
Secretory protein or membrane protein  
Patent: EP 1067182-A 203 10-JAN-2001;  
Helix Research Institute (JP)  
TITLE  
JOURNAL  
HELIK RESEARCH INSTITUTE (JP)  
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Oy	2	GCACCTTTTGCGGATTTGTTCTTGCTTCCAGGCTTTGGCGTGCAAATCCAGTGTACCAG	61
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Db	406	TGTGAAGATTTCCAGGCTGGAACAACGATTTCTCATCTCCCTGAGTTTCATGTAAATTGCACC	465
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DEFINITION	Homo sapiens, clone MGC:29643 IMAGE:3641660, mRNA, complete cds.				
ACCESSION	Homo sapiens				
VERSION	BC017318.1	GI:16878239			
KEYWORDS	MGC.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 946)				
TITLE	Straussberg,R				
JOURNAL	Direct Submission				
	Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a>				
COMMENT	Contact: MGC help desk				

## FEATURES

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAT Plate: 39 Row: D Column: 19  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis. Similarly but not identically to protein.  
Location/Qualifiers

Location/Qualifiers





[illegible][illegible]

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HEV

BASE COUNT 263 a 435 c 362 g 302 t  
ORIGIN

Query Match 30.7% Score 497.6; DB 6; Length 1362;  
Best Local Similarity 99.0% Pred. No. 7.5e-125;  
Matches 511; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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DB 1362 TCAACTTCATGCTCTGAAACCATTCCTGCGAGCAATGTCGCTTCCTCCGCTGA 1303  
QY 905 GTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGTGGGCTTCGCTCGCT 964  
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QY 1025 GAAGAGCAAGCGGGCGCTGCACAAAGCGCGCTGTGCGTGGAGTGGCAATGTACGCG 1084  
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LOCUS  
DEFINITION  
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AF034633.1 GI:2654160  
SOURCE  
ORGANISM  
Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1362)  
McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Felgner, S.D.,  
Hreniuk, D.L., Smith, R.G., Howard, A.D. and Van Der Ploeg, L.H.  
Cloning and characterization of two human G protein-coupled  
receptor genes (GPR38 and GPR39) related to the growth hormone  
secretagogue and neurotensin receptors  
Genomics 46 (3), 428-434 (1997)  
9441746  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 1362)  
McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Felgner, S.D.,  
Hreniuk, D.L., Smith, R.G., Van Der Ploeg, L.H.T. and Howard, A.D.  
Direct Submission  
Submitted (17-NOV-1997) Biochemistry and Physiology. Merck and Co.,  
Inc., PO Box 2000, Rahway, NJ 07065, USA

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Source

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HEV"

BASE COUNT 263 a 435 c 362 g 302 t  
ORIGIN

Query Match 30.7% Score 497.6; DB 9; Length 1362;  
Best Local Similarity 99.0% Pred. No. 7.5e-125;  
Matches 511; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 845 TCACATTCATGCTCTGAAACCATTCCTGCGAGCAATGTCGCTTCCTCCGCTGA 904  
DB 1362 TCAACTTCATGCTCTGAAACCATTCCTGCGAGCAATGTCGCTTCCTCCGCTGA 1303  
QY 905 GTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGTGGGCTTCGCTCGCT 964  
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RESULT 13  
AC112072

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 DEFINITION Rattus norvegicus clone CH230-286021. \*\*\* SEQUENCING IN PROGRESS  
 \*\*\* 50 unordered pieces.  
 ACCESSION AC112072 GI:21744373  
 VERSION AC112072.3  
 KEYWORDS HTG; HTGS\_PHAHEL.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 92874)  
 Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C.,  
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 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
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 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S.,  
 Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K.,  
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
 Weinstein,G. and Gibbs,R.  
 TITLE Unpublished  
 JOURNAL Direct Submission  
 REFERENCE 2 (bases 1 to 92874)  
 AUTHORS Worley,K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 92874)  
 REFERENCE Direct Submission  
 AUTHORS Worley,K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 COMMENT On Jul 13, 2002 this sequence version replaced gi:20303189.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information

Center project name: GRJD  
 Center clone name: CH230-286021  
 ----- Summary Statistics  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye 100% of reads  
 Assembly program: Phrap; version 0.990329  
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 Consensus quality: 35930 bases at least Q20  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 50 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
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 1158 2410: contig of 1253 bp in length  
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 38486 38586: gap of unknown length  
 38586 40145: contig of 1559 bp in length





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 17:54:48 ; Search time 2169.32 Seconds  
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Word size : 10

Total number of hits satisfying chosen parameters: 1916787

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	35.3	888	14	BQ689771
2	531	32.8	879	14	BQ689033
3	507	31.3	702	14	BQ006545
4	506	31.3	743	10	BE385797
5	467	28.8	676	10	BE385990
6	466	28.8	696	13	BM547680

7	463	28.6	530	12	BF726459	BF726459 by06h03.y
8	461	28.5	537	12	BF594242	BF594242 7n10d03.x
9	437	27.0	457	9	A1459805	A1459805 ap17910.x
10	436	26.9	591	9	A1884686	A1884686 w183d07.x
11	434	26.8	540	12	BF939693	BF939693 nac80b12
12	432	26.7	696	12	BF439382	BF439382 nab3906
13	429	26.5	538	13	BM667957	BM667957 UI-E-DW0-
14	429	26.5	627	13	BM669397	BM669397 UI-E-DW1-
15	426	26.3	457	9	A1936826	A1936826 wp69h10.x
16	425	26.3	678	9	A1150931	A1150931 qb53c04.x
17	424	26.2	527	10	AM338938	AM338938 ha68h04.x
18	424	26.2	527	10	AM338938	AM338938 qx86g11.x
19	413	25.5	515	9	A1336858	A1336858 UI-E-CR1-
20	412	25.4	500	10	AM075598	AM075598 xb24e07.x
21	411	25.4	551	12	BE858216	BE858216 7919g07.x
22	411	25.4	616	9	A1990500	A1990500 w4d0d07.x
23	411	25.4	649	10	AM590950	AM590950 hg51e12.x
24	411	25.4	452	9	A1391683	A1391683 qv93f04.x
25	394	24.3	704	13	B1919074	B1919074 603180881
26	386	23.8	456	9	A1765236	A1765236 w172h08.x
27	379	23.4	821	12	BG752229	BG752229 w938h03.x
28	372	23.0	821	12	BG752229	BG752229 7171h01.y
29	369	22.8	381	12	BF054837	BF054837 7169f08.y
30	368	22.7	371	12	BF054837	BF054837 7169f08.y
31	364	22.5	465	10	AV725028	AV725028 AV725028
32	364	22.5	578	9	A1742092	A1742092 w938h03.x
33	363	22.4	379	9	AA084248	AA084248 zn17f09.r
34	353	22.2	534	10	BE350014	BE350014 hc07g12.x
35	359	22.2	573	10	BE395206	BE395206 601309558
36	353	21.8	432	10	AM087372	AM087372 xb19g02.x
37	353	21.8	537	9	A1018769	A1018769 ov32e04.x
38	349	21.6	707	13	B1913989	B1913989 603180565
39	348	21.5	920	10	BE386060	BE386060 601276753
40	347	21.4	933	9	AL538562	AL538562 AL538562
41	338	20.9	368	12	BF935708	BF935708 MR2-NY013
42	336	20.8	454	10	AM191974	AM191974 x178a02.x
43	336	20.8	747	13	B1917149	B1917149 603181571
44	334	20.6	540	10	AM954549	AM954549 EST366619
45	328	20.3	690	13	B1669845	B1669845 603295440

## ALIGNMENTS

RESULT 1  
BQ689771  
LOCUS 888 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8344092 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6248684  
ACCESSION BQ689771  
VERSION BQ689771.1 GI:21815087  
KEYWORDS EST.  
SOURCE human.  
ORANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 888)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LICM2388 row: O column: 21  
High quality sequence stop: 665.  
Location/Qualifiers  
1. 888

FEATURES  
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="6207625"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pORF7; Site:1: XhoI; Site:2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

```

```

BASE COUNT      217 a      219 c      264 g      187 t
ORIGIN

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Query Match      35.3%; Score 571; DB 14; Length 888;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 691; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 583 AATTGAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGAGTGAAGTGA 642
DB 13 AATTGAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGAGTGAAGTGA 72
QY 643 CCCCCATGCTGTGTACCGGAGTCAAGCCAGCTGCGAGAGTCAATTCAGTCA 702
DB 73 CCCCCATGCTGTGTACCGGAGTCAAGCCAGCTGCGAGAGTCAATTCAGTCA 132
QY 703 CTGAGGTGGGAGTCCCTTTTGTAAACCTCTCAATTCATCCATCCATGAGG 762
DB 133 CTGAGGTGGGAGTCCCTTTTGTAAACCTCTCAATTCATCCATCCATGAGG 192
QY 763 ATAGTTGAGAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 822
DB 193 ATAGTTGAGAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 252
QY 823 TCAAGGCTCCCTCGCTTGTACATTCATTCATTCATTCATTCATTCATTCAT 882
DB 253 TCAAGGCTCCCTCGCTTGTACATTCATTCATTCATTCATTCATTCATTCAT 312
QY 883 AATTGAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGAGTGAAGTGA 942
DB 313 AATTGAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGAGTGAAGTGA 372
QY 943 TAGACTGGGCTCGGCTCTGTAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 1002
DB 373 TAGACTGGGCTCGGCTCTGTAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 432
QY 1003 CAGAGGAGTGGGCTCGGCTCTGTAAGAGTGAAGAGTGAAGAGTGAAGAGT 1062
DB 433 CAGAGGAGTGGGCTCGGCTCTGTAAGAGTGAAGAGTGAAGAGTGAAGAGT 492
QY 1063 TGTGTAGAGTGCATGTACGCGAGGAGTGTGAGTGTGAGTGTGAGTGTGAG 1122
DB 493 TGTGTAGAGTGCATGTACGCGAGGAGTGTGAGTGTGAGTGTGAGTGTGAG 552
QY 1123 GGCAGGAGTGGGCTCGGCTCTGTAAGAGTGAAGAGTGAAGAGTGAAGAGT 1182
DB 553 GGCAGGAGTGGGCTCGGCTCTGTAAGAGTGAAGAGTGAAGAGTGAAGAGT 611
QY 1183 AGCGGAGTGTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 1242
DB 612 AGCGGAGTGTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 671
QY 1243 TACGCCCCGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 1274
DB 672 TACGCCCCGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 703

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RESULT 2
BO689033
LOCUS      BO689033      879 bp      mRNA      linear      EST 15-JUL-2002

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DEFINITION      AGENCOURT 8063959 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207625
                  5' mRNA sequence.
ACCESSION      BO689033
VERSION      BO689033.1 GI:21814349
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 879)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
                Email: cgabs-remail.nih.gov
                Tissue Procurement: ATCC
                CDNA Library Preparation: Rubin Laboratory
                CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                plate: LLCW2364 row: a column: 02
                High quality sequence stop: 555.
                Location/Qualifiers

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FEATURES
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            /db_xref="taxon:9606"
            /clone_image="6207625"
            /clone_lib="NIH_MGC_110"
            /tissue_type="ductal carcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: pancreas; Vector: pORF7; Site:1: XhoI; Site:2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

```

```

BASE COUNT      203 a      260 c      241 g      175 t
ORIGIN

```

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Query Match      32.8%; Score 531; DB 14; Length 879;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 583 AATTGAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGAGTGAAGTGA 642
DB 13 AATTGAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGAGTGAAGTGA 72
QY 643 CCCCCATGCTGTGTACCGGAGTCAAGCCAGCTGCGAGAGTCAATTCAGTCA 702
DB 73 CCCCCATGCTGTGTGTACCGGAGTCAAGCCAGCTGCGAGAGTCAATTCAGTCA 132
QY 703 CTGAGGTGGGAGTCCCTTTTGTAAAGCTCCATTCATTCATTCATTCATTCAT 762
DB 133 CTGAGGTGGGAGTCCCTTTTGTAAAGCTCCATTCATTCATTCATTCATTCAT 192
QY 763 ATAGTTGAGAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 822
DB 193 ATAGTTGAGAGTGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 252
QY 823 TCAAGGCTCCCTCGCTTGTACATTCATTCATTCATTCATTCATTCATTCAT 882
DB 253 TCAAGGCTCCCTCGCTTGTACATTCATTCATTCATTCATTCATTCATTCAT 312
QY 883 AATTGAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGAGTGAAGTGA 942
DB 313 AATTGAGCTGACTGAATTTTCAATGATGACTTGAAGAGAGAGTGAAGTGA 372
QY 943 TAGACTGGGCTCGGCTCTGTAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 1002

```



[illegible]

RESULT 3	LOCUS	DEFINITION	IMAGE:5846228 3'	702 bp	mRNA	linear	EST 26-MAR-2007
B0006545/c	B0006545	UI-H-E11-a2a-p-21-0-UI-s1 NCI CGAP_E11 Homo sapiens	CDNA clone				
		IMAGE:5846228 3'	mRNA sequence.				

ACCESSION	BC000645	GI:19731445
VERSION	BC006545.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE AUTHORS TITLE	
1 (bases 1 to 702)	
NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)	

**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.

Email: cgaaps-remail.1nl.gov  
Tissue Procurement: Dr. Jose Mercuende  
CNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Seq primer: M13 FORWARD  
POLYA-yes.

FEATURES	Location/Qualifiers
source	1. .702

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ORIGIN
BASE COUNT
137 a      200 c      163 g      202 t

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5846228"
/clone_1lb="NCI.CGAP.E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10b (Life Technologies)"
/notes="Organ: Left Pelvis; Vector: pTR73-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I
NCI.CGAP.E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pTR73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(CT)18 tail. The sequence tag for this library is
ACACTTGAC."
TAG_LIB="UI-H-E11"
TAG_TISSUE="chondrosarcoma"
TAG_SRO="ACACTTGAC"

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Query Match	31.3%	Score 507;	DB 14;	Length 702;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 677;	Conservative	0;	Mismatches 1;	Indels 1;
Gaps				

QY 939 GACTTACACGCGGCGCTCGCTCTGAATAAATGTTAAGAAATCTTCAGTTCTC 998  
 |||||

Db	678	GACATTAGACTGGGGCTGGGCTCGCTCTGAAAAATGCTTAAGAAAATCTTCTCAGTTCTC	619
Qy	999	CTTCGACAGGACATGGCCCGCGGGAGACCCGAAGCAACGGCCGCTGCACAAAGCGGGCCCTG	1098
Db	618	CTTGGAGGAGCATGGCGCGGGAGCGCAAGAGCAACGGCGCTCTCACAAAGCGGGCCCTG	559
Qy	1059	TCGGGTGGGAGTGGCGCATGTATGACGCGCAGCGCGCTTCTGTGGTGGGTGCTGCAGGCAC	1118
Db	558	TCGGGTGGGAGTGGCGCATGTATGACGCGCAGCGCGCTTCTGTGGTGGGTGCTGCAGGCAC	499
Qy	1119	AGGCGCGACACAGCACCCTTGACAGACACCCCGGAACTGTCTGCGAGCACACCGTGT	1178
Db	498	AGGCGCGACACAGCACCCTTGACAGACACCCCGGAACTGTCTGCGAGCACACCGTGT	440
Qy	1179	CAGGAGCGGGTTGATGACCGAGCTAGAGGTAGAAAACGTCCGAGAAAGGAGAGAGAT	1238
Db	439	CAGGAGCGGGTTGATGACCGAGCTAGAGGTAGAAAACGTCTCCGAGAAAGGAGAGAGAT	380
Qy	1239	CATGTACGCCCGGGAAGTAGGACCTCGTCACAGTCGTGTTGGGTTGGCGGACCATGAT	1298
Db	379	CATGTACGCCCGGGAAGTAGGACCTCGTCACAGTCGTGTTGGGTTGGCGGACCATGAT	320
Qy	1299	CCTCCGAATCTGTGTGGGCATTCAGCATACGGCCAAATGTCAACAATCAGCCCTGGGCA	1358
Db	319	CCTCCGAATCTGTGTGGGCATTCAGCATACGGCCAAATGTCAACAATCAGCCCTGGGCA	260
Qy	1359	GACACGACAGAGGAGGAGAGACAGAGAAAGAAAACACAGCATAGAAACACAGTAAATG	1418
Db	259	GACACGACAGAGGAGGAGAGAGACAGAGAAAGAAAACACAGCATAGAAACACAGTAAATG	200
Qy	1419	AATTAACCATTAATAATATTATAGCCCTCTGTTCTGTGCTTACTGGCCAGGAATGGTACC	1478
Db	199	AATTAACCATTAATAATATTATAGCCCTCTGTTCTGTGCTTACTGGCCAGGAATGGTACC	140
Qy	1479	AATTTTTCAGTTTGAGACTTGACAGCTTCCTTTGGCACAAAGCAAGAGAAATTTAACT	1538
Db	139	AATTTTTCAGTTTGAGACTTGACAGCTTCCTTTGGCACAAAGCAAGAGAAATTTAACT	80
Qy	1539	GTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAGACATG	1598
Db	79	GTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAGACATG	20
Qy	1599	TAAAAAATTTTTTTTTTTT	1617
Db	19	TAAAAAATTTTTTTTTTTT	1

RESULT 4	BE395797	743 bp	mRNA	linear	EST 21-JUL-2000
LOCUS	BE395797				
DEFINITION	601310028f1 NIH_MGC_44	homo sapiens	CDNA clone	IMAGE:3631543 5',	
ACCESSION	BE395797				
VERSION	BE395797.1	GI:9341162			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 743)				
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				

Email: [cgabbs-remail.nln.gov](mailto:cgabbs-remail.nln.gov)  
 Tissue Procurement: AVCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E..Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LILCM321 row: h column: 08

High quality sequence stop: 600.

FEATURES  
Location/Qualifiers  
1..743

Source  
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/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:361543"  
/clone\_lib="NIH\_MGC\_44"  
/issue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: uterus; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 160 a 189 c 214 g 180 t

Query Match 31.3%; Score 506; DB 10; Length 743;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

473 CTGAGGAGATTTCTCTGGGCTCCTTTATTCGGTAGGAGGAGGAGTCCGTTCT 532  
|||||  
65 CTGAGGAGATTTCTCTGGGCTCCTTTATTCGGTAGGAGGAGGAGTCCGTTCT 124  
|||||  
533 CTTTGTTCCTGTGCAATATGAAAGAGCTGTGAAGCATTCGATTAATTCAGCT 592  
|||||  
125 CTTTGTTCCTGTGCAATATGAAAGAGCTGTGAAGCATTCGATTAATTCAGCT 184  
|||||  
593 GACTGATTTTCAGTATGACTTGAAGAGAGGTGAGTGAAGATTACCCCATGTC 652  
|||||  
185 GACTGATTTTCAGTATGACTTGAAGAGAGGTGAGTGAAGATTACCCCATGTC 244  
|||||  
653 TGTGTACCGAGTACAGGCGGCTGGCAGAGTACCTTAAGAGTCACTGAGGTGG 712  
|||||  
245 TGTGTACCGAGTACAGGCGGCTGGCAGAGTACCTTAAGAGTCACTGAGGTGG 304  
|||||  
713 CATGTGCTTTTGTAAAGCCCTCAGTGTCCATTCCTCATGAGGAGGAGTATGAG 772  
|||||  
305 CATGTGCTTTTGTAAAGCCCTCAGTGTCCATTCCTCATGAGGAGGAGTATGAG 364  
|||||  
773 ACTGAGAGTGAAGTACGCTTTTCTAGGGCTGAGGAGGAGTCCCATCAAGGCTCC 832  
|||||  
365 ACTGAGAGTGAAGTACGCTTTTCTAGGGCTGAGGAGGAGTCCCATCAAGGCTCC 424  
|||||  
833 CTGCGTTGACATTCGATTCATGCTCTGAAAGCATTCCTGAGAGAGATTTGGCTGG 892  
|||||  
425 CTGCGTTGACATTCGATTCATGCTCTGAAAGCATTCCTGAGAGAGATTTGGCTGG 484  
|||||  
893 TTTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGAGTATGAGTGGG 952  
|||||  
485 TTTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGAGTATGAGTGGG 544  
|||||  
953 CTGCGCTCGCTCGTGAAGAGTCTTA 978  
|||||  
545 CTGCGCTCGCTCGTGAAGAGTCTTA 570

RESULT 5  
BE385990 676 bp mRNA linear EST 21-JUL-2000  
LOCUS BE385990  
DEFINITION mRNA sequence.  
VERSION BE385990  
KEYWORDS BE385990.1 GI:9331355  
SOURCE EST.  
ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 676)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
COMMENT Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: ATCC/DCMP

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Inceye Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LICM285 row: 9 column: 09  
High quality sequence stop: 653.

FEATURES  
Location/Qualifiers  
1..676

Source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:3617696"  
/clone\_lib="NIH\_MGC\_20"  
/issue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 168 a 172 c 199 g 137 t

Query Match 28.8%; Score 467; DB 10; Length 676;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 587; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

830 TCCCTGCTTGAATTCGATTCATGCTCTGAAAGCATTCCTGAGAGATTTGGC 889  
|||||  
1 TCCCTGCTTGAATTCGATTCATGCTCTGAAAGCATTCCTGAGAGATTTGGC 60  
|||||  
890 TGGTTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGGACTTACGTC 949  
|||||  
61 TGGTTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGGACTTACGTC 120  
|||||  
950 GGGCTGGCGCTCCTCGTGAAGAGTGTGTAAGAAATCTTCAGTCTGCTGAGAGGA 1009  
|||||  
121 GGGCTGGCGCTCCTCGTGAAGAGTGTGTAAGAAATCTTCAGTCTGCTGAGAGGA 180  
|||||  
1010 CTGCGCGGCGGAGCGGAAGCAACGAGGCGCTGCAAGAGCGGCGCTGCTGAGTGA 1069  
|||||  
181 CTGCGCGGCGGAGCGGAAGCAACGAGGCGCTGCAAGAGCGGCGCTGCTGAGTGA 240  
|||||  
1070 GTGCGGATGACCGGAGGCGCTCTCTGTTGGTGGTCTCTGAGCGAGACGCGGAGCA 1129  
|||||  
241 GTGCGGATGACCGGAGGCGCTCTCTGTTGGTGGTCTCTGAGCGAGACGCGGAGCA 300  
|||||  
1130 CAGCACCCTTGCAAGACACCGCGGAACCTGCTGAGAGAGACCGGTTACAGAGGGGT 1189  
|||||  
301 CAGCACC-TCGACGAGACACCGCGGAACCTGCTGAGAGAGACCGGTTACAGAGGGGT 359  
|||||  
1190 TGAATGACGAGCTGAGTGAAGAAAGCTCTCGAGAAAGGAGAGAGATCATGACGCC 1249  
|||||  
360 TGAATGACGAGCTGAGTGAAGAAAGCTCTCGAGAAAGGAGAGAGATCATGACGCC 419  
|||||  
1250 GGAAGTGAAGACCTCGTCCAGTGTGTTGGTGGTGGCGGACCATGATCTCCGAATCT 1309  
|||||  
420 GGAAGTGAAGACCTCGTCCAGTGTGTTGGTGGTGGCGGACCATGATCTCCGAATCT 479  
|||||  
1310 GGTGGGATTCAGATAGCGCAATGTCACAAATCATGAGCCCTGGGAGACAGAGAGC 1369  
|||||  
480 GGTGGGATTCAGATAGCGCAATGTCACAAATCATGAGCCCTGGGAGACAGAGAGC 539  
|||||  
1370 GAGGGAAGACAGAGAAAGAAACACAGCATGAGAAACAGTAAT 1417

Db	540	GAGGAGACAGACAGAAAAAAGAAACACACGATGAGAGACAGTAAT	587
RESULT 6	BM547680	696 bp	linear EST 20-FEB-2002
LOCUS	BM547680		
DEFINITION	AGENCOURT 6507108 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:57277588		
ACCESSION	BM547680		
VERSION	BM547680.1	GI:18781656	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 696)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.lnl.gov Plate: LMNL2722 row: h column: 07 High quality sequence stop: 641. Location/Qualifiers 1..696 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5727798" /issue_11b="NIH_MGC_124" /tissue_type="hippocampus" /lab_host="DH10B" /note="Organ: brain; Vector: pCMV-SPORT6; site_1: Ecory (destroyed); site_2: NotI; RNA source: male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (Ecory site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."		
BASE COUNT	188 a 160 c 197 g 134 t	17 others	
ORIGIN			
Query Match	28.8%	Score 466;	DB 13; Length 696;
Best Local Similarity	99.7%;	Pred. No. 0;	
Matches 636;	Conservative 0;	Mismatches 1;	Indels 1; Gaps 1;
931	ATGACTGGGACTTACACTGGGCTCGGCTCGCTCTGAAAAGTGGCTTAAGAAAATCTTCT	990	
4	ATGACTGGGACTTACACTGGGCTCGGCTCGCTCTGAAAAGTGGCTTAAGAAAATCTTCT	63	
991	CAGTCTCTCTTGACAGAGACTTGGCCCGGAGCGCAAGAGCAACGGCGCTGCACAAAGC	1050	
64	CAGTCTCTCTTGACAGAGACTTGGCCCGGAGCGCAAGAGCAACGGCGCTGCACAAAGC	123	
1051	GGGCGCTCTGGTGGTAGTGCAGTGCATGTACGCCGAGCGGCTTCTCGTGGTGGCGTGT	1110	
124	GGGCGCTCTGGTGGTAGTGCAGTGCATGTACGCCGAGCGGCTTCTCGTGGTGGCGTGT	183	
1111	GCAGGCAACGCGCGACACACACCTTTCACAGAAACCCCGGAAATGCTTCGACAGAC	1170	
184	GCAGGCAACGCGCGACACACACCTTTCACAGAAACCCCGGAAATGCTTCGACAGAC	242	
1171	ACCGGTACAGAGGCGGTGATGACCGAGCTGAGAGTGAAGAAAGCTCCGACAGAGGG	1230	
243	ACCGGTACAGAGGCGGTGATGACCGAGCTGAGAGTGAAGAAAGCTCCGACAGAGGG	302	

Oy	1231	AGGAGATCATGTACGCCCGGAAGAAGAGCACTCCGCACAGTGGTGCTTTGGTTGGCCCCA	1290
Db	303	AGGAGATCATGTACGCCCGGAAGAAGAGCACTCCGCACAGTGGTGCTTTGGCCCCA	362
Oy	1291	GCCATGATCCTCCGAAATCTGGTTGGGCGATTCGACGATACGGCCAATGTACAACATTCAGC	1350
Db	363	GCCATGATCCTCCGAAATCTGGTTGGGCGATTCGACGATACGGCCAATGTACAACATTCAGC	422
Oy	1351	CCTGGGCGAGACACGACGAGCGAGGAGACACAGAAAAAAAACACAGCATGTAGAACAC	1410
Db	423	CCTGGGCGAGACACGAGCGAGGAGGAGACAGAAAAAAAACACAGCATGTAGAACAC	482
Oy	1411	AGTAATAAATAAACCATTAAATTTATTAAGCCCCCTCTGTGTGCTACTACGGCCAGGAA	1470
Db	483	AGTAATAAATAAACCATTAAATTTATTAAGCCCCCTCTGTGTGCTACTACGGCCAGGAA	542
Oy	1471	ATGGTACCAATTTTTTCAGTGTGGACTTGAGACTTCTTTTGCACAAGACAGAGAAAT	1530
Db	543	ATGGTACCAATTTTTTCAGTGTGGACTTGAGACTTCTTTTGCACAAGACAGAGAAAT	602
Oy	1531	TTCACACTGTTTCAAACCCGGGGGAGTTGGCTGTCTTA	1568
Db	603	TTCACACTGTTTCAAACCCGGGGGAGTTGGCTGTCTTA	640
RESULT 7			
LOCUS	Bf726459	530 bp	mRNA linear EST 05-JAN-2001
DEFINITION	bv06h03.y1 Human Lens cDNA (Un-normalized, unamplified): By Homo sapiens cDNA clone bv06h03 5', mRNA sequence.		
ACCESSION	Bf726459		
VERSION	Bf726459.1	GI:12042370	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Wistow G.J., Bernstein S., Beitel A. and Smith D.		
TITLE	NEIBANK: EST analysis and bioinformatics for ocular genomics		
JOURNAL	Invest. Ophthalmol. Vis. Sci. 41, (2000) In press		
COMMENT	Contact: Wistow G Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 06 row: h column: 03 Seq primer: M13RPL reverse primer (ABI). Location/Qualifiers		
FEATURES			
SOURCE	1..530		
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	/db_xref="taxon:9606"		
	/clone="bv06h03"		
	/clone_lib="Human lens cDNA (Un-normalized, unamplified): By"		
	/tissue_type="Lens"		
	/dev_stage="Adult"		
	/lab_host="EMDHI0B"		
	/note="Organ: Eye; Vector: PCWSPORT6; Two human lenses from different adults (both approximately 40 years old) together yielded 20ug of total RNA and 150ng mRNA for CDNA library synthesis. A directionally cloned cDNA library in the PCWSPORT6 vector was constructed at Life Technologies , essentially following the protocols of the Superscript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pgacatgctttagatcgccggcgcgcc(TrI5-3')]. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the		







/clone.lib="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled: Vector: pRT73-Pac (Pharmacia) with  
 a modified polylinker; Site1: Not I; Site2: Eco RI;  
 Equal amounts of plasmid DNA from five normalized  
 libraries were mixed, and ss circles were made in vitro.  
 Following HAP purification, this DNA was used as tracer in  
 a subtractive hybridization reaction. The driver was  
 PCR-amplified cDNAs from pools of 5,000 clones made from  
 the same 5 libraries. The pools consisted of the following  
 libraries and clones: Soares NBHSF pool 1:  
 309384-310919, 323208-325895 Soares ND2HP pool 1:  
 145032-147335, 147720-148103, 148872-149255, 15002 -  
 150407, 151176-152327 Soares NB2HP-9W pool 1:  
 758280-760583, 772104-774407 Soares NBHPA pool 1:  
 304776-306311, 320136-322823 326280-326603 Soares NBHOT  
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento  
 Soares and M. Patricia Bonaldo."

BASE COUNT 138 a 202 c 164 g 192 t  
 ORIGIN

Query Match 26.7%; Score 432; DB 12; Length 696;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 602; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1001 TGCAGAGACTGCGCGCGGAGCGGAGCAAGCGGCGCTGCACAAAGCGGCGCTGTC 1060  
 |||||||  
 DB 603 TGCAGAGACTGCGCGCGGAGCGGAGCAAGCGGCGCTGCACAAAGCGGCGCTGTC 544

OY 1061 GGTGTGAGTGGCATGTATGACGCGGCGGCGTTCGCTGGTGGCTGTGACGACAG 1120  
 |||||||  
 DB 543 GGTGTGAGTGGCATGTATGACGCGGCGGCGTTCGCTGGTGGCTGTGACGACAG 484

OY 1121 GCGGACAGACAGACCTTGCACAGACCGCGGAAATGCTGCGAGAGACACCGTGTACA 1180  
 |||||||  
 DB 483 GCGGACAGACAGACCGCGGAAATGCTGCGAGAGACACCGTGTACA 425

OY 1181 GAGACGGGTGATGATGACGAGCTGAGGTAGAAAAAGCTCTCCAGAAAGGAGAGAGATCA 1240  
 |||||||  
 DB 424 GAGACGGGTGATGATGACGAGCTGAGGTAGAAAAAGCTCTCCAGAAAGGAGAGATCA 365

OY 1241 TGTACGCGCGGAAAGTATGACACTCTGTCAGTGGTGGCGGCGAGCATGATCC 1300  
 |||||||  
 DB 364 TGTACGCGCGGAAAGTATGACACTCTGTCAGTGGTGGCGGCGAGCATGATCC 305

OY 1301 TCCGATCTGCTGGGATCCAGCATACGCCAATGTCAACAATCAGCCCTGGGCGAGA 1360  
 |||||||  
 DB 304 TCCGATCTGCTGGGATCCAGCATACGCCAATGTCAACAATCAGCCCTGGGCGAGA 245

OY 1361 CACGACGAGAGAGAGACAGAAAAAGAAAAACAGCATGAGAACACAGTAAATGAA 1420  
 |||||||  
 DB 244 CACGACGAGAGAGAGAGACAGAAAAAGAAAAACAGCATGAGAACACAGTAAATGAA 185

OY 1421 TAAAAACATAAATATTTAGCCCTCTGCTGTGCTTACTGCGCAGGAATGTACCAA 1480  
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 DB 184 TAAAAACATAAATATTTAGCCCTCTGCTGTGCTTACTGCGCAGGAATGTACCAA 125

OY 1481 TTTTCAAGTGTGAGCTGACAGCTTCTTTGCCAAGAGAGATTTAACTGTT 1540  
 |||||||  
 DB 124 TTTTCAAGTGTGAGCTGACAGCTTCTTTGCCAAGAGAGATTTAACTGTT 65

OY 1541 TTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGTTTAGACAGTGA 1600  
 |||||||  
 DB 64 TTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGTTTAGACAGTGA 5

OY 1601 AAAA 1604  
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 DB 4 AAAA 1

RESULT 13  
 BM667957/c 538 bp mRNA 1linear EST 27-FEB-2002  
 LOCUS BM667957

DEFINITION UI-E-DW0-agg-j-01-0-UI.s1 UI-E-DW0 Homo sapiens cDNA clone  
 UI-E-DW0-agg-j-01-0-UI 3', mRNA sequence.  
 ACCESSION BM667957  
 VERSION BM667957.1 GI:18975788  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 538)  
 TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: mscares@blue.weeg.uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing Arrayed by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Forward  
 POLYA=yes.

#### FEATURES

source Location/Qualifiers  
 1..538  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-DW0-agg-j-01-0-UI"  
 /clone.lib="UI-E-DW0"  
 /tissue.type="lens"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: pRT73-Pac (Pharmacia) with a  
 modified polylinker; Site1: EcoR I; Site2: Not I;  
 UI-E-DW0 is a cDNA library containing the following  
 tissue(s): lens. The library was constructed according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. First strand cDNA synthesis was primed with an  
 oligo-dT primer containing a Not I site. Double stranded  
 cDNA was ligated to an EcoR I adaptor, digested with Not  
 I, and cloned directionally into pRT73-Pac vector. The  
 oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is CGATTAGCGA. This library  
 was created for the program, Gene Discovery in the Visual  
 System, supported by National Eye Institute (NEI).  
 TAG\_LIB=UI-E-DW0  
 TAG\_TISSUE=human lens  
 TAG\_SEQ=CGATTAGCGA"  
 BASE COUNT 104 a 144 c 122 g 167 t 1 others  
 ORIGIN

Query Match 26.5%; Score 429; DB 13; Length 538;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1138 TGCAGACACCGCGCGGAAATGCTGCGAGACACCGTGTACAGAGACGGGTGATGACC 1197  
 |||||||  
 DB 480 TGCAGACACCGCGCGGAAATGCTGCGAGACACCGTGTACAGAGACGGGTGATGACC 421

OY 1198 GAGCTGAGTGAAGAAAAAGTCTCCGAGAAGGAGGAGATCATGTACGCCGAGAGTAG 1257  
 |||||||  
 DB 420 GAGCTGAGTGAAGAAAAAGTCTCCGAGAAGGAGGAGATCATGTACGCCGAGAGTAG 361

OY 1258 GACCTGTCACGCTGCTGGTGGTGGCGCGACCATGATCTCCGAATCTGTTGGGC 1317



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|||||
Db 360 GACCTGTCACATCGTGGCTTGGCCGAGCATGATCTCCGAATCGCTTGGGC 301
QY 1318 ATCCAGCATACGCCCAATGTCTACACATCAGCCCTGGGCGAGACGAGGAGGAGA 1377
Db 300 ATCCAGCATACGCCCAATGTCTACACATCAGCCCTGGGCGAGACGAGGAGGAGA 241
QY 1378 GACAGAGAAAAGAAAACACAGCATGAGAACACATTAATGAATTAACCATTAATATT 1437
Db 240 GACAGAGAAAAGAAAACACAGCATGAGAACACATTAATGAATTAACCATTAATATT 181
QY 1438 TAGCCCTCTGTTCTGTCTGCTTACTGCGCCAGCAATGTGATACCAATTTTCAGTGGAGCT 1497
Db 180 TAGCCCTCTGTTCTGTCTGCTTACTGCGCCAGCAATGTGATACCAATTTTCAGTGGAGCT 121
QY 1498 TGACAGCTTCTTTTGGCAGACAGAGAGAAATTAACACTGTTTCAAAACCCGGGGAGT 1557
Db 120 TGACAGCTTCTTTTGGCAGACAGAGAGAAATTAACACTGTTTCAAAACCCGGGGAGT 61
QY 1558 TGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGACACTGTAATAAAAAAAAAAAAA 1617
Db 60 TGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGACACTGTAATAAAAAAAAAAAAA 1

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RESULT 14
BM669397 627 bp mRNA linear EST 27-FEB-2002
LOCUS BM669397
DEFINITION UI-E-DWI-and-c-11-0-UI-s1 UI-E-DWI Homo sapiens cDNA clone
ACCESION BM669397
VERSION BM669397.1 GI:18979294
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 627)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLY-A=yes

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## FEATURES

## SOURCE

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1..627
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-DWI-and-c-11-0-UI"
/clone_id="UI-E-DWI"
/tissue_type="lens"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DWI is a normalized cDNA library containing the
following tissue(s): lens. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double

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stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dId)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG-UI-E-DWI  
TAG-RTSUE-human lens  
TAG-SEQ-CGATTAGCGA"

```

BASE COUNT      118 a      180 c      145 g      183 t      1 others
Query Match      26.5%; Score 429; DB 13; Length 627;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1138 TGACAGACACCCCGCCGAACCTGTCGAGACACCGGTACAGAGCGGTTATGACC 1197
Db 480 TGACAGACACCCCGCCGAACCTGTCGAGACACCGGTACAGAGCGGTTATGACC 421
QY 1198 GACCTGAGTAGAAAAACCTCTCCGAGAGGAGAGATCATGTACGCCCGAAGTAG 1257
Db 420 GACCTGAGTAGAAAAACCTCTCCGAGAGGAGAGATCATGTACGCCCGAAGTAG 361
QY 1258 GACCTGTCAGTCGTCGTTGGTTGGCCGAGCATGATCTCCGATCTGTTGGGC 1317
Db 360 GACCTGTCAGTCGTCGTTGGTTGGCCGAGCATGATCTCCGATCTGTTGGGC 301
QY 1318 ATCCAGCATACGCCCAATGTCTACACATCAGCCCTGGGCGAGACGAGGAGGAGA 1377
Db 300 ATCCAGCATACGCCCAATGTCTACACATCAGCCCTGGGCGAGACGAGGAGGAGA 241
QY 1378 GACAGAGAAAAGAAAACACAGCATGAGAACACAGTAATGAATTAACCATTAATATT 1437
Db 240 GACAGAGAAAAGAAAACACAGCATGAGAACACAGTAATGAATTAACCATTAATATT 181
QY 1438 TAGCCCTCTGTTCTGTCTGCTTACTGCGCCAGCAATGTGATACCAATTTTCAGTGGAGCT 1497
Db 180 TAGCCCTCTGTTCTGTCTGCTTACTGCGCCAGCAATGTGATACCAATTTTCAGTGGAGCT 121
QY 1498 TGACAGCTTCTTTTGGCAGACAGAGAGAAATTAACACTGTTTCAAAACCCGGGGAGT 1557
Db 120 TGACAGCTTCTTTTGGCAGACAGAGAGAAATTAACACTGTTTCAAAACCCGGGGAGT 61
QY 1558 TGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGACACTGTAATAAAAAAAAAAAAA 1617
Db 60 TGCGTGTGTTAAAGAAAGACCATTAATGCTTTAGACACTGTAATAAAAAAAAAAAAA 1

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RESULT 15
A1936826 678 bp mRNA linear EST 08-MAR-2000
LOCUS A1936826/c
DEFINITION w669h10 x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2467075 3'
similar to SW:GP39.HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39.; mRNA sequence.

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```

ACCESSION A1936826
VERSION A1936826.1 GI:5675696
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 678)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRINAP), Tumor Gene Index
(unpublished (1998))
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapb-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

```



Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bdrp/image/image.html  
 Insert Length: 1143 Std Error: 0.00  
 Seq primer: -40UP from Glibco  
 High quality sequence stop: 454.  
 Location/Qualifiers  
 1. 678  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="2467075"  
 /clone\_id="NCI CGAP Brn23"  
 /tissue\_type="anaplastic oligodendroglioma"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCCGCAATCTTTTGTGTTTGTGTTT  
 T 3'] double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified p773 vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M.Fatima Bonaldo."

BASE COUNT 133 a 199 c 161 g 182 t 3 others  
 ORIGIN

Query Match 26.3%; Score 426; DB 9; Length 678;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 596; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

QY 1001 TCGAGAGAGCTGGCGCCGCGAGCGAAGACACAGCGCGCTGCACAAAGCGCGCTGTC 1060
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DB 597 TCGAGAGAGCTGGCGCCGCGAGCGAAGACACAGCGCGCTGCACAAAGCGCGCTGTC 538
    |||
QY 1061 GGTGGTGAATGCGCATGTACGCGCAGAGCGCTTCTCGTGGTGGCGTGTGACGACAG 1120
    |||
DB 537 GGTGGTGAATGCGCATGTACGCGCAGAGCGCTTCTCGTGGTGGCGTGTGACGACAG 478
    |||
QY 1121 GCGGACACAGACACCTTGACGACACACCGCGGAAATCTCTCGAGAGACACCTGTACA 1180
    |||
DB 477 GCGGACACACAGACACCTTGACGACACACCGCGGAAATCTCTCGAGAGACACCTGTACA 419
    |||
QY 1181 GAGCGGGTGTGATGACCGAGCTGAGTAAAGCTCTCCGAGAGGGAGAGGATCA 1240
    |||
DB 418 GAGCGGGTGTGATGACCGAGCTGAGTAAAGCTCTCCGAGAGGGAGAGGATCA 359
    |||
QY 1241 TGTACGCGCGGAGTGAAGACCTGTCAGTCTGCTGGGTTGGCCGACGACCATGATCC 1300
    |||
DB 358 TGTACGCGCGGAGTGAAGACCTGTCAGTCTGCTGGGTTGGCCGACGACCATGATCC 299
    |||
QY 1301 TCGGAATCTGTTGGGATTCACAGATACGCGCAATGTCAACAACATCACCCGCGGACAGA 1360
    |||
DB 298 TCGGAATCTGTTGGGATTCACAGATACGCGCAATGTCAACAACATCACCCGCGGACAGA 239
    |||
QY 1361 CACGACACAGAGGAGAGACAGAGAAAAGAAAACACAGCATGAGAACACAGTAAATGAA 1420
    |||
DB 238 CACGACACAGAGGAGAGACAGAGAAAAGAAAACACAGCATGAGAACACAGTAAATGAA 179
    |||
QY 1421 TAAACCAATTAATATTTAGCCCTCTGTTCTGTGCTTCTGCGCAAGAAATGTTACCAA 1480
    |||
DB 178 TAAACCAATTAATATTTAGCCCTCTGTTCTGTGCTTCTGCGCAAGAAATGTTACCAA 119
    |||
QY 1481 TTTTTCAGTGTGGAGCTTGACAGCTTCTTTTGCACAAAGAGAGATTTAAACAGTGT 1540
    |||
DB 118 TTTTTCAGTGTGGAGCTTGACAGCTTCTTTTGCACAAAGAGAGATTTAAACAGTGT 59
    |||
QY 1541 TTCAAAACCGGGGGAGTGGCTGTGTAAAGAAAGACCTTTAAATGCTTTAGACAGTG 1598
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DB 58 TTCAAAACCGGGGAGTGGCTGTGTAAAGAAAGACCTTTAAATGCTTTAGACAGTG 1

RESULT 16  
 A1150931/c  
 LOCUS  
 DEFINITION

A1150931 467 bp mRNA linear EST 26-OCT-1998  
 gb53c04.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:1703814.3  
 similar to SW:NTRI\_RAT F20789 NEUROKININ RECEPTOR TYPE 1; mRNA  
 sequence.

ACCESSION A1150931  
 VERSION A1150931  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 467)  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke; Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index  
 Unpublished (1998)

COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bdrp/image/image.html  
 Insert Length: 1149 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 425.  
 Location/Qualifiers

FEATURES  
 source

1. 467

/organism="Homo sapiens"  
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 /clone\_id="NCI CGAP Brn23"  
 /tissue\_type="gliblastoma (pooled)"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCCGCAATCTTTTGTGTTTGTGTTT  
 T 3'] double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified p773 vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M.Fatima Bonaldo."

BASE COUNT 106 a 119 c 92 g 150 t  
 ORIGIN

Query Match 26.3%; Score 425; DB 9; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1176 GTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAGAGAGGAGAG 1235
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DB 467 GTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAGAGAGGAGAG 408
    |||
QY 1236 GATCATGTACCGCCGGAAGTAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295
    |||
DB 407 GATCATGTACCGCCGGAAGTAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 348
    |||
QY 1296 GATCTCCGAATCTGTTGGGATTCACAGATACGCGCAATGTCAACAATTCAGCCCTGG 1355
    |||
DB 347 GATCTCCGAATCTGTTGGGATTCACAGATACGCGCAATGTCAACAATTCAGCCCTGG 288
    |||
QY 1356 GCAGACACAGACAGAGAGAGACAGAGAAAAGAAAACACAGCATGAGAACACAGTAA 1415
    |||

```



reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1463064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 103 a 142 c 119 g 151 t

ORIGIN

Query Match 25.6%; Score 415; DB 9; Length 515;

Best Local Similarity 99.8%; Pred. No. 0; Matches 465; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1138 TGCACCAACACCCCGGAAACCTGCTCCGAGACACCGGTACAGAGCGGGTTGATACC 1197  
 466 TGCACCAACACCCCGGAAACCTGCTCCGAGACACCGGTACAGAGCGGGTTGATACC 407  
 1198 GACCTGAGGTAGAAAACCTCCGAGAGGGAGAGGATCATGTACCGCGGAAATAG 1257  
 406 GACCTGAGGTAGAAAACCTCCGAGAGGGAGAGGATCATGTACCGCGGAAATAG 347  
 1258 GACCTGAGGTAGAAAACCTCCGAGAGGGAGAGGATCATGTACCGCGGAAATAG 1317  
 346 GACCTGAGGTAGAAAACCTCCGAGAGGGAGAGGATCATGTACCGCGGAAATAG 287  
 1318 ATCCACATACGCGCAATTCACAAATCAGCCCTGGGAGACAGACAGAGAGGAGA 1377  
 286 ATCCACATACGCGCAATTCACAAATCAGCCCTGGGAGACAGACAGAGAGGAGA 227  
 1378 GACGAGAAAAGAAAACACACATGAGAACAGTAATGATTAATTAATTAATTAAT 1437  
 226 GACGAGAAAAGAAAACACACATGAGAACAGTAATGATTAATTAATTAATTAAT 167  
 1438 TACCCCTCTGTTCTGCTTCTACTGCGAGAAATGTAACAAATTTTTCAGTTGGACT 1497  
 166 TACCCCTCTGTTCTGCTTCTACTGCGAGAAATGTAACAAATTTTTCAGTTGGACT 107  
 1498 TGACACCTCTTTTGGCAACAGAGAGAAATTAACCTGTTCAACCCGGGGAGT 1557  
 106 TGACACCTCTTTTGGCAACAGAGAGAAATTAACCTGTTCAACCCGGGGAGT 47  
 1558 TGCGCTGTTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAA 1603  
 46 TGCGCTGTTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAA 1

RESULT 19 421 bp mRNA linear EST 28-FEB-2002  
 BM686824  
 LOCUS  
 DEFINITION UI-E-CRI-aec-b-10-0-UI.r1 UI-E-CRI Homo sapiens cDNA clone  
 BM686824  
 VERSION UI-E-CRI-aec-b-10-0-UI 5', mRNA sequence.  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 421)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 JOURNAL  
 MEDLINE  
 COMMENT 97044477  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

FEATURES  
 source 1..421

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
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 /clone\_lib="UI-E-CRI"  
 /rname="eye anterior segment"  
 /dev\_stage="adult"  
 /note="Host: DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: pRT3-Pac (Pharmacia) with a modified polylinker. Site.1: EcoR I; Site.2: Not I; UI-E-CRI is a normalized cDNA library containing the following tissue(s): eye anterior segment. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tag for this library is AATGCCCAT. This library was created for the program Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 96 a 99 c 118 g 108 t

ORIGIN

Query Match 25.5%; Score 413; DB 14; Length 421;

Best Local Similarity 100.0%; Pred. No. 0; Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

564 CGGTAAAGCATTTGTAATTAATTCAGCTGATTAATTTTCAATGATGATTAAGGAG 623  
 9 CGGTAAAGCATTTGTAATTAATTCAGCTGATTAATTTTCAATGATGATTAAGGAG 68  
 624 GAGGAGAGTAAAGTTCACCCCATGCTGCTTAACCCGAGTAAGCCAGCTGCGAG 683  
 69 GAGGAGAGTAAAGTTCACCCCATGCTGCTTAACCCGAGTAAGCCAGCTGCGAG 128  
 684 AGTCACTCTTAGAAGTACAGTGAAGTGGGATGCTGCTTTTAAAGCTCCAGTGTCA 743  
 129 AGTCACTCTTAGAAGTACAGTGAAGTGGGATGCTGCTTTTAAAGCTCCAGTGTCA 188  
 744 TTCCATCCCTGATGGGGCATAGTTTGAAGCTGCAGAGTGAAGTGAAGTGTCTT 803  
 189 TTCCATCCCTGATGGGGCATAGTTTGAAGCTGCAGAGTGAAGTGAAGTGTCTT 248  
 804 CTGGAGGGCCAGTCCCACTCAAGGCTCCGCTGTAACATTAATTAATGCTCTGA 863  
 249 CTGGAGGGCCAGTCCCACTCAAGGCTCCGCTGTAACATTAATTAATGCTCTGA 308  
 864 AAACCATCTCTGAGAGAGAAATGCTGTTTCCGCGCTAGTGGGCTTAAGTACTCG 923  
 309 AAACCATCTCTGAGAGAGAAATGCTGTTTCCGCGCTAGTGGGCTTAAGTACTCG 368  
 924 AGACTCAATGACTGGAGTAACTGAGTGGGCTGGGCTCTGAAAAGTCT 976  
 369 AGACTCAATGACTGGAGTAACTGAGTGGGCTGGGCTCTGAAAAGTCT 421

RESULT 20 500 bp mRNA linear EST 13-OCT-1999  
 AM075598/c  
 LOCUS  
 DEFINITION XM24607.x1 NCI\_CGAP\_Kid3 Homo sapiens cDNA clone IMAGE:257752.3,  
 similar to SW:GP39, HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39.; mRNA sequence.  
 ACCESSION AM075598  
 VERSION AM075598.1 GI:6030596  
 KEYWORDS EST.

Source	Organism	Human
REFERENCE 1 (bases 1 to 500)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
ADDITIONAL TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	
JOURNAL COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
	Unpublished (1997)	
	Contact: Robert Stransberg, Ph.D.	
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>	
	Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center	
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/MLNL at: <a href="http://www-bio.livnl.gov/bbrp/image/image.html">www-bio.livnl.gov/bbrp/image/image.html</a>	
FEATURES	Possible reversed clone: similarity on wrong strand	
Source	Seq primer: -40UP from Gibco	
	High quality sequence stop: 413.	
	Location/Qualifiers	
	1..500	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:2577252"	
	/clone_11b="NCI-CGAP_K1d13"	
	/tissue_type="2, pooled WILMS" tumors, one primary and one metastatic to brain"	
	/lab_host="DH10B"	
	/note="Organ: Kidney; Vector: pCMV-Sport6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."	
BASE COUNT	99 a 139 c 114 g 148 t	
ORIGIN		
Query Match	25.4%	Score 412; DB 10; Length 500;
Best Local Similarity	99.8%	Pred. No. 0;
Matches 462: Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
1138	TGCACGAACACCCCGCGAAGACTCTGCGAGACACCGCTACAGAGCGGGTTGATGACC	1197
463	TGCACGAACACCCCGCGAAGACTCTGCGAGACACCGCTACAGAGCGGGTTGATGACC	404
1198	GAGCTGAGGTAGAAAAACCTCTCCGAGAGGGGAGGAGGATCATGTACCCCGGAAGTAG	1257
403	GAGCTGAGGTAGAAAAACCTCTCCGAGAGGGGAGGAGGATCATGTACCCCGGAAGTAG	344
1258	GACCTGTCACATGCTGCTTGGGTTTGGCGGAGCGCATGATCCTCGAATCTGCTGGGCG	1317
343	GACCTGTCACATGCTGCTTGGGTTTGGCGGAGCGCATGATCCTCGAATCTGCTGGGCG	284
1318	ATCCAGCATATCGCCCAATGTCAACAACATCAGCCCTGGCGACAGACAGAGAGGAGA	1377
283	ATCCAGCATATCGCCCAATGTCAACAACATCAGCCCTGGCGACAGACAGAGAGGAGA	224
1378	GACAGAGAAAAAACAACACAGCATGAGAACACAGTAATGATTAATAAACCTATAATATT	1437
223	GACAGAGAAAAAACAACACAGCATGAGAACACAGTAATTAATAATAAACCTATAATATT	164
1438	TAGCCCTCTGCTTGTGCTTACTGTGCGCCAGAAATGGTACCAATTTTTCAGTGTGGACT	1497
163	TAGCCCTCTGCTTGTGCTTACTGTGCGCCAGAAATGGTACCAATTTTTCAGTGTGGACT	104
1498	TGACAGACTTCTTTTGGCACAGACAGAGAGAAATTAACTGTTTCAACCCGGGGAGCT	1557
103	TGACAGACTTCTTTTGGCACAGACAGAGAGAAATTAACTGTTTCAACCCGGGGAGCT	44
1558	TGGGTGTGTTAAGAAGACCAATTAACTCTTAACTAGCACTGTA 1600	
43	TGGGTGTGTTAAGAAGACCAATTAACTCTTAACTAGCACTGTA 1	

RESULT 21	BE858216/c	551 bp	mRNA	linear	EST 29-SEP-2000
LOCUS	BE858216				
DEFINITION	7919907.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:33069972 3'				
	Similar to SW:G939_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39.1; mRNA sequence.				
ACCESSION	BE858216				
VERSION	BE858216.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 551)				
AUTHORS	NCI/NINDS-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .				
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAAP), Tumor Gene Index				
JOURNAL	Unpublished (1998)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapb-rt@mail.nih.gov">cgapb-rt@mail.nih.gov</a> Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfield M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> Seq primer: -400P from Glibco High quality sequence stop: 490. Location/Qualifiers 1..551 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:33069972" /clone_lib="NCI-CGAP_Brn23" /tissue_type="glioblastoma (pooled)" /lab_host="IDH10B" /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site:1; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5 TGTATCCCATCTGATGAGTGGGACGCCGCCGCAATATTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."				
BASE COUNT	110 a 161 c 128 g 152 t				
ORIGIN					
Query Match	25.4%; Score 411; DB 12; Length 551;				
Best Local Similarity	99.8%; Pred. No. 0;				
Matches 461; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
Y	1138 TGCACGACACCCCGCGAAACGTCTGCGAGGACACCGGTATACAGGAGGGGTGATGACC	1197			
Db	462 TGCACGAAACCCCGCGAAACGTCTGCGAGGACACCGGTATACAGGAGGGGTGATGACC	403			
Y	1198 GAGCTGAGGTAGAAAAAGCTCTCCAGAAAGGAGGAGAGATCATGCGCCCGGAAGTAG	1257			
Db	402 GAGCTGAGGTAGAAAAAGCTCTCCAGAAAGGAGGAGAGATCATGCGCCCGGAAGTAG	343			
Y	1258 GACCTGTCACAGTCTGCTTGGGTTTGGCCGACGACCATGATCTCTCCGAATCTGGTTGGCC	1317			
Db	342 GACCTGTCACAGTCTGCTTGGGTTTGGCCGACGACCATGATCTCTCCGAATCTGGTTGGCC	283			
Y	1318 ATCCAGCATPAGGGCAATGTCAACAATCACCCCTGGGCAACAGCAGAGAGAGGAGA	1377			
Db	282 ATCCAGCATPAGGGCAATGTCAACAATCACCCCTGGGCAACAGCAGAGAGAGGAGA	223			

QY 1378 GACAGAGAAAAAGAACACACATGAGACACAGTAATGATATAAACATTAATATT 1437  
 DB 222 GACAGAGAAAAAGAACACACATGAGACACAGTAATGATATAAACATTAATATT 163  
 QY 1438 TAGCCCTCTGTTGTTGTTACTGCGGAGAAATGTTACCAATTTTTCAGTTGGACT 1497  
 DB 162 TAGCCCTCTGTTGTTGTTACTGCGGAGAAATGTTACCAATTTTTCAGTTGGACT 103  
 QY 1498 TGACAGCTTCTTTTGCACACAGAGAGAAATTAACACTTTTCAACCCGGGGAGCT 1557  
 DB 102 TGACAGCTTCTTTTGCACACAGAGAGAAATTAACACTTTTCAACCCGGGGAGCT 43  
 QY 1558 TGCGCTGTGTTAAAGAAAGACATTAATGCTTTAGCAGCTGT 1599  
 DB 42 TGCGCTGTGTTAAAGAAAGACATTAATGCTTTAGCAGCTGT 1  
 RESULT 22  
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 DEFINITION ws40d07.x1 NCI\_CGAP\_GC6 Homo sapiens CDNA clone IMAGE:2499661.3  
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 GPR39. ; mRNA sequence.  
 ACCESSION AI990500  
 VERSION AI990500.1 GI:5837381  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 616)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/dbp/image/image.html  
 Insert Length: 1212 Std Error: 0.00  
 Seq primer: -40UP from gibco  
 High quality sequence stop: 459.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
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 /clone\_lib="NCI\_CGAP\_GC6"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
 from the normalized library NCI\_CGAP\_GC4 was prepared, and  
 as circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 120 a 182 c 147 g 167 t  
 ORIGIN  
 Query Match 25.4%; Score 411; DB 9; Length 616;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1138 TGACAGAACACCCGCGAACTGCTGCGAGACACCGCTGTACAGAGACCGGGTGTATGACC 1197  
 DB 462 TGACAGAACACCCGCGAACTGCTGCGAGACACCGCTGTACAGAGACCGGGTGTATGACC 403  
 QY 1198 GAGCTGAGGTGAGAAAACGCTCCGAGAGGGAGAGATCATGTACGCCCGGAGTAG 1257  
 DB 402 GAGCTGAGGTGAGAAAACGCTCCGAGAGGGAGAGATCATGTACGCCCGGAGTAG 343  
 QY 1258 GAGCTGCTCCAGTGTGTTGGTTGGCCGAGCAGTATGATCCCGAATCTGGTTGGCC 1317  
 DB 342 GAGCTGCTCCAGTGTGTTGGTTGGCCGAGCAGTATGATCCCGAATCTGGTTGGCC 283  
 QY 1318 ATCCAGCTATGCGCCCAATGTCACACATTCAGCCCTGGCGAGACAGCAGAGGAGAGA 1377  
 DB 282 ATCCAGCTATGCGCCCAATGTCACACATTCAGCCCTGGCGAGACAGCAGAGGAGAGA 223  
 QY 1378 GACAGAGAAAAAGAACACACATGAGACACAGTAATGATATAAACATTAATATT 1437  
 DB 222 GACAGAGAAAAAGAACACACATGAGACACAGTAATGATATAAACATTAATATT 163  
 QY 1438 TAGCCCTCTGTTGTTGTTACTGCGGAGAAATGTTACCAATTTTTCAGTTGGACT 1497  
 DB 162 TAGCCCTCTGTTGTTGTTACTGCGGAGAAATGTTACCAATTTTTCAGTTGGACT 103  
 QY 1498 TGACAGCTTCTTTTGCACACAGAGAGAAATTAACACTTTTCAACCCGGGGAGCT 1557  
 DB 102 TGACAGCTTCTTTTGCACACAGAGAGAAATTAACACTTTTCAACCCGGGGAGCT 43  
 QY 1558 TGCGCTGTGTTAAAGAAAGACATTAATGCTTTAGCAGCTGT 1599  
 DB 42 TGCGCTGTGTTAAAGAAAGACATTAATGCTTTAGCAGCTGT 1  
 RESULT 23  
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 DEFINITION hgs1e12.x1 NCI\_CGAP\_GC6 Homo sapiens CDNA clone IMAGE:2949166.3  
 similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39. ; mRNA sequence.  
 ACCESSION AM590950  
 VERSION AM590950.1 GI:7278094  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 649)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 image.llnl.gov/image/html/iresources.shtml  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -40UP from gibco  
 High quality sequence stop: 457.  
 Location/Qualifiers  
 FEATURES  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:2949166"  
 /clone\_lib="NCI\_CGAP\_GC6"

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/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/Note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP_G4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      132 a      189 c      155 g      173 t
ORIGIN
Query Match      25.4%; Score 411; DB 10; Length 649;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1138 TGCAGAACACCCGCCGAACTGTCGAGAGACACCGTGTACAGAGCGGGTGTGACG 1197
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|
|
Db 462 TGCAGAACACCCGCCGAACTGTCGAGAGACACCGTGTACAGAGCGGGTGTGACG 403
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|
|
QY 1198 GAGCTGAGTAGAAAAACGCTCTCGAAGAGGAGAGATCATGTACGCCGGAAGTAG 1257
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|
|
Db 402 GAGCTGAGTAGAAAAACGCTCTCGAAGAGGAGAGATCATGTACGCCGGAAGTAG 343
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|
|
QY 1258 GACCTGTCACAGTCGTGGTGGTGGCCGACGACATGATCCGCAATGCTGTGGTGGC 1317
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|
|
Db 342 GACCTGTCACAGTCGTGGTGGTGGCCGACGACATGATCCGCAATGCTGTGGTGGC 283
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|
|
QY 1318 ATCCAGCATACGCCCAATGTCACAACAATGACCCCTGGGCGACAGAGAGAGAGAGA 1377
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|
|
Db 282 ATCCAGCATACGCCCAATGTCACAACAATGACCCCTGGGCGACAGAGAGAGAGAGA 223
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|
|
QY 1378 GACAGAGAAAAAAGAACACAGCATGAGAACAGTAATGAATAAACCTAAATATT 1437
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|
|
Db 222 GACAGAGAAAAAAGAACACAGCATGAGAACAGTAATGAATAAACCTAAATATT 163
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QY 1438 TAGCCCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1497
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|
|
Db 162 TAGCCCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 103
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QY 1498 TGACAGCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1557
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|
|
Db 102 TGACAGCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 43
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QY 1558 TGCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1599
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Db 42 TGCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1
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RESULT 24      452 bp      mRNA      linear      EST 17-MAR-1999
AI391683/c      452 bp      mRNA      linear      EST 17-MAR-1999
LOCUS      qy93f04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2019583 3'
DEFINITION      similar to SW:NTFL_RAT p20789 NEUROTENSIN RECEPTOR TYPE 1 ;, mRNA
sequence.
ACCESSION      AI391683
VERSION      AI391683.1 GI:4217687
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 452)
AUTHORS      NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES      National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
JOURNAL      Unpublished (1998)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

```

```

Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1183 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 451.
FEATURES
source
1..452
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2019583"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/Note="Organ: Brain; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTCACATCTGAGTAGTGAGACCGCCGCAATGCTTTTGTGTGTGTGTGTGTGT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      94 a      122 c      99 g      137 t
ORIGIN
Query Match      24.3%; Score 394; DB 9; Length 452;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1155 AAATGCTCGAGAGACACCGTGTACAGAGCGGGTGTATGACCGAGCTAGAGAAA 1214
|
|
|
Db 445 AAATGCTCGAGAGACACCGTGTACAGAGCGGGTGTATGACCGAGCTAGAGAAA 386
|
|
|
QY 1215 CGTCTCCGAAGAGGAGAGATCATGTACGCCGGAAGTACGCTGTCTGTCTGT 1274
|
|
|
Db 385 CGTCTCCGAAGAGGAGAGATCATGTACGCCGGAAGTACGCTGTCTGTCTGT 326
|
|
|
QY 1275 CTTGGGTTGGCGGACGATGATCTCGATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1334
|
|
|
Db 325 CTTGGGTTGGCGGACGATGATCTCGATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 266
|
|
|
QY 1335 TGTCAACAATCAGCCCTGGGCGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1394
|
|
|
Db 265 TGTCAACAATCAGCCCTGGGCGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 206
|
|
|
QY 1395 CACAGCATGAGAGACAGTAATGAATTAATTAATTAATTAATTAATTAATTAATTA 1454
|
|
|
Db 205 CACAGCATGAGAGACAGTAATGAATTAATTAATTAATTAATTAATTAATTAATTA 146
|
|
|
QY 1455 GCTTACTGGCCAGAAATGATACCAATTTTCAAGTGTGAGCTGAGAGCTTTTGGC 1514
|
|
|
Db 145 GCTTACTGGCCAGAAATGATACCAATTTTCAAGTGTGAGCTGAGAGCTTTTGGC 86
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|
|
QY 1515 ACAAGCAAGAGAGATTAACAGTGTTCAAACCCGGGGAGTGGCTGTAAAGAA 1574
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|
|
Db 85 ACAAGCAAGAGAGATTAACAGTGTTCAAACCCGGGGAGTGGCTGTAAAGAA 26
|
|
|
QY 1575 GACCATTAATGCTTTAGACAGTGT 1599
|
|
|
Db 25 GACCATTAATGCTTTAGACAGTGT 1
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|
|
RESULT 25      704 bp      mRNA      linear      EST 16-OCT-2001
BI919074      704 bp      mRNA      linear      EST 16-OCT-2001
LOCUS      603180881.F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244956 5',
DEFINITION      mRNA sequence.

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ACCESSION	B1919074
VERSION	B1919074.1
KEYWORDS	GI:16200128
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	1 (bases 1 to 704)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@bcm.tmc.edu Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: InCyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L1A1M1618 row: a column: 21 High quality sequence start: 4 High quality sequence stop: 702. Location/Qualifiers 1..704 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5244956" /clone_1kb="NIH_MGC_121" /lab_host="DH10B" /note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb. Insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH/MGC Library."
BASE COUNT	132 a 237 c 204 g 131 t
ORIGIN	
Query Match	23.8%; Score 386; DB 13; Length 704;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 386; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GGCACTTTTCGCGATTTCTTGCTTCAGAGCTTGGCTGCAAAATCAGTGTACCA 60
DB	318 GGCACTTTTCGCGATTTCTTGCTTCAGAGCTTGGCTGCAAAATCAGTGTACCA 377
OY	61 GTGTGAAGAATTCCAGCTGACACAGACTGTCCTCCGCCGAGTTCATTGTGAATTGCAC 120
DB	378 GTGTGAAGAATTCCAGCTGACACAGACTGTCCTCCGCCGAGTTCATTGTGAATTGCAC 437
OY	121 GGTGAACGTTCAAGCATCTGTCCAGAAAACAATGATGAGGACAAAGTCCGGGATCATGTA 180
DB	438 GGTGAACGTTCAAGCATCTGTCCAGAAAACAATGATGAGGACAAAGTCCGGGATCATGTA 497
OY	181 CGGCAAGTCTGTGATCATCATCAGCGGCTGTGTTCATCGGCTGTGCGGGTACCAGTCTTA 240
DB	498 CGGCAAGTCTGTGATCATCATCAGCGGCTGTGTTCATCGGCTGTGCGGGTACCAGTCTTA 557
OY	241 CTGCTCTCCAGGAAATGTAAGTCACTCACTGATGATGATGATGATGATGATGATGAT 300
DB	558 CTGCTCTCCAGGAAATGTAAGTCACTCACTGATGATGATGATGATGATGATGATGAT 617
OY	301 CGGGCCAAGGCCCAAGAAAAGGGAAGTCTGTGCTGGCGCTTCAGGCAAGGGCTCCGCAC 360
DB	618 CGGGCCAAGGCCCAAGAAAAGGGAAGTCTGTGCTGGCGCTTCAGGCAAGGGCTCCGCAC 677
OY	361 CACCATCTGTTCTTCAATTAGCCC 386

Db	678	CACCATCCTGTCTCCAAATATGAGCC	703
RESULT	26		
LOCUS	AI765236/c		
DEFINITION	w172h08.x1 NCI.GCAP.Kid12 Homo sapiens cDNA clone IMAGE:2398911 3'	456 bp	mRNA linear EST 21-DEC-1999
ACCESSION	AI765236		
VERSION	AI765236.1	GI:5231745	
KEYWORDS	EST.		
ORGANISM	human.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria (to 456)		
AUTHORS	NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmerl-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-GCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbdp/image/image.html Insert Length: 961 Std Error: 0.00 Seq primer: -400P from Gidco High quality sequence stop: 453.		
FEATURES	location/Qualifiers		
source	1. 456 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2398911" /clone_lib="NCI.GCAP_Kid12" /tissue_type="2 pooled tumors (clear cell type)" /lab_host="DH10B" /note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI.GCAP-Kid12 was prepared, and ss circles were made in vitro. Following HAT purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA from a pool of 5,000 clones made from the same library (cloneids 1322912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Faltma Bonaldo.		
BASE COUNT	93 a 122 c 99 g 142 t		
ORIGIN			
Query Match	23.5%; Score 380; DB 9; Length 456;		
Best Local Similarity	99.8%; Fred. No. 0;		
Matches 430; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
1149	CCGCCGAAACTCTCCGAGACACCGTGACAGAGCGGGTGGATGACCGACTGAGTA	1208	
456	CGCGCGAAACTCTCTCGAGACACCGCTGTACAGAGCGGGTGTGATGACCGACTGAGTA	397	
1209	GAAAAACGTTCTCGAGAGAGGAGAGAGATCATGTACGCCCGGAAATAGAGACTCGTCCA	1268	
396	GAATAACGTTCTCGAGAGAGGAGAGAGATCATGTACGCCCGGAAATAGAGACTCGTCCA	337	
1269	GTTCGAGCTTGGTTGGCCGAGCCATGATGCTCCGAATCTGTTGGGATCAGCATAC	1328	
336	GTTCGAGCTTGGTTGGCCGAGCCATGATGCTCCGAATCTGTTGGGATCAGCATAC	277	
1329	GCCCATGTGCACAAATATGAGCCCTGTGGCGACAGCAGCAGGAGGAGAGACAGAAAA	1388	

Db 276 GGGCAATGTACACAAATCATGCGCTGGCAGACAGGAGGAGGAGACAGAGAAAA 217  
 QY 1389 GAAAAACACAGCATGGAACACAGTAATGAATAAATTAATTTACCCCTCTG 1448  
 Db 216 GAAAAACACAGCATGGAACACAGTAATGAATAAATTAATTTACCCCTCTG 157  
 QY 1449 TTCTGTGCTTACTGGCCAGGAATGTACCAATTTTTCAGTTGTGAGCTTGACCTTCT 1508  
 Db 156 TTCTGTGCTTACTGGCCAGGAATGTACCAATTTTTCAGTTGTGAGCTTGACCTTCT 97  
 QY 1509 TTTCGCCACAGCAGAGAGATTTTAACACTGTTTCAAAACCGGGGAGTTGGCTGTGA 1568  
 Db 96 TTTCGCCACAGCAGAGAGATTTTAACACTGTTTCAAAACCGGGGAGTTGGCTGTGA 37  
 QY 1569 AAGAAAGACCA 1579  
 Db 36 AAGAAAGACCA 26  
 RESULT 27 738 bp mRNA linear EST 21-MAR-2002  
 LOCUS BM981455  
 DEFINITION UI-CF-EN1-adh-b-10-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
 ACCESSION BM981455  
 VERSION BM981455.1 GI:19603962  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 738)  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: McCreay, PB  
 McCreay Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccreay@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 FORWARD  
 POLYA=Yes.  
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 source location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-EN1-adh-b-10-0-UI"  
 /clone\_lib="UI-CF-EN1"  
 /tissue\_type="Primary Lung Cystic Fibrosis Epithelial  
 Cells"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: Lung; Vector: pT73-Pac (pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 UI-CF-EN1 is a normalized cDNA library containing the  
 following tissue(s): Primary Lung Cystic Fibrosis  
 Epithelial Cells. The library was constructed according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. First strand cDNA synthesis was primed with an  
 oligo-dT primer containing a Not I site. Double stranded  
 cDNA was ligated to an EcoR I adaptor, digested with Not  
 I, and cloned directionally into pT73-Pac vector. The  
 oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is CTGCTCAGGT.  
 TAG\_LIB=UI-CF-EN1  
 TAG\_TISSUE=Human Lung Epithelial Cell lines untreated LPS  
 6hr to LPS 24h  
 TAG\_SF0=CTGCTCAGGT"  
 BASE COUNT 151 a 199 c 164 g 221 t 3 others  
 ORIGIN  
 Query Match 23.4%; Score 379; DB 14; Length 738;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 170 GGAATCATGATACCGCAAGTCTGTGATCATCAGGCGCTGTCTATGCGCTTGCCGGG 229  
 Db 290 GGGATCATGTACCCGCAAGTCTGTGATCATCAGGCGCTGTCTATGCGCTTGCCGGG 349  
 QY 230 TACAGTCTTCTGCTCCCGCAAGTCTGTGATCATCAGGCGCTGTCTATGCGCTTGCCGGG 289  
 Db 350 TACAGTCTTCTGCTCCCGCAAGTCTGTGATCATCAGGCGCTGTCTATGCGCTTGCCGGG 409  
 QY 290 CCTCTTTGTAAAGGCGCCAGGCGCCAGAAAGGGAAGTTCTGCTCTGCGCTCAGGCCA 349  
 Db 410 CCTCTTTGTAAAGGCGCCAGGCGCCAGAAAGGGAAGTTCTGCTCTGCGCTCAGGCCA 469  
 QY 350 GGGCTCCGACACCAATCCTGTTCTCAATTAAGCCTCTTCTGCGCACCTCTGAAGC 409  
 Db 470 GGGCTCCGACACCAATCCTGTTCTCAATTAAGCCTCTTCTGCGCACCTCTGAAGC 529  
 QY 410 TGAAGGAGATGCCAGCCCGCTGATGTTCTTCCAGCGCTGCGCCAGCCCGCCAGC 469  
 Db 530 TGAAGGAGATGCCAGCCCGCTGATGTTCTTCCAGCGCTGCGCCAGCCCGCCAGC 569  
 QY 470 TCCCTGAGTGAATTTCTTCTGAGTCTCTTATTTCTGAGTGAAGGAGGAGTCCGTG 529  
 Db 590 TCCCTGAGTGAATTTCTTCTGAGTCTCTTATTTCTGAGTGAAGGAGGAGTCCGTG 649  
 QY 530 TCTCTTTTGTCTCCGTGCA 548  
 Db 650 TCTCTTTTGTCTCCGTGCA 668  
 RESULT 28  
 LOCUS BG752229 821 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602731372F1 NIH\_MGC.43 Homo sapiens cDNA clone IMAGE:4875113 5',  
 ACCESSION BG752229  
 VERSION BG752229.1 GI:14062882  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 821)  
 TITLE NIH-MGC http://mgi.nci.nih.gov/  
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 plate: LLCM1755 row: 0 column: 18  
 high quality sequence stop: 770.  
 Location/Qualifiers  
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/db\_xref="taxon:9606"  
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 /clone\_lib="NIH\_MGC\_43"  
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 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: eye; Vector: pORF7; Site: 1; XhoI; Site: 2; EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library. |"

BASE COUNT  
 ORIGIN

Query Match 23.0%; Score 372; DB 12; Length 821;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

555 GAAGAGCTCGGTAAAGCAATTCGATTAATTAATTCACCTGACTGAATTTTCAGTATGACT 614  
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 2 GAAGAGCTCGGTAAAGCAATTCGATTAATTAATTCACCTGACTGAATTTTCAGTATGACT 61  
 |||||||  
 615 TGAAGAGAGAGCTGAGTGAAGTCAACCCCATGCTGTGTAACGAGTCAAGGCCA 674  
 |||||||  
 62 TGAAGAGAGAGCTGAGTGAAGTCAACCCCATGCTGTGTAACGAGTCAAGGCCA 121  
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 675 GCGTGGCAGAGTCACTGCTTGAAGTCACTGAGTGGGATCTGCTTTTGTAAAGCCTC 734  
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 122 GCGTGGCAGAGTCACTGCTTGAAGTCACTGAGTGGGATCTGCTTTTGTAAAGCCTC 181  
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 735 CAGTGTCCATTCATCCCTGATGAGGGGCACTAGTTGAGACTCAAGATGAGTACGTT 794  
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 182 CAGTGTCCATTCATCCCTGATGAGGGGCACTAGTTGAGACTCAAGATGAGTACGTT 241  
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 795 TTCTTGGCTGGAGGGCAGTCCCATCAAGGCTCCCTGCTTGAATTAACCTCA 854  
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 242 TTCTTGGCTGGAGGGCAGTCCCATCAAGGCTCCCTGCTTGAATTAACCTCA 301  
 |||||||  
 855 TGCTCTGAAAACCATTCCTGCGACAGAAATGGCTGTTGGCGCTGAGTTGGGCTCT 914  
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 302 TGCTCTGAAAACCATTCCTGCGACAGAAATGGCTGTTGGCGCTGAGTTGGGCTCT 361  
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 915 AGTGAAGTCCGAGA 926  
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 362 AGTGAAGTCCGAGA 373

RESULT 29  
 LOCUS BP054837 381 bp mRNA linear EST 16-OCT-2000  
 DEFINITION 7171h01.y1 NCI\_CGAP\_Brn20 Homo sapiens cDNA clone IMAGE:3340177 5' similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39. ;, mRNA sequence.

ACCESSION BP054837  
 VERSION BP054837.1 GI:10808733  
 KEYWORDS EST.

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 381)  
 AUTHORS NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index  
 JOURNAL Unpublished (1998)  
 COMMENT Other ESFs: 7171h01.x1  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim Jacobson, Ph.D.

cDNA Library Preparation: David B. Kitzman, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov  
 The vector to vector length is 382  
 Seq primer: -40RP from Gluco.  
 Location/Qualifiers  
 1. 381  
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 /clone="IMAGE:3340177"  
 /clone\_lib="NCI\_CGAP\_Brn20"  
 /tissue\_type="oligodendroglioma"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: Brain; Vector: PAMPI; mRNA made from oligodendroglioma tissue, cDNA made by oligo-dT priming. Directionally cloned. Size selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."

FEATURES  
 source

BASE COUNT 123 a 81 c 83 t

Query Match 22.8%; Score 369; DB 12; Length 381;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1229 GGAGAGAGATCATGTAGCCCGGAGTAGAGACTGTCAGTCTGCTGGTGGCCG 1288  
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 1 GGAGAGAGATCATGTAGCCCGGAGTAGAGACTGTCAGTCTGCTGGTGGCCG 60  
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 1289 CAGCATATCTCTCCGATCTGCTGGGCAATCCAGATAGGCGCAATGATCAACATCA 1348  
 |||||||  
 61 CAGCATATCTCTCCGATCTGCTGGGCAATCCAGATAGGCGCAATGATCAACATCA 120  
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 1349 GCCCTGGCAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1408  
 |||||||  
 121 GCCCTGGCAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
 |||||||  
 1409 ACAGTAAATGAATTAACCATTAATTTAGCCCTCTGCTGCTGCTTCTGCGCCAG 1468  
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 181 ACAGTAAATGAATTAACCATTAATTTAGCCCTCTGCTGCTGCTTCTGCGCCAG 240  
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 1469 AATGTATCAATTTTTCAGTGTGAGCTTGACAGCTCTTTTGCACAAAGAGAGA 1528  
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 241 AATGTATCAATTTTTCAGTGTGAGCTTGACAGCTCTTTTGCACAAAGAGAGA 300  
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 1529 ATTAACTGTTTCAAAACCCGGGAGTGGCTGTGTTAAAGAAACCATTAATGCT 1588  
 |||||||  
 301 ATTAACTGTTTCAAAACCCGGGAGTGGCTGTGTTAAAGAAACCATTAATGCT 360  
 |||||||  
 1589 TTAGACAGT 1597  
 |||||||  
 361 TTAGACAGT 369

RESULT 30  
 LOCUS BP054680 371 bp mRNA linear EST 16-OCT-2000  
 DEFINITION 7169f08.y1 NCI\_CGAP\_Brn20 Homo sapiens cDNA clone IMAGE:3339875 5' similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39. ;, mRNA sequence.

ACCESSION BP054680  
 VERSION BP054680.1 GI:10808576  
 KEYWORDS EST.

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 371)

## AUTHORS

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## TITLE

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/RTGAP), Tumor Gene Index

## JOURNAL

Unpublished (1998)

## COMMENT

Other-ESTs: 7169f08.xl

Contact: Robert Strausberg, Ph.D.

Email: [cgapdb-rt@mail.nih.gov](mailto:cgapdb-rt@mail.nih.gov)

Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim Jacobson, Ph.D.

CDNA Library Preparation: David B. Kitzman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to:

[info@image.llnl.gov](mailto:info@image.llnl.gov)

Seq primer: -40RP from Gibco

High quality sequence stop: 361.

## FEATURES

Location/Qualifiers

1..371

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3339975"

/clone\_lib="NCI CGAP\_Brn20"

/tissue\_type="Oligodendroglioma"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Organ: brain; Vector: PAMPI; mRNA made from oligodendroglioma tissue, cDNA made by oligo-dT priming. directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."

## BASE COUNT

114 a 81 c 93 g 83 t

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 368; DB 12; Length 371;

Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1230 GAGAGAGATCATGTACGCCGGAAGTAGACGTCGTCAGTCTGCTGGGTTGGCCGC 1289

1 GAGAGAGATCATGTACGCCGGAAGTAGACGTCGTCAGTCTGCTGGGTTGGCCGC 60

1290 AGCCATGATCTCGAATCTGTTGGGCATCCAGCATAGGCCCAATGTCACAAATCAG 1349

61 AGCCATGATCTCGAATCTGTTGGGCATCCAGCATAGGCCCAATGTCACAAATCAG 120

1350 CCTTGGGACACAGACGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGACA 1409

121 CCTTGGGACACAGACGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGACA 180

1410 CAGTAATGATTAACCAATTAATTTAGCCCTCTGCTGCTTACTGAGCCAGGA 1469

181 CAGTAATGATTAACCAATTAATTTAGCCCTCTGCTGCTTACTGAGCCAGGA 240

1470 AATGTACCAATTTTCACTGTTGACATGACAGCTTTCTTTGCCACAGCAAGAGAGA 1529

241 AATGTACCAATTTTCACTGTTGACATGACAGCTTTCTTTGCCACAGCAAGAGAGA 300

1530 TTTTAACACTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTT 1589

301 TTTTAACACTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTT 360

1590 TAGACAGT 1597

361 TAGACAGT 368

RESULT 31

AV725028 465 bp mRNA linear EST 16-OCT-2000

LOCUS AV725028 HTC Homo sapiens cDNA clone HTCBRH07 5', mRNA sequence.

DEFINITION AV725028 HTC Homo sapiens cDNA clone HTCBRH07 5', mRNA sequence.

ACCESSION AV725028

## VERSION

AV725028.1 GI:10830006

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 465)

## AUTHORS

Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z., and Han, Z.

## TITLE

Homo sapiens cDNA HTC clones

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: [hanzg@chgc.sh.cn](mailto:hanzg@chgc.sh.cn)

This clone is available at CHGC in Shanghai.

## FEATURES

Location/Qualifiers

1..465

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="HTCBRH07"

/clone\_lib="HTC"

/tissue\_type="Hypothalamus"

/dev\_stage="Adult"

/lab\_host="SOLR"

/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

## BASE COUNT

103 a 136 c 112 g 114 t

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 364; DB 10; Length 465;

Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

227 GGGTACCAAGTCTTCTGCTCCCGGAGAACTGAATGATGTTGGATCAGTGTGACAC 286

1 GGGTACCAAGTCTTCTGCTCCCGGAGAACTGAATGATGTTGGATCAGTGTGACAC 60

287 ACCCTCTTTTGAAGGGCCCAAGGCCAAGAAAGGGAATGTCGCTGGCCCTCAGG 346

61 ACCCTCTTTTGAAGGGCCCAAGGCCAAGAAAGGGAATGTCGCTGGCCCTCAGG 120

347 CCAGGCTCCGACACCATCTGTTCTCAATTAAGCCCTCTTCTGGCACACTGCTGA 406

121 CCAGGCTCCGACACCATCTGTTCTCAATTAAGCCCTCTTCTGGCACACTGCTGA 180

407 AGCTAAGAGATGGACACCCCTCTGATGTTCTTCCAGCCCTCCGCCCAACCCCCC 466

181 AGCTAAGAGATGGACACCCCTCTGATGTTCTTCCAGCCCTCCGCCCAACCCCCC 240

467 ACCTCCCTGAGTGAAGTTCTTCTGAGTGTCTTTTATTCGTGGAGAGAGAGAGTCCG 526

241 ACCTCCCTGAGTGAAGTTCTTCTGAGTGTCTTTTATTCGTGGAGAGAGAGAGTCCG 300

527 TGTCTCTTTTGTCTCCGTCGTAATTAATGAAGAGCTCGGTAAGCATTTGTAATAATT 586

301 TGTCTCTTTTGTCTCCGTCGTAATTAATGAAGAGCTCGGTAAGCATTTGTAATAATT 360

587 CAGC 590

361 CAGC 364

RESULT 32

AV72092 578 bp mRNA linear EST 19-DEC-1999

LOCUS AV72092/c w938h03.x1 Soares NSF\_F8\_9W\_OT\_PA.P\_St Homo sapiens cDNA clone

DEFINITION IMAGE:2367413 3' similar to SW:GP39\_HUMAN O43194 PUTATIVE G

IMAGE:2367413 3' similar to SW:GP39\_HUMAN O43194 PUTATIVE G

IMAGE:2367413 3' similar to SW:GP39\_HUMAN O43194 PUTATIVE G

IMAGE:2367413 3' similar to SW:GP39\_HUMAN O43194 PUTATIVE G

IMAGE:2367413 3' similar to SW:GP39\_HUMAN O43194 PUTATIVE G

PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.  
 AT142092  
 VERSION AT142092.1 GI:5110380  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 578)  
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nlm.nih.gov  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 806 Std Error: 0.00  
 Seq primer: -400p from Glibco  
 High quality sequence stop: 460.  
 Location/Qualifiers  
 1..578  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2367413"  
 /clone\_lib="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 102 a 176 c 142 g 158 t  
 ORIGIN  
 Query Match 22.5%; Score 364; DB 9; Length 578;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 534; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 Db 873 TCTGCACGACAATTTGGCTTTCGGCCCTGAGTGGGCTCTAGTACCTGAGACTCAAT 932  
 574 TCTGCACGACAATTTGGCTTTCGGCCCTGAGTGGGCTCTAGTACCTGAGACTCAAT 515  
 933 GACTGGACTTACCTGAGTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTAAAGAAATCTTCTCA 992  
 514 GACTGGACTTACCTGAGTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTAAAGAAATCTTCTCA 455  
 993 GTTCTCTTTCAGAGACTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTAAAGAAATCTTCTCA 1052  
 454 GTTCTCTTTCAGAGACTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTAAAGAAATCTTCTCA 395  
 1053 GCGCTGTCGGTGTGAGTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTAAAGAAATCTTCTCA 1112  
 394 GCGCTGTCGGTGTGAGTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTAAAGAAATCTTCTCA 335  
 1113 AGCAGACAGGCGGAGCAGACACCTTTCAGAGACTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTCTCA 1172  
 334 AGCAGACAGGCGGAGCAGACACCTTTCAGAGACTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTCTCA 276  
 1173 CGTGTACAGGAGCGGCTTTCAGAGACTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTCTCA 1232  
 275 CGTGTACAGGAGCGGCTTTCAGAGACTGGGCTTTCGGCCCTGAGTGGGCTCTAGTAAAGCTTCTCA 216

1233 GAGGATCATGTACGCGCCGGAAGTAGACCTCTCCAGTCTGCTTGGGTTGGCCGACG 1292  
 215 GAGGATCATGTACGCGCCGGAAGTAGACCTCTCCAGTCTGCTTGGGTTGGCCGACG 156  
 1293 CATGATCTCCGGAATTCGTTGGGCTCATGAGCATACGCGCAATGTACAAATCAAGCCG 1352  
 155 CATGATCTCCGGAATTCGTTGGGCTCATGAGCATACGCGCAATGTACAAATCAAGCCG 96  
 1353 TGGCAGACAGCAGGAGGAGAGACAGCAAGAAAGAAACACAGCATGAGAAC 1408  
 95 TGGCAGACAGCAGGAGGAGAGAGACAGCAAGAAAGAAACACAGCATGAGAAC 40  
 RESULT 33  
 AA084248 379 bp mRNA linear EST 31-JUL-1997  
 LOCUS 2117109.r1 Striatogene neuroepithelium NT2RAM1 937234 Homo sapiens  
 DEFINITION CDNA clone IMAGE:547721 5', mRNA sequence.  
 ACCESSION AA084248  
 VERSION AA084248.1 GI:1626368  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 379)  
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B., Chissee, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Maris, E., Moore, B., Morris, M., Parsons, J., Prange, C., Riklin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevas, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
 Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)  
 TITLE JOURNAL MEDLINE  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 980 Std Error: 0.00  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 357.  
 Location/Qualifiers  
 1..379  
 /organism="Homo sapiens"  
 /db\_xref="GDB:3926237"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:547721"  
 /clone\_lib="Striatogene neuroepithelium NT2RAM1 937234"  
 /dev\_stage="Ntera-2/RH-MI neuroepithelial cells"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Cloned unidirectionally. Precursor cells induced with Retinoic acid for 1 week, followed by 3 weeks in mitotic inhibitors (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR vector; ~5' adaptor sequence: 5' GATTCGGCAGAC 3' -3' adaptor sequence: 5' CTCGATGTTTTTTTTTTT 3'."  
 BASE COUNT 77 a 95 c 114 g 93 t  
 ORIGIN  
 Query Match 22.4%; Score 363; DB 9; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 720 CTTTGTAAAGCTTCAGATGTCATTCATCCCTGATGGGCGCATAGTTGAGACTGCG 779  
 17 CTTTGTAAAGCTTCAGATGTCATTCATCCCTGATGGGCGCATAGTTGAGACTGCG 76

QY 780 AGTGAAGTACGTTTCTTAAAGGCTGAGAGGCGCAGTTCACATCAAGGCTCCCTGCT 839  
 DB 77 AGTGAAGTACGTTTCTTAAAGGCTGAGAGGCGCAGTTCACATCAAGGCTCCCTGCT 136  
 QY 840 GACATTCAACCTTCACTGCTCCCTGAGAAACCAATCTCTGACAGCAGAAATGGCTTTCGCG 899  
 DB 137 GACATTCAACCTTCACTGCTCCCTGAGAAACCAATCTCTGACAGCAGAAATGGCTTTCGCG 196  
 QY 900 CCTGAGTTGGGCTCTAGTACTGAGACATGATGCTGGGACTTGGAGTGGGCTCGGCC 959  
 DB 197 CCTGAGTTGGGCTCTAGTACTGAGACATGATGCTGGGACTTGGAGTGGGCTCGGCC 256  
 QY 960 TCGCTCTGAAAAGTCTTAAGAAAATCTTCTCAGTTCTCTGACAGAGACTGGCGCCG 1019  
 DB 257 TCGCTCTGAAAAGTCTTAAGAAAATCTTCTCAGTTCTCTGACAGAGACTGGCGCCG 316  
 QY 1020 GACGGGAGAGCAAGGGGCGCTGCACAAAGGGGCGCTGTGGTGGTGGAGTGGCGCATGT 1079  
 DB 317 GACGGGAGAGCAAGGGGCGCTGCACAAAGGGGCGCTGTGGTGGTGGAGTGGCGCATGT 376  
 QY 1080 ACG 1082  
 DB 377 ACG 379

RESULT 34  
 BE350014/c 534 bp mRNA linear EST 18-JUL-2000  
 LOCUS ht07912.x1 NCI-CGAP Kid13 Homo sapiens cDNA clone IMAGE:3146086.3  
 DEFINITION similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GP39, mRNA sequence.

ACCESSION BE350014  
 VERSION BE350014.1 GI:9261867  
 KEYWORDS EST.  
 ORGANISM human.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 534)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life  
 Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The  
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
 Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL, send email to:  
 InfoImage.llnl.gov  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 408.

FEATURES  
 source Location/Qualifiers  
 1..534  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3146086"  
 /clone\_1b="NCI-CGAP Kid13"  
 /tissue\_type="2 pooled Wilms' tumors, one primary and one  
 metastatic to brain"  
 /lab\_host="DH10B"  
 /note="Organ: Kidney; Vector: PCMV-SPORE6; Site: 1: SalI;  
 Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies."

BASE COUNT 98 a 172 c 143 g 121 t

Query Match 22.2%; Score 359; DB 10; Length 534;  
 Best Local Similarity 99.6%; Pred. No. 0;

Matches 529; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 852 TCATGCTCTGAAAACCATTCCTGTGACAGCAAAATGGCTGTTTCGGCGCTGAGTTGGCG 911  
 DB 530 TCATGCTCTGAAAACCATTCCTGTGACAGCAAAATGGCTGTTTCGGCGCTGAGTTGGCG 471  
 QY 912 TCTAGTACTGAGACATCATGACTGGGACTTGTAGACTGGGCTCGGCTCTGTAAGA 971  
 DB 470 TCTAGTACTGAGACATCATGACTGGGACTTGTAGACTGGGCTCGGCTCTGTAAGA 411  
 QY 972 GTGCTTAAAGAAAATCTTCTCAGTTCTCTGACAGAGACTGGCGCGGAGCGGAAGAGC 1031  
 DB 410 GTGCTTAAAGAAAATCTTCTCAGTTCTCTGACAGAGACTGGCGCGGAGCGGAAGAGC 351  
 QY 1032 AAGGGCGCTGCAAAAAGCGGCGCTGTGGTGGTGGAGTGGCGCATGTACGGCGAGCGC 1091  
 DB 350 AAGGGCGCTGCAAAAAGCGGCGCTGTGGTGGTGGAGTGGCGCATGTACGGCGAGCGC 291  
 QY 1092 TTCTCGTGTGGCGTGTGCTGACGAGACAGCGCGGACACAGACCTTGCACGAAACCCG 1151  
 DB 290 TTCTCGTGTGGCGTGTGCTGACGAGACAGCGCGGACACAGACCTTGCACGAAACCCG 232  
 QY 1152 CGAAAACCTGCTGCGAGACACCTGTACAGAGCGGTTGATGACCGAGCTGAGTAGAA 1211  
 DB 231 CGAAAACCTGCTGCGAGACACCTGTACAGAGCGGTTGATGACCGAGCTGAGTAGAA 172  
 QY 1212 AAACGCTCTCGAAGAGGAGAGATCATGTACGCCCGGAAGTAGACCTGTCCAGTC 1271  
 DB 171 AAACGCTCTCGAAGAGGAGAGATCATGTACGCCCGGAAGTAGACCTGTCCAGTC 112  
 QY 1272 GTGCTTGGGTTGGCGCGGACCATGATCTCGGAATCTGTTGGGCAATCCAGCATACGCG 1331  
 DB 111 GTGCTTGGGTTGGCGCGGACCATGATCTCGGAATCTGTTGGGCAATCCAGCATACGCG 52  
 QY 1332 CAATGTACACAAATCAGCCCTGGCGAGACAGACAGAGAGAGAGAGAC 1382  
 DB 51 CAATGTACACAAATCAGCCCTGGCGAGACAGACAGAGAGAGAGAGAC 1

RESULT 35  
 BE395206 573 bp mRNA linear EST 21-JUL-2000  
 LOCUS 601309558P1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3631047.5,  
 DEFINITION mRNA sequence.  
 ACCESSION BE395206  
 VERSION BE395206.1 GI:9340571  
 KEYWORDS EST.  
 ORGANISM human.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 573)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://Image.llnl.gov  
 Plate: LICM320 row: C column: 16  
 High quality sequence stop: 573.

FEATURES  
 source Location/Qualifiers  
 1..573  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3631047"  
 /clone\_1b="NIH\_MGC\_44"  
 /tissue\_type="endometrium, adenocarcinoma cell line"

/lab\_host="DH10B (phage-resistant)"  
/note="Organ: uterus; Vector: pORF7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 119 a 192 c 154 g 108 t  
ORIGIN

Query Match 21.9%; Score 355; DB 10; Length 573;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

82 CACGACGCTCTCTCCCGAGTTCATTTGTAATGCAAGGTAAGTTCAGACATGTG 141  
1 CAACGACGCTCTCTCCCGAGTTCATTTGTAATGCAAGGTAAGTTCAGACATGTG 60  
142 TCAGAAAGAGTATGAGCAAGTCCGGATCATATCCGCAAGTCTCTGCATCATC 201  
61 TCAGAAAGAGTATGAGCAAGTCCGGATCATATCCGCAAGTCTCTGCATCATC 120  
202 AGCGGCTCTCTCATGCGCTGCGGGATACCAAGTCTCTGCTCCCGAGGAAGTGA 261  
121 AGCGGCTCTCTCATGCGCTGCGGGATACCAAGTCTCTGCTCCCGAGGAAGTGA 180  
262 CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTTAAAGGCGCAAGCAAGAA 321  
181 CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTTAAAGGCGCAAGCAAGAA 240  
322 GGAAGTTTGCCTCGGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 381  
241 GGAAGTTTGCCTCGGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
382 AGGCTCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 436  
301 AGGCTCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 355

RESULT 36  
AM087372 432 bp mRNA linear EST 15-OCT-1999  
LOCUS X019602.x1 NCI CGAP Kid13 Homo sapiens cDNA clone IMAGE:2576786 3'  
DEFINITION similar to SW:GP93\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
GPR39.1; mRNA sequence.  
ACCESSION AM087372  
VERSION AM087372.1 GI:6043177  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 432)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D. cDNA Library Preparation: Life  
Technologies, Inc. cDNA Library Arrayed by: Christa Pirange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbp/image/image.html

FEATURES  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 306.  
Location/Qualifiers

source

1. 432  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2576786"  
/clone\_1b="NCI-CGAP Kid13"  
/tissue\_type="2 pooled Wilms' tumors, one primary and one  
metastatic to brain"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies."  
BASE COUNT 92 a 116 c 89 g 134 t 1 others  
ORIGIN

Query Match 21.8%; Score 353; DB 10; Length 432;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1252 AAGTAGACCT 1311  
353 AAGTAGACCT 294  
1312 TTGGGATTCACATGACGCGCAATGTCACAAATATCAGCCTGGGCGAGACGACG 1371  
293 TTGGGATTCACATGACGCGCAATGTCACAAATATCAGCCTGGGCGAGACGACG 234  
1372 GGGAGACAG 1431  
233 GGGAGACAG 174  
1432 AATATTTAGCCCT 1491  
173 AATATTTAGCCCT 114  
1492 TCGACTTGACACT 1551  
113 TCGACTTGACACT 54  
1552 GGGAGTTGGCTGTGTTAAAGAACATTAATGCTTTAGACAGTGTAA 1604  
53 GGGAGTTGGCTGTGTTAAAGAACATTAATGCTTTAGACAGTGTAA 1

RESULT 37  
A1018769 537 bp mRNA linear EST 27-AUG-1998  
LOCUS A1018769/c  
DEFINITION ov32e04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1639038  
3' similar to SW:NTNL\_RAT P20789 NEUROFENSIN RECEPTOR TYPE 1 ;  
mRNA sequence.  
ACCESSION A1018769  
VERSION A1018769.1 GI:3232567  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 537)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbp/image/image.html  
Insert length: 1394 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 452.

FEATURES  
source

Location/Qualifiers  
1. .537  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1639038"  
/clone\_lib="Soares\_testis\_NHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories Inc., and primed with a Not I - oligo(dT) primer (5' TGTTCACATCTGAAGTGGAGCGCGCCCAATTTTGTGTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization to Cots, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 147 c 126 g 139 t

ORIGIN

Query Match 21.8%; Score 353; DB 9; Length 537;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 453; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1138 TGCAGAACACCCCGGAACTGCTGCAGACACCGTGTACAGAGCGGGTGTATGACC 1197  
|||||  
DB 475 TGCAGAACACCCCGGAACTGCTGCAGACACCGTGTACAGAGCGGGTGTATGACC 416  
|||||

QY 1198 GAGCTGAGTGAAGAAAGCTCTCGAGAGGAGGAGATCATGTACCGCCGGAAGTAG 1257  
|||||  
DB 415 GAGCTGAGTGAAGAAAGCTCTCGAGAGGAGGAGATCATGTACCGCCGGAAGTAG 356  
|||||

QY 1258 GACCTGCTGCAGTGTGCTGGTGGTGGCGCAGCCATGATCTCCGAATCTGGTGGGC 1317  
|||||  
DB 355 GACCTGCTGCAGTGTGCTGGTGGTGGCGCAGCCATGATCTCCGAATCTGGTGGGC 296  
|||||

QY 1318 ATCCAGCATATGAGGCAATGTACAAACATCAGCCCTGGGAGACAGACAGAGGAGAGA 1377  
|||||  
DB 295 ATCCAGCATATGAGGCAATGTACAAACATCAGCCCTGGGAGACAGACAGAGGAGAGA 236  
|||||

QY 1378 GACGAGAGAAAGAAACACAGCATGAGAACACAGTAATGAATAAACATAAATATT 1437  
|||||  
DB 235 GACGAGAGAAAGAAACACAGCATGAGAACACAGTAATGAATGAATAAACATAAATATT 176  
|||||

QY 1438 TAGCCCTCTGCTGCTGCTTACTGCGCAGGAATGTACCAATTTTTCAGTGTGACT 1497  
|||||  
DB 175 TAGCCCTCTGCTGCTGCTTACTGCGCAGGAATGTACCAATTTTTCAGTGTGACT 116  
|||||

QY 1498 TGACAGCTCTTTTGCACAGACAGAGAGATTTAACTGTTTCAACCCGGGGAGT 1557  
|||||  
DB 115 TGACAGCTCTTTTGCACAGACAGAGAGATTTAACTGTTTCAACCCGGGGAGT 56  
|||||

QY 1558 TGGCTGTGTTAAAGAAAGACCATTAATGCTTAG 1592  
|||||  
DB 55 TGGCTGTGTTAAAGAAAGACCATTAATGCTTAG 21  
|||||

RESULT 38  
BI913989 707 bp mRNA linear EST 16-OCT-2001  
LOCUS 603180565F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5244569 5',  
DEFINITION mRNA sequence.  
ACCESSION BI913989  
VERSION BI913989.1 GI:16178286  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 707)  
AUTHORS NIH-MGC http://mgi.mcl.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINTL at:  
http://image.llnl.gov  
Plate: L1M1617 row: a column: 18  
High quality sequence stop: 698.

FEATURES  
source

Location/Qualifiers  
1. .707  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5244569"  
/clone\_lib="NIH\_MGC\_121"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

BASE COUNT 133 a 233 c 209 g 132 t

ORIGIN

Query Match 21.6%; Score 349; DB 13; Length 707;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGAGTGTCTTGTCCAGGCTTGGCTGCAAAATCAGTGTACCA 60  
|||||  
DB 286 GGCACCTTTTGGGAGTGTCTTGTCCAGGCTTGGCTGCAAAATCAGTGTACCA 345  
|||||

QY 61 GGTGAAGATTCACAGCTTAACACAGCATGCTCTCCCGCAGTTTCATTTGATTCAC 120  
|||||  
DB 346 GGTGAAGATTCACAGCTTAACACAGCATGCTCTCCCGCAGTTTCATTTGATTCAC 405  
|||||

QY 121 GGTGAAGCTTCAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180  
|||||  
DB 406 GGTGAAGCTTCAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 465  
|||||

QY 181 CCGCAAGTCTGTGATCATTCAGCGGCTGTCTATGCTTGTGCGGGATCAAGTCTT 240  
|||||  
DB 466 CCGCAAGTCTGTGATCATTCAGCGGCTGTCTATGCTTGTGCGGGATCAAGTCTT 525  
|||||

QY 241 CTGCTCCCGCAGGAAGTGAATCACTGTTGCATCGCTGCTGCGCAACACCCCTTTGTA 300  
|||||  
DB 526 CTGCTCCCGCAGGAAGTGAATCACTGTTGCATCGCTGCTGCGCAACACCCCTTTGTA 585  
|||||

QY 301 CGGGCCAAAGGCCCAAGAAAGGGAGTTTGTGCTGCGCCCTCAGGCCA 349  
|||||  
DB 586 CGGGCCAAAGGCCCAAGAAAGGGAGTTTGTGCTGCGCCCTCAGGCCA 634  
|||||

RESULT 39  
BE386060 593 bp mRNA linear EST 21-JUL-2000  
LOCUS BE386060  
DEFINITION 601276753F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3617749 5',  
ACCESSION BE386060  
VERSION BE386060.1 GI:9331425  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 593)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: ATCC/DCTD/DRP  
 DNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/MLNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: L1CM285 row: 1 column: 14  
 High quality sequence stop: 593.

## FEATURES

source

1..593  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="3617749"  
 /clone\_lib="NIH-MGC\_20"  
 /tissue\_type="melanocytic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 BASE COUNT 139 a 166 c 183 g 105 t  
 ORIGIN

Query Match 21.5%; Score 348; DB 10; Length 593;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 31 AGCGTTTGGCGTCAATTCAGTGTACAGTGTGAAGATTCAGTCAACAGACTG 90  
 DB 246 AGCGTTTGGCGTCAATTCAGTGTACAGTGTGAAGATTCAGTCAACAGACTG 305  
 QY 91 CTTCCCTCCCGGATTCATTTGTAATTCGACGGTGAACGTTCAAGCATGTGTCAAGAA 150  
 DB 306 CTTCCCTCCCGGATTCATTTGTAATTCGACGGTGAACGTTCAAGCATGTGTCAAGAA 365  
 QY 151 AGTGAATGAGCAAAAGTCCCGGATCATGTATGACGCAAGTCCGTGATCATGAGCGCGT 210  
 DB 366 AGTGAATGAGCAAAAGTCCCGGATCATGTATGACGCAAGTCCGTGATCATGAGCGCGT 425  
 QY 211 TCTCATCGCTCTGCGGGTACCACTCTTCTGCTCCCGAGGAAGTGAACATCAAGTTTG 270  
 DB 426 TCTCATCGCTCTGCGGGTACCACTCTTCTGCTCCCGAGGAAGTGAACATCAAGTTTG 485  
 QY 271 CATCAAGCTGTCTCAACACCCCTCTTTTGAAGGGCCCAAGAAAGGGAAGTTTC 330  
 DB 486 CATCAAGCTGTCTCAACACCCCTCTTTTGAAGGGCCCAAGAAAGGGAAGTTTC 545  
 QY 331 TGCCTCGGCGCTCAGGCGGCGGACGACCATCTCTGTCACAA 378  
 DB 546 TGCCTCGGCGCTCAGGCGGCGGACGACCATCTCTGTCACAA 593

RESULT 40  
 AL538562 920 bp mRNA linear EST 16-FEB-2001  
 LOCUS AL538562.LT1.FL013.FBn1 Homo sapiens cDNA CS0DF024Y004.5  
 DEFINITION prime, mRNA sequence.  
 ACCESSION AL538562  
 VERSION AL538562.1 GI:12866967  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 920)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polyes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

## FEATURES

source

1..920  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="CS0DF024Y004"  
 /clone\_lib="LT1.FL013.FBn1"  
 /dev\_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"  
 /lab\_host="DH10B"  
 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL : <http://fulllength.invitrogen.com>"  
 BASE COUNT 172 a 285 c 257 g 199 t 7 others  
 ORIGIN

Query Match 21.4%; Score 347; DB 9; Length 920;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGCACATTTTGGCGAATTTCTTCTCCAGGCTTTGCGTCAATTCAGTGTACCA 60  
 DB 279 GGCACATTTTGGCGAATTTCTTCTCCAGGCTTTGCGTCAATTCAGTGTACCA 338  
 QY 61 GTGGAAGATTTCCAGTGAACACGACTGCTCTCCCGAGATTCATTTGATTCAC 120  
 DB 339 GTGGAAGATTTCCAGTGAACACGACTGCTCTCCCGAGATTCATTTGATTCAC 398  
 QY 121 GGTGAAGTTCAGACATGTGTCAAGAAAGATGATGAGCAAGTCCGGGATCATGTA 180  
 DB 399 GGTGAAGTTCAGACATGTGTCAAGAAAGATGATGAGCAAGTCCGGGATCATGTA 438  
 QY 181 CCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCGCTGCGGATACAGTCTT 240  
 DB 459 CCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCGCTGCGGATACAGTCTT 518  
 QY 241 CTGCTCCCGAAGGAAGTGAACATGATTTGATGATGCTGTCAACACCCCTCTTTGTA 300  
 DB 519 CTGCTCCCGAAGGAAGTGAACATGATTTGATGATGCTGTCAACACCCCTCTTTGTA 578  
 QY 301 CGGCGCAAGGCGCCAAAGAAAGGGAAGTTTCTGCTCGGCGCTCAGGC 347  
 DB 579 CGGCGCAAGGCGCCAAAGAAAGGGAAGTTTCTGCTCGGCGCTCAGGC 625

RESULT 41  
 BF935708 368 bp mRNA linear EST 22-JAN-2001  
 LOCUS BF935708.MR2.NT0138-281200-008-f08 NT0138 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION MR2.NT0138-281200-008-f08 NT0138 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF935708  
 VERSION BF935708.1 GI:12353032  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 368)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

**JOURNAL MEDLINE COMMENT**

**TITLE**  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

**JOURNAL**  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

**CONTACT:** Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&cl=MR2-NT0138-281200-008-f08&cl=2000-12-28&cl=1)

**Seq primer:** puc 18 forward  
High quality sequence start: 14  
High quality sequence stop: 368.  
Location/Qualifiers

**FEATURES**  
source 1..368  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="NT0138"  
/dev\_stage="Adult"  
/note="Organ: nervous tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

**BASE COUNT**  
88 a 109 c 96 g 75 t  
**ORIGIN**

**Query Match**  
Best Local Similarity 100.0%; Score 338; DB 12; Length 368;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 746 CCATCCCTATGGGGGAGTTTGGAGTGCAGAGTGAAGTGAAGTCTTTCTTGAAGGCT 805  
Db 352 CCATCCCTATGGGGGAGTTTGGAGTGCAGAGTGAAGTGAAGTCTTTCTTGAAGGCT 293

QY 806 GGAGGGCCAGTTCGCCACTCAGAGTCCCTCCCTGACATTCAACTGATGCTCCCTGAAA 865  
Db 292 GGAGGGCCAGTTCGCCACTCAGAGTCCCTCCCTGACATTCAACTGATGCTCCCTGAAA 233

QY 866 ACCATTTCTGCAGCAGAAATTTGGCTGTTTCGCCCTGAGTTGGGCTCTAGTGCAG 925  
Db 232 ACCATTTCTGCAGCAGAAATTTGGCTGTTTCGCCCTGAGTTGGGCTCTAGTGCAG 173

QY 926 ACTCAATGACTGGGAGTGAAGTGGGCTGGGCTGCTGCTGTAAGAAAGTCTTAAGAAAT 985  
Db 172 ACTCAATGACTGGGAGTGAAGTGGGCTGGGCTGCTGCTGTAAGAAAGTCTTAAGAAAT 113

QY 986 CTCTCTAGTTCTCTTGCAGAGAGTGGCGCGGAGCGGAGAGAGAGAGAGAGAGAGAG 1045  
Db 112 CTCTCTAGTTCTCTTGCAGAGAGTGGCGCGGAGCGGAGAGAGAGAGAGAGAGAGAG 53

QY 1046 AAAGCGGGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1083  
Db 52 AAAGCGGGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 15

RESULT 42  
AM191974/c AM191974 454 bp mRNA linear EST 29-NOV-1999  
LOCUS  
DEFINITION x178a02.x1 NCI\_CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2680778 3'

**ACCESSION**  
AM191974  
**VERSION**  
AM191974.1 GI:6470673  
**KEYWORDS**  
EST.  
**SOURCE**  
human.  
**ORGANISM**  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

**REFERENCE**  
AUTHORS  
TITLE  
NCI-CGAP  
Tumor Gene Index  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdrp/image/image.html

**FEATURES**  
source 1..454  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="IMAGE:2680778"  
/clone\_1lb="NCI\_CGAP\_Pan1"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site\_1: SmaI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

**BASE COUNT**  
96 a 123 c 95 g 138 t 2 others  
**ORIGIN**

**Query Match**  
Best Local Similarity 99.5%; Score 336; DB 10; Length 454;  
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1165 GAGGACACCTGTACAGAGAGGGGTTGATGACGAGTGTGAGTGAAGAAAGTCTCCGAG 1224  
Db 438 GAGGACACCTGTACAGAGAGGGGTTGATGACGAGTGTGAGTGAAGAAAGTCTCCGAG 379

QY 1225 AAGGGAGAGAGATCATGTACGCGCGGAGATGAGACTCTGCAAGTCTGCTGGGTTTG 1284  
Db 378 AAGGGAGAGAGATCATGTACGCGCGGAGATGAGACTCTGCAAGTCTGCTGGGTTTG 319

QY 1285 GCCGACGACATGATCTCCGATCTGTTGGGATCCAGATACGGCCAAATGTACACACA 1344  
Db 318 GCCGACGACATGATCTCCGATCTGTTGGGATCCAGATACGGCCAAATGTACACACA 259

QY 1345 ATCAGCCCTGGGAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGA 1404  
Db 258 ATCAGCCCTGGGAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGA 199

QY 1405 GAACACAGTAATGAATAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1464  
Db 198 GAACACAGTAATGAATAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 139

QY 1465 CAGGAATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1524  
Db 138 CAGGAATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 79

QY 1525 GAGAAATTAACAGTGTTCAAACCCGGGGAGAGTGGTGTGTTAAAGAAAGACATTAA 1584  
Db 78 GAGAAATTAACAGTGTTCAAACCCGGGGAGAGTGGTGTGTTAAAGAAAGACATTAA 19



OY 1585 TCCTTAGACAGTGTAA 1602  
DB 18 TCGTTAGACAGTGTAA 1

RESULT 43  
BI917149 747 bp mRNA linear EST 16-OCT-2001  
LOCUS 60318157.F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5245648 5',  
DEFINITION mRNA sequence.  
ACCESSION BI917149  
VERSION BI917149.1 GI:16181111  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 747)  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LHAM1619 row: n column: 17  
High quality sequence stop: 737.  
Location/Qualifiers  
1..747  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="5245648"  
/clone\_lib="NIH\_MGC\_121"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: PCMV-SPORE6; Site:1; NotI;  
Site:2; EcoRV (destroyed); RNA source anonymous pool of 3  
fetal brains, female age 20 weeks, female age 24 weeks,  
and male age 26 weeks. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
0.7-3.5 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 017. Note:  
this is a NIH\_MGC Library."

BASE COUNT 140 a 245 c 216 g 146 t  
ORIGIN

Query Match 20.8%; Score 336; DB 13; Length 747;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCACCTTTTGGCGATGTTCTTGTCTCCAGGCTTGGCTGCAATTCAGTGTACCA 60  
DB 325 GGCACCTTTTGGCGATGTTCTTGTCTCCAGGCTTGGCTGCAATTCAGTGTACCA 384

OY 61 GTGTGAAGATTCAGCTGCAACAGCAGTCTCTCCCGGAGTTTGTGAATGCAC 120  
DB 385 GTGTGAAGATTCAGCTGCAACAGCAGTCTCTCCCGGAGTTTGTGAATGCAC 444

OY 121 GGTGAAGCTTGAAGACATGTGTGAGAAAGATGATGAGAGCAAGTCCGGGATCATGTA 180  
DB 445 GGTGAAGCTTGAAGACATGTGTGAGAAAGATGATGAGAGCAAGTCCGGGATCATGTA 504

OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTCGCGGTACACAGTCTT 240  
DB 505 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTCGCGGTACACAGTCTT 564

OY 241 CTGCTCCCAAGGAACTGAACTAGTTTGCATCAGCTGCTGCAACACCCCTTTGTAA 300

DB 565 CTGCTCCCAAGGAACTGAACTAGTTTGCATCAGCTGCTGCAACACCCCTTTGTAA 624  
OY 301 CCGGCCAAGGCCCAAGAAAGGGAAGTCTGCTC 336  
DB 625 CCGGCCAAGGCCCAAGAAAGGGAAGTCTGCTC 660

RESULT 44  
AW954549 540 bp mRNA linear EST 01-JUN-2000  
LOCUS EST36619 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.  
DEFINITION AW954549  
ACCESSION AW954549  
VERSION AW954549.1 GI:8144232  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 540)  
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt,  
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and  
Quackenbush, J.  
TITLE Assessment of gene expression patterns in a model of colon tumor  
metastasis using a 19,200 element cDNA microarray  
JOURNAL Unpublished (2000)  
COMMENT Contact: John Quackenbush  
The Institute for Genomic Research  
7712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: johnq@tigr.org  
Plate: 65  
Seq primer: Reverse.  
Location/Qualifiers  
1..540  
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/db\_xref="taxon:9606"  
/clone\_lib="MAGE resequences, MAGE"  
/note="Vector: pBluescriptSM"

BASE COUNT 122 a 150 c 134 g 134 t  
ORIGIN

Query Match 20.6%; Score 334; DB 10; Length 540;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 434; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 155 ATGAGCAAGTCCGCGATCATGTACCGCAAGTCTGTGCATCATCAGCGCTGTCTC 214  
DB 56 ATGAGCAAGTCCGCGATCATGTACCGCAAGTCTGTGCATCATCAGCGCTGTCTC 115

OY 215 ATGCGCTTCCCGGATACAGTCTTCTGTCTCCCAAGGAACTGAACTCATTTGCATC 274  
DB 116 ATGCGCTTCCCGGATACAGTCTTCTGTCTCCCAAGGAACTGAACTCATTTGCATC 175

OY 275 AGCTGTGCAACACCCCTCTTGTACGGGCGCAAGGCCCAAGAAAGGGAAGTTTGGC 334  
DB 176 AGCTGTGCAACACCCCTCTTGTACGGGCGCAAGGCCCAAGAAAGGGAAGTTTGGC 235

OY 335 TGGGCGCTGAGGCGGATCGGACACACCATCTTCTCTCAATTAAGCCCTCTTCTG 394  
DB 236 TGGGCGCTGAGGCGGATCGGACACACCATCTTCTCTCAATTAAGCCCTCTTCTG 295

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DB 296 GCACACGTGTGAAGTGAAGAGATGCCACCCCTCTCATTTTGTTCACAGCCTGCG 355

OY 455 CCGCAACCCCACTCTCTGATGAGTTTCTTCTGCTGCTCTTATTCGGGTAGGG 514  
DB 356 CCGCAACCCCACTCTCTGATGAGTTTCTTCTGCTGCTCTTATTCGGGTAGGG 415

OY 515 AGCGGAGTCCGTCTCTTTTGTCTGTGCAATTAAGAGCTCGGTAAAGCAT 574  
DB 415 AGCGGAGTCCGTCTCTTTTGTCTGTGCAATTAAGAGCTCGGTAAAGCAT 574

Db 416 AGCGGAGTCCCTGTTCTTTTCTTCTGCAAAATGAAGAGCTCGTAAGCAT 475  
 QY 575 TCTGAATAATTTCAGC 590  
 Db 476 TCTGAATAATTTCAGC 491

## RESULT 45

BI669845 690 bp mRNA linear EST 12-SEP-2001  
 LOCUS 603293440F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:531289 5',  
 DEFINITION mRNA sequence.

ACCESSION BI669845  
 VERSION BI669845.1 GI:15584078

## KEYWORDS

EST.

## SOURCE

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 690)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: L1A11792 row: p column: 10

High quality sequence stop: 690.

Location/Qualifiers

1..690

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5312889"

/clone\_lib="NIH\_MGC\_96"

/tissue\_type="hypothalamus"

/lab\_host="DH10B"

/note="Organ: brain; Vector: Bluescript (modified

Pluscript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcgag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',

size-selected for average insert size 2.3 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NHGRI, National

Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 127 a 231 c 202 g 130 t

ORIGIN

Query Match 20.3%; Score 328; DB 13; Length 690;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 GTGTGAAGATTCCAGCTGAACAACGACTGCTCTCCCGAGTTGTAATGGCAC 120  
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 Db 423 GGTGAACGTTCAAGCATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 482  
 QY 181 CCGCAAGTCCTGTCATCATGAGCGGCTGTCTCATGCTGCGGGGTACAGTCTT 240  
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Db 543 CTGCTCCCGAGGAACTGAATCAATTGATCAGCTGTCGAACACCCCTTTTGTAA 602  
 QY 301 CGGGCCAGGCCCCAAGAAAAGGGAAGTTCTGCTCGGCTCAGGCGAGGCTCCGCAC 360  
 Db 603 CGGGCCAGGCCCCAAGAAAAGGGAAGTTCTGCTCGGCTCAGGCGAGGCTCCGCAC 662  
 QY 361 CACCATCTGTTCTCTCAAAATTAGCCCTC 388  
 Db 663 CACCATCTGTTCTCTCAAAATTAGCCCTC 690

Search completed: November 7, 2002, 23:08:04  
 Job time: 2196.32 secs





14-NOV-2000: 2000US-0713550.  
PR 03-APR-2001: 2001US-0825294.  
PR 02-OCT-2001: 2001US-0970966.

(CORI-) CORIXA CORP.

Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

WPI: 2002-500186/53.

Novel ovarian cancer polypeptide and polynucleotide, useful for  
detecting the presence of ovarian cancer in a patient, and in  
pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

Claim 2: Page 195; 197pp: English.

The present invention provides human ovarian cancer associated proteins  
and coding sequences. The sequences can be used in the diagnosis and  
treatment of ovarian cancers. The present sequence is a coding sequence  
of the invention.

Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other:

Query Match 100.0%; Score 1619; DB 24; Length 1619;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCACATTTTGGCGATGTTCTTCTCCAGGCTTGGCGTGAATTCAGTCTACCA 60  
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61 GTGTGAAGATTCACCTGACACAGACAGTCTCTCCCGAGTTATTTGTATTCAC 120  
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121 GTGTGAAGATTCACCTGACACAGACAGTCTCTCCCGAGTTATTTGTATTCAC 180  
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361 CACCATCTCTCTCTCAATTAAGCCCTCTCTCTGCGACACTGCTGAAGCTGAAG 420  
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421 CCAACCCCTCTCTGATGTTCTTCCAGCCCTCGGCGCGCCCAACCCCTCTGAT 480  
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481 GTTCT 540  
481 GTTCT 540  
541 CCGTGTGAATTAATGAAGAGCTGCTGAAGCATTCGAATTAATTAATTAATTAAT 600  
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601 TTTCAGTATGATCTTGAAGAGAGGTGAGTGAAGATTCAACCCCATGCTGTGTA 660  
601 TTTCAGTATGATCTTGAAGAGAGGTGAGTGAAGATTCAACCCCATGCTGTGTA 660

661 CGAGTCAAGGCGAGGCTGCGAGATCAGTCTTACAGTCTGAGTGGCATCTGCC 720  
661 CGAGTCAAGGCGAGGCTGCGAGATCAGTCTTACAGTCTGAGTGGCATCTGCC 720  
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781 GTGAGAGTGAAGTCTTCTTACGAGGCGAGTCTCCACTCAAGGCTCCCTCGCT 840  
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841 ACATTCAACTCTTCACTCTCTGAAACCATTCCTGACAGAGAAATTTGCTGCT 900  
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1561 CTGCTGTTAAAGAAAGCAATTAATGCTTGTAGACAGTGTAAAGAAAGAA 1619  
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RESULT 3  
ABL40345  
ID ABL40345 standard; cDNA; 1619 BP.

XX ABL40345;  
XX AC  
XX DT 28-JUN-2002 (first entry)  
XX

DE Ovarian carcinoma sequence isolate 57887 extended cDNA.  
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 KM Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KW ss.  
 XX  
 OS Homo sapiens.  
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 PN US2002004491-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 03-APR-2001; 2001US-0825294.  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PA (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALCA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 DR WPI: 2002-171027/22.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 PT prevention and/or treatment of cancer, especially ovarian cancer -  
 XX  
 PS Claim 1a; Page 119-120; 131pp; English.  
 XX  
 CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the extended cDNA sequence of ovarian carcinoma  
 CC isolate 57887 given in record ABL48956.  
 CC  
 XX  
 SO Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;  
 Query Match 100.0%; Score 1619; DB 24; Length 1619;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CTGCTCCCGAGGAACTGAAGTTCATGCTGCTGCAACACCCCTTTGTAA 300  
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 DB 241 CTGCTCCCGAGGAACTGAAGTTCATGCTGCTGCAACACCCCTTTGTAA 300  
 QY 301 CGGGCAAGGCCCAAGAAAGAGTTCGCTGGCCCTCAGGCGAGGCTCCGCAC 360  
 |||||||  
 DB 301 CGGGCAAGGCCCAAGAAAGAGTTCGCTGGCCCTCAGGCGAGGCTCCGCAC 360  
 QY 361 CACCATCTGTTCTCAAAATTAAGCCCTCTCTCGGCACTGCTGAAGTGAAGAGATG 420  
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 DB 361 CACCATCTGTTCTCAAAATTAAGCCCTCTCTCGGCACTGCTGAAGTGAAGAGATG 420  
 QY 421 CCACCCCTCTCGATGTTCTTCACAGCCCTCGCCCAACCCCACTCTCTAGTGA 480  
 |||||||  
 DB 421 CCACCCCTCTCGATGTTCTTCACAGCCCTCGCCCAACCCCACTCTCTAGTGA 480  
 QY 481 GTTCTTCTGGGTGCTCTTTATTTCTGGTGAAGAGGAGTCCGTTCTTTGTT 540  
 |||||||  
 DB 481 GTTCTTCTGGGTGCTCTTTATTTCTGGTGAAGAGGAGTCCGTTCTTTGTT 540  
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 DB 541 CTGTGCAAAATTAATGAAGAGCTGGTAAAGCATTTCTGAATTAATTCAGCTGATGAT 600  
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 DB 601 TTTCAGTATGATCTGAAGAGAGGTGAGTGAAGTTCACCCCACTGCTGTATAC 660  
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 |||||||  
 DB 721 TTTTGTAAAGCCCTCCAGTGTCCATTTCCATCCCTGATGGGGCATTTGAGACTGACA 780  
 QY 781 GTGAGAGTACGTTTCTTAGGGCTGAGGGCCAGTTCACACTCAAGGCTCCCTGCTTG 840  
 |||||||  
 DB 781 GTGAGAGTACGTTTCTTAGGGCTGAGGGCCAGTTCACACTCAAGGCTCCCTGCTTG 840  
 QY 841 ACATTTAACTTATCTCTCTGTAAGAAACCTTCTGACAGACAAATTTGCTGCTGCCG 900  
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 DB 841 ACATTTAACTTATCTCTCTGTAAGAAACCTTCTGACAGACAAATTTGCTGCTGCCG 900  
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 DB 1141 ACGAACAACCCCGCAAACTGCTGAGAGACACCGTGTACAGAGCGGCTTATGACCGAG 1200  
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 QY 1321 CAGCATACGGCCAAATGTCAACAATACAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1380



```

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Db 1021 ACGCGAAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTCGGTGGTGGAGTGGACATGA 1080
Qy 1081 CGGCGAAGGCGCTTCTGCTGGTGGCTGCTGCAAGCGAGCGGCGGACAGACACCTTTC 1140
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Qy 1141 ACGAAGACCGCGGAGAACTGCGCGAGACACCGCTGACAGAGAGGGGTGATGACCGAG 1200
Db 1141 ACGAAGACCGCGGAGAACTGCGCGAGACACCGCTGACAGAGAGGGGTGATGACCGAG 1200
Qy 1201 CTGAGGTAGAAAACGCTCTCCGAGAAAGGAGAGATCATGTAGCCCGGAGATGAGAC 1260
Db 1201 CTGAGGTAGAAAACGCTCTCCGAGAAAGGAGAGATCATGTAGCCCGGAGATGAGAC 1260
Qy 1261 CTGCTCAAGTCTGCTGGGCTTGGCGGCGGACGATGATCTCCGAATCTGTTGGGCAATC 1320
Db 1261 CTGCTCAAGTCTGCTGGGCTTGGCGGCGGACGATGATCTCCGAATCTGTTGGGCAATC 1320
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Db 1321 CAGCATACGCGCAATGTCAACAATCAACCCCTGGGAGACGAGAGAGAGAGAGAC 1380
Qy 1381 AAGAGAAAGAAAACACAGCATGAGAACACAGTAATGATTAATTAATTAATTAATTAAT 1440
Db 1381 AAGAGAAAGAAAACACAGCATGAGAACACAGTAATGATTAATTAATTAATTAATTAAT 1440
Qy 1441 CCCCTCTGCTGCTGCTTACTGCGAGAAATGATTAATTAATTAATTAATTAATTAATTAAT 1500
Db 1441 CCCCTCTGCTGCTGCTTACTGCGAGAAATGATTAATTAATTAATTAATTAATTAATTAAT 1500
Qy 1501 CAGCTTCTTTTGGCCACAGCAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Db 1501 CAGCTTCTTTTGGCCACAGCAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Qy 1561 CTGCTTTAAGAAAGACATTAATGCTTTGAGACAGTGTAAAAAAGAAAAA 1619
Db 1561 CTGCTTTAAGAAAGACATTAATGCTTTGAGACAGTGTAAAAAAGAAAAA 1619

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RESULT 5  
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 ID ABT03284 standard; cDNA: 1897 BP.  
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AC ABT03284;
DT 05-SEP-2002 (first entry)
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.
XX
KM Human: ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX cytosolic; gene; ss.
XX Homo sapiens.
XX OS
XX PN WO200239885-A2.
XX PD
XX 23-MAY-2002.
XX PF
XX 13-NOV-2001; 2001WO-US45395.
XX PR
XX 14-NOV-2000; 2000US-0713550.
XX 03-APR-2001; 2001US-0825294.
XX 02-OCT-2001; 2001US-0970966.
XX PA (CORI-) CORIXA CORP.

```

```

XX Xu J, Stolk JA, Algate PA, Filing SP, Molesch DA;
XX WPI: 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for
XX detecting the presence of ovarian cancer in a patient, and in
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
XX Claim 2; Page 196; 197pp; English.
XX
XX The present invention provides human ovarian cancer associated proteins
XX and coding sequences. The sequences can be used in the diagnosis and
XX treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention.
XX
XX Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other:

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Query Match 99.28; Score 1606.2; DB 24; Length 1897;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

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Qy 1 GCGAAGTCTTTGGGATGTTCTGCTTCCAGGCTTGGCGCTGCAATTCAGTGTACCA 60
Db 280 GCGAAGTCTTTGGGATGTTCTGCTTCCAGGCTTGGCGCTGCAATTCAGTGTACCA 339
Qy 61 GTTGAAGAAATTCAGCTGAAACAAGACTGCTCTCCCGGAGTTCATTTGAAATGAC 120
Db 340 GTTGAAGAAATTCAGCTGAAACAAGACTGCTCTCCCGGAGTTCATTTGAAATGAC 399
Qy 121 GGTGAAGTTCACATGTTGTGAGAAAGAGTGTGAGACAAAGTCCGGATCATGTA 180
Db 400 GGTGAAGTTCACATGTTGTGAGAAAGAGTGTGAGACAAAGTCCGGATCATGTA 459
Qy 181 CCGCAAGTCTGCTGATCATCAGGCGCTGCTCATAGCCTGCGGGATCAGTCTT 240
Db 460 CCGCAAGTCTGCTGATCATCAGGCGCTGCTCATAGCCTGCGGGATCAGTCTT 519
Qy 241 CTGCTCCCGAGGAAACTGAACTGATTTGCAATGCTGCTGCAACACCTTTTGTAA 300
Db 520 CTGCTCCCGAGGAAACTGAACTGATTTGCAATGCTGCTGCAACACCTTTTGTAA 579
Qy 301 CGGGCCAGGCGCCAAAGAAAGGGAAGTTCTGCTGGGCTCTGAGCCAGGCTCCGCAC 360
Db 580 CGGGCCAGGCGCCAAAGAAAGGGAAGTTCTGCTGGGCTCTGAGCCAGGCTCCGCAC 639
Qy 361 CACCATCTGTTCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
Db 640 CACCATCTGTTCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 699
Qy 421 CCAACCCCTGCTGATTTGTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGAGTGA 480
Db 700 CCAACCCCTGCTGATTTGTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGAGTGA 759
Qy 481 GTTCTTCTGAGTGTCTTTTATTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 760 GTTCTTCTGAGTGTCTTTTATTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
Qy 541 CTTGTCAATTAATTAAGAGCTCGGTTAAAGCATTTCTGAATTAATTAATTAATTAAT 600
Db 820 CTTGTCAATTAATTAAGAGCTCGGTTAAAGCATTTCTGAATTAATTAATTAATTAAT 879
Qy 601 TTTCAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 880 TTTCAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
Qy 661 CGGAGTCAAGGCGGCTGCGAGAGTCACTTGAATCACTGAGTGGGATCTGCC 720
Db 940 CGGAGTCAAGGCGGCTGCGAGAGTCACTTGAATCACTGAGTGGGATCTGCC 999
Qy 721 TTTTGAAGGCTCCAGTGTCCATTCATCCCTGATGGGGGATAGTTGAGACTGACAGA 780

```



Db 1000 TTTTGAAGCCTCCAGTGTCCATTCCTCGATGGGGGAGTATTGAGACTGCAGA 1059  
 Oy 781 GTGAGAGTACGCTTTTCTTAGGGCTGGAGGGCCATTTCCCATCAAGCTCCCTGGCTTG 840  
 Db 1060 GTGAGAGTACGCTTTTCTTAGGGCTGGAGGGCCATTTCCCATCAAGCTCCCTGGCTTG 1119  
 Oy 841 ACATTCACATTCATGCTCTGAAACCATCTCTGACAGACAAATTTGGCTGGTTCGGGC 900  
 Db 1120 ACATTCACATTCATGCTCTGAAACCATCTCTGACAGACAAATTTGGCTGGTTCGGGC 1179  
 Oy 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTTAGACTGGGCTGGGCT 960  
 Db 1180 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTTAGACTGGGCTGGGCT 1239  
 Oy 961 CGGCTGAAAAGTGTCTTAAGAAAATCTTCTCAGTCTCTCTTCCAGAGAGCTGGCCCGGG 1020  
 Db 1240 CGGCTGAAAAGTGTCTTAAGAAAATCTTCTCAGTCTCTCTTCCAGAGAGCTGGCCCGGG 1299  
 Oy 1021 ACAGGAAGACAAAGGGGCTGACAAAGCGGGCTGTCGGTGTGAGTGCATGTA 1080  
 Db 1300 ACAGGAAGACAAAGGGGCTGACAAAGCGGGCTGTCGGTGTGAGTGCATGTA 1359  
 Oy 1081 CCGGAGGGGCTTCTGCTGTGGCTGCTGCTGACAGCAGCGGGGACAGACAGACCTTGC 1140  
 Db 1360 CCGGAGGGGCTTCTGCTGTGGCTGCTGCTGACAGCAGCGGGGACAGACAGACCTTGC 1418  
 Oy 1141 ACAGAACCCCGGAAACGCTCCGAGAGAGGAGATCATGATGAGGAGGGGTTGATGACCGAG 1200  
 Db 1419 ACAGAACCCCGGAAACGCTCCGAGAGAGGAGATCATGATGAGGAGGGGTTGATGACCGAG 1478  
 Oy 1201 CTGAGGTAGAAAACGCTCCGAGAGAGGAGATCATGATGAGGAGGGGTTGATGAGGAG 1260  
 Db 1479 CTGAGGTAGAAAACGCTCCGAGAGAGGAGATCATGATGAGGAGGGGTTGATGAGGAG 1538  
 Oy 1261 CTGCTCCAGTCTGCTGTGGCTTGGCCGACCATATCTCCGAACTCTGTGGCTGATC 1320  
 Db 1539 CTGCTCCAGTCTGCTGTGGCTTGGCCGACCATATCTCCGAACTCTGTGGCTGATC 1598  
 Oy 1321 CAGCATGCGGCAATGTCACAAACATCAGCCCTGGGACAGACAGCAGAGGAGGAGAGAC 1380  
 Db 1599 CAGCATGCGGCAATGTCACAAACATCAGCCCTGGGACAGACAGCAGAGGAGGAGAGAC 1658  
 Oy 1381 AGAGAAAAGAAAACACAGCATAGAAACACAGTAATGAATAAACCATTAATTTAG 1440  
 Db 1659 AGAGAAAAGAAAACACAGCATAGAAACACAGTAATGAATAAACCATTAATTTAG 1718  
 Oy 1441 CCCTCTGCTCTGCTGTAGTCTGCGCAGGAATGTACCAATTTTTCAGTGTGAGCTGTA 1500  
 Db 1719 CCCTCTGCTCTGCTGTAGTCTGCGCAGGAATGTACCAATTTTTCAGTGTGAGCTGTA 1778  
 Oy 1501 CAGCTTCTTGGCCACAGAGAGAGAAATTTAACTGTTTCAAAACCCGGGGAGTTGG 1560  
 Db 1779 CAGCTTCTTGGCCACAGAGAGAGAAATTTAACTGTTTCAAAACCCGGGGAGTTGG 1838  
 Oy 1561 CTGCTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619  
 Db 1839 CTGCTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1897  
 RESULT 6  
 ABL40352  
 ID ABL40352 standard; cDNA: 1897 BP.  
 XX  
 AC ABL40352;  
 XX  
 DT 28-JUN-2002 (first entry)  
 XX  
 DE Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.  
 XX  
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KW ss.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 260..685  
 FT //tag= a  
 FT /product= "Ovarian carcinoma protein O1034C/O591S"  
 XX  
 PN US2002004491-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PP 03-APR-2001; 2001US-0825294.  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PA (X0J/J) XU J.  
 PA (STOL/J) STOLK J A.  
 PA (ALGA/J) ALGATE P A.  
 PA (FLIN/J) FLING S P.  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 XX  
 DR WPI: 2002-171027/22.  
 XX  
 DR P-PSDB: ABB09417.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 XX prevention and/or treatment of cancer, especially ovarian cancer  
 PS Claim 1a: Page 127-128; 131pp; English.  
 CC  
 CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma O1034C/O591S consensus  
 CC nucleotide sequence.  
 CC  
 CC  
 SQ Sequence 1897 BP; 435 A; 532 G; 407 T; 2 other:  
 XX  
 XX  
 Query Match 99.2%; Score 1606.2; DB 24; Length 1897;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;  
 Oy 1 GGCACCTTTTGGGAGATTGTTCTGCTTCAGGCTTTGGCTGCAAAATCCAGTGTACCA 60  
 Db 280 GGCACCTTTTGGGAGATTGTTCTGCTTCAGGCTTTGGCTGCAAAATCCAGTGTACCA 339  
 Oy 61 GTGTGAAGAAATTCACACTGAACAGACGTCCTCCCGGAGTTCATGTGAATTGCAC 120  
 Db 340 GTGTGAAGAAATTCACACTGAACAGACGTCCTCCCGGAGTTCATGTGAATTGCAC 399  
 Oy 121 GTGTGAAGTTCAGACATGTGTCAGAAAGAGTGTAGAGCAAAAGTCCGGGATCATGTA 180  
 Db 400 GTGTGAAGTTCAGACATGTGTCAGAAAGAGTGTAGAGCAAAAGTCCGGGATCATGTA 459  
 Oy 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGGTACCATGCTTT 240  
 Db 460 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGGTACCATGCTTT 519

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QY 241 CTGCTCCCGAGGGAACAGTCACTGTTGATGACAGTCTGCAACACCCCTCTTTGTA 300
    |||||||
Db 520 CTGCTCCCGAGGGAACAGTCACTGTTGATGACAGTCTGCAACACCCCTCTTTGTA 579
QY 301 CGGGCCCAAGGCCCAAGAAAAGGGAAGTTCTCCCTGCGCCCTCAGGCCAGGGCTCCGAC 360
    |||||||
Db 580 CGGGCCCAAGGCCCAAGAAAAGGGAAGTTCTCCCTGCGCCCTCAGGCCAGGGCTCCGAC 639
QY 361 CACCATCTGTTCTCAAAATTAAGCCCTCTTCGCGACACCTGACAGTGAAGAGATG 420
    |||||||
Db 640 CACCATCTGTTCTCAAAATTAAGCCCTCTTCGCGACACCTGACAGTGAAGAGATG 699
QY 421 CCACCCCTCTCTGATGTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGATGA 480
    |||||||
Db 700 CCACCCCTCTCTGATGTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGATGA 759
QY 481 GTTCTCTGCGGTGTCCTTTTATCTGGGTAGGAGCGGGAGTCCGTCTCTTTGTT 540
    |||||||
Db 760 GTTCTCTGCGGTGTCCTTTTATCTGGGTAGGAGCGGGAGTCCGTCTCTTTGTT 819
QY 541 CCTGTGCAAAATTAAGAGAGCTCGGTAAAGCATTTGAAATTAATTCAGCCGATGAAT 600
    |||||||
Db 820 CCTGTGCAAAATTAAGAGAGCTCGGTAAAGCATTTGAAATTAATTCAGCTGATGAAT 879
QY 601 TTTCACTATGTTCTGAAGAGAGAGAGTGAAGTGAACCCCACTGCTGTGTATAC 660
    |||||||
Db 880 TTTCACTATGTTCTGAAGAGAGAGAGTGAAGTGAACCCCACTGCTGTGTATAC 939
QY 661 CGGAGTCAAGGCCAGGCTGCGAGAGTCACTGCTTGAAGTCACTGAGTGGGCAATCTGCC 720
    |||||||
Db 940 CGGAGTCAAGGCCAGGCTGCGAGAGTCACTGCTTGAAGTCACTGAGTGGGCAATCTGCC 999
QY 721 TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAGACTGCAGA 780
    |||||||
Db 1000 TTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAGACTGCAGA 1059
QY 781 GTGAGAGTGAAGTTTCTTAAGGGGGGAGGGCCAGTTCCCACTAAGGCTCCCTCGCTTG 840
    |||||||
Db 1060 GTGAGAGTGAAGTTTCTTAAGGGGGGAGGGCCAGTTCCCACTAAGGCTCCCTCGCTTG 1119
QY 841 ACATTCAAACTTCATGCTCTGAAAACCATTCCTGACAGCAAGAAATGGCTGTTTCGGCG 900
    |||||||
Db 1120 ACATTCAAACTTCATGCTCTGAAAACCATTCCTGACAGCAAGAAATGGCTGTTTCGGCG 1179
QY 901 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGGACTGAGCTGGGCTCGGCT 960
    |||||||
Db 1180 CTGAGTTGGGCTCTAGTACTCGAGACTCAATGACTGGGACTGAGCTGGGCTCGGCT 1239
QY 961 CGCTCTGAAAAGCTCTTAAGAAAATCTTTCAGTTCTCTTGGCAGAGACTGGGCGCGG 1020
    |||||||
Db 1240 CGCTCTGAAAAGCTCTTAAGAAAATCTTTCAGTTCTCTTGGCAGAGACTGGGCGCGG 1299
QY 1021 ACGGGAAGAGCAACGGGCGCTGACAAAGGGGCGCTGTGCTGTGTGAGTGGCATGTA 1080
    |||||||
Db 1300 ACGGGAAGAGCAACGGGCGCTGACAAAGGGGCGCTGTGCTGTGTGAGTGGCATGTA 1359
QY 1081 CGGCAAGGCGTTCTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1140
    |||||||
Db 1360 CGGCAAGGCGTTCTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1418
QY 1141 ACGAACAACCGCCGCAAACTGCTGAGAGAGACCGTGTGACAGAGGGGCTTGAATCCGAG 1200
    |||||||
Db 1419 ACGAACAACCGCCGCAAACTGCTGAGAGAGACCGTGTGACAGAGGGGCTTGAATCCGAG 1478
QY 1201 CTGAGGTAGAAAACGTTCTCGAAGAGGAGAGATGATGATACGCCGGAATGAGAC 1260
    |||||||
Db 1479 CTGAGGTAGAAAACGTTCTCGAAGAGGAGAGATGATGATACGCCGGAATGAGAC 1538
QY 1261 CTGCTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1320
    |||||||
Db 1539 CTGCTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1598
QY 1321 CAGCATACGGCCAAATGTCACAAACATCAGCCCTGGGAGACAGACAGGAGGAGAC 1380

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Db 1599 CAGCATACGGCCAAATGTCACAAATCAGCCCTGGGAGACAGACAGGAGAGAC 1658
    |||||||
QY 1381 AGAGAAAAGAAAACACAGCATGAGAACACAGTAAATGAATTAATTAATTTAG 1440
    |||||||
Db 1659 AGAGAAAAGAAAACACAGCATGAGAACACAGTAAATGAATTAATTAATTTAG 1718
    |||||||
QY 1441 CCCCTCTGTTTGTGCTTACTGCGCAGGAAATGGTACCATTTTTCAGTGTGACTGA 1500
    |||||||
Db 1719 CCCCTCTGTTTGTGCTTACTGCGCAGGAAATGGTACCATTTTTCAGTGTGACTGA 1778
    |||||||
QY 1501 CAGCTTTTGTGCGACAGCAGAGAGATTTTAACACTGTTTCAACCCGGGGAGTTGG 1560
    |||||||
Db 1779 CAGTCTCTTTTGGCCACAGCAGAGAGAAATTTAACTGTTTCAACCCGGGGAGTTGG 1838
    |||||||
QY 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAA 1619
    |||||||
Db 1839 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAA 1897
    |||||||

```

## RESULT 7

AAE22400/C  
ID AAE22400 standard; cDNA; 1953 BP.

XX AAE22400;

XX 26-MAR-2001 (first entry)

DE Human secreted protein gene 28 SEQ ID NO:38.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
 XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
 XX cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;  
 XX fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;  
 XX rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;  
 XX cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;  
 XX angiogenesis; nervous system disorder; Alzheimer's disease; infection;  
 XX ocular disorder; corneal infection; wound healing; skin aging;  
 XX food additive; preservative; ss.

OS Homo sapiens.

PN WO200061629-A1.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09071.

PR 09-APR-1999; 99US-0128694.

PR 20-JAN-2000; 2000US-0176931.

PA (HUMA-) HUMAN GENOME SCI INC.

PI (ROSE/) ROSEN C A.

PI Ruben SM, Komatsoulis G;

DR WPI: 2000-647420/62.

PT P-PSDB; AAB63161.

PT Isolated nucleic acid molecule encoding a human secreted protein is  
 used in preventing, treating or ameliorating a medical condition -

PS Claim 1; Page 440; 533pp; English.

CC AAE22373 to AAE22421 encode the human secreted proteins given in AAB63134  
 CC to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins  
 CC and polypeptides homologous to them. Human secreted proteins have  
 CC activities based on the tissues and cells the genes are expressed in.  
 CC Examples of activities include: immunosuppressive; antiarthritic;  
 CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
 CC cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;  
 CC fungicide; and ophthalmological. The polynucleotides and proteins can be  
 CC used to prevent, treat or ameliorate a medical condition in e.g. humans,

CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are  
 CC also used in diagnosing a pathological condition or susceptibility to a  
 CC autoimmune condition. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular  
 CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral  
 CC ischemia, angiodysplasia, nervous system disorders e.g. Alzheimer's  
 CC disease, infections caused by bacteria, viruses and fungi and also  
 CC disorders e.g. corneal infection. The polypeptides can also be used to  
 CC aid wound healing and epithelial cell proliferation, to prevent skin  
 CC aging due to sunburn, to maintain organs before transplantation, for  
 CC supporting cell culture of primary tissues, to regenerate tissues and in  
 CC chemotaxis. The polypeptides can also be used as a food additive or  
 CC preservative to increase or decrease storage capabilities. AAF22364 to  
 CC AAF22372 and AAB63133 represent sequences used in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other;

Query Match 97.2% Score 1574.2; DB 21; Length 1953;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1993; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 GGCACATTTTGGCGATGTTCTTCTCCAGGCTTTGGCTGCAATTCAGTGTACCA 60  
 DB 1674 GGCACATTTTGGCGATGTTCTTCTCCAGGCTTTGGCTGCAATTCAGTGTACCA 1615  
 QY 61 GTGTGAAGATTCACAGCTACACAGCAGCTGCTCTCCCGAGTTCATGTGAATTCGAC 120  
 DB 1614 GTGTGAAGATTCACAGCTACACAGCAGCTGCTCTCCCGAGTTCATGTGAATTCGAC 1555  
 QY 121 GGTGAAGCTTCAAGCATGTGTGCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180  
 DB 1554 GGTGAAGCTTCAAGCATGTGTGCAAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 1495  
 QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGTACCAATGCTT 240  
 DB 1494 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGTACCAATGCTT 1435  
 QY 241 CTGCTCTCCAGGAACTCAACATGTTGATGATGATGATGATGATGATGATGATGATGAT 300  
 DB 1434 CTGCTCTCCAGGAACTCAACATGTTGATGATGATGATGATGATGATGATGATGATGAT 1375  
 QY 301 CCGGCAAGGCGCCAGAAAGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 DB 1374 CCGGCAAGGCGCCAGAAAGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1316  
 QY 361 CACCATCTGTTCTCAATTAAGCCCTCTTCTGCGACACACTGCTGAAGCTGAAGAGATG 420  
 DB 1315 CACCATCTGTTCTCAATTAAGCCCTCTTCTGCGACACACTGCTGAAGCTGAAGAGATG 1256  
 QY 421 CCAACCCCTCTCATGTTGTTCTTCAAGCCCTGCGCCCAACCCCGCCCAACCCCGCTGAGTGA 480  
 DB 1255 CCAACCCCTCTCATGTTGTTCTTCAAGCCCTGCGCCCAACCCCGCCCAACCCCGCTGAGTGA 1196  
 QY 481 GTTCTCTCTGCTGCTCTTCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 DB 1195 GTTCTCTCTGCTGCTCTTCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1136  
 QY 541 CCTGTGCAAAATTAAGAAAGCTGCTGAAGCAATTCGAATTAATTCAGCTTCACTGAAT 600  
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 QY 601 TTTTCAGTATGATGTTGAAGAGAGAGTGAAGCAATTCACCCCATGCTGTGTAAAC 660  
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 QY 721 TTTTGTAAAGCTTCAAGTGTCAATCCCTGATGGGGCATAGTTTGAAGTGTGAGA 780  
 DB 1111 TTTTGTAAAGCTTCAAGTGTCAATCCCTGATGGGGCATAGTTTGAAGTGTGAGA 780

DB 955 TTTTGTAAAGCTTCAAGTGTCAATCCCTGATGGGGCATAGTTTGAAGTGTGAGA 896  
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 DB 895 GTGAGTCAAGTGTGTTTGAAGGCTGAGGCGCAGTTCCTCACTCAAGGCTCTCTGCTT 836  
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 DB 835 ACATTTCAACTTCACTGCTCTGAAAACCATTCCTGCAAGCAAGATTTGGCTTGGCGC 776  
 QY 901 CTGAGTGGGCTGCTAGAGTCACTGCAAGTCAATGATGCTGGAGTCAATGCTGGGCT 960  
 DB 775 CTGAGTGGGCTGCTAGAGTCACTGCAAGTCAATGATGCTGGAGTCAATGCTGGGCT 716  
 QY 961 CGCTCTGAAAAGTCTTCAAGAAATCTTCTCAGTTCCTTCTGCAAGAGTGGCGCGCG 1020  
 DB 715 CGCTCTGAAAAGTCTTCAAGAAATCTTCTCAGTTCCTTCTGCAAGAGTGGCGCGCG 656  
 QY 1021 ACGGCAAGAGCAAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 DB 655 ACGGCAAGAGCAAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTG 596  
 QY 1081 CCGCAGGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 DB 595 CCGCAGGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 537  
 QY 1141 ACGAAGACCCCGCAAGTCTGCGAGAGACACCGTGTACAGAGCGGGTGTATGCCAG 1200  
 DB 536 ACGAAGACCCCGCAAGTCTGCGAGAGACACCGTGTACAGAGCGGGTGTATGCCAG 477  
 QY 1201 CTGAGTGAAGAAACGTTCTCCGAGAGGAGAGAGATCATGTACGCCCGGAATAGAG 1260  
 DB 476 CTGAGTGAAGAAACGTTCTCCGAGAGGAGAGAGATCATGTACGCCCGGAATAGAG 417  
 QY 1261 CTGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
 DB 416 CTGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 357  
 QY 1321 CAGCATAGCGGCAATGTCAACAATACAGCCCTGGGCGAGACAGAGAGAGAGAGAC 1380  
 DB 356 CAGCATAGCGGCAATGTCAACAATACAGCCCTGGGCGAGACAGAGAGAGAGAGAC 297  
 QY 1381 AGAGAAAGAAAGAAACAGAGATGAGACACAGTAAATTAATTAATTAATTAATTAAT 1440  
 DB 296 AGAGAAAGAAAGAAACAGAGATGAGACACAGTAAATTAATTAATTAATTAATTAAT 237  
 QY 1441 CCGCTCTGCTGCTGCTTACAGGCGCAGGAAATGTACCAATTTTCACTGTTGCACTGA 1500  
 DB 236 CCGCTCTGCTGCTGCTTACAGGCGCAGGAAATGTACCAATTTTCACTGTTGCACTGA 177  
 QY 1501 CAGCTTCTTTTCCCAAGCAAGAGAGAAATTAACACTGTTTCAAAACCCGGGAGATTGG 1560  
 DB 176 CAGCTTCTTTTCCCAAGCAAGAGAGAAATTAACACTGTTTCAAAACCCGGGAGATTGG 117  
 QY 1561 CTGTGTTAAAGAAAGCAATTAATGCTTTAGACAGTGA 1600  
 DB 116 CTGTGTTAAAGAAAGCAATTAATGCTTTAGACAGTGA 77

RESULT 8  
 AAF64188/c  
 ID AAF64188 standard; cDNA, 1956 BP.  
 XX  
 AC AAF64188;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human secreted protein gene 13 SEQ ID NO:23.  
 XX  
 XX Human: secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytotoxic; cardiac; vasotropic; cerebroprotective;  
 KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;  
 KW optical; vulnary; autoimmune disease; cardiovascular disorder;

KW hyperproliferative disorders; cerebrovascular disorder; wound healing;  
KW nervous system disorder; ocular disorder; skin ageing; chemotaxis;  
KW food additive; ss.  
OS Homo sapiens.  
XX WO200077026-A1.  
XX  
XX  
XX 21-DEC-2000.  
XX  
XX 01-JUN-2000; 2000WO-US14973.  
XX  
XX 11-JUN-1999; 99US-0138630.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.  
XX  
XX Rosen CA, Ruben SM, Komatsoulis GA;  
XX WPI: 2001-071258/08.  
XX P-PSDB: AAB75518.  
XX  
XX Nucleic acid molecules encoding human secreted proteins, used in  
XX preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
XX Parkinson's diseases and cancers -  
XX  
XX Claim 1: Page 443-444; 542pp: English.  
XX  
XX Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide  
XX sequences AAB64176 - AAB64224. The specification includes amino acid  
XX sequences AAB75555 - AAB75606 which represent fragments of the human  
XX secreted proteins, and protein sequences with which they share homology.  
XX The proteins and polynucleotides, their agonists and antagonists have  
XX activities dependent on the tissues and cells in which they are  
XX expressed, examples of these activities include; immunosuppressive;  
XX antirheumatic; antiproliferative; cytostatic; cardiant;  
XX vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;  
XX vitucide; fungicide; opthalmological; and vulnerrary. The proteins,  
XX polynucleotides, agonists and antagonists can be used to treat or detect  
XX or diagnose various diseases and disorders including, autoimmune  
XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders  
XX e.g. neoplasms of the breast or liver, cardiovascular disorders  
XX e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
XX angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
XX infections caused by bacteria, viruses and fungi and ocular disorders  
XX e.g. corneal infection. The polypeptides can also be used to aid wound  
XX healing and epithelial cell proliferation, to prevent skin ageing due to  
XX sunburn, to maintain organs before transplantation, for supporting cell  
XX culture of primary tissues, to regenerate tissues and in chemotaxis. The  
XX polypeptides can also be used as a food additive or preservative to  
XX increase or decrease storage capabilities. Included in the invention are  
XX polynucleotide sequences AAB64167 - AAB64175 and peptide AAB75505 which  
XX are used in the isolation, identification and characterisation of the  
XX proteins of the invention.  
XX  
XX Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other;  
XX  
XX Query Match 97.28; Score 1574.2; DB 22; Length 1956;  
XX Best Local Similarity 99.78; Pred. No. 0;  
XX Matches 1595; Conservative 2; Mismatches 1; Indels 2; Gaps 2;  
XX  
XX 1 GGCACATTTTGGCGATTTGTTGCTTCCAGGCTTGGCGTCAAAATCCAGTCAACA 60  
XX |  
XX 1674 GCGCACTTTTGGCGATTTGTTGCTTCCAGGCTTGGCGTCAAAATCCAGTCAACA 1615  
XX |  
XX 61 GTGTGAAGAAATTCAGCTGAACAAGACTGCTCTCCCGAGTTCATTGTGAATTGCAC 120  
XX |  
XX 1614 GTGTGAAGAAATTCAGCTGAACAAGACTGCTCTCCCGAGTTCATTGTGAATTGCAC 1555  
XX |  
XX 121 GGTGAAGCTTCAGAGACTGTGTGTGAGAAAGAGTGTGAGCAAGTCCGGGATCATGTA 180  
XX |  
XX 1554 GGTGAAGCTTCAGAGACTGTGTGTGAGAAAGAGTGTGAGCAAGTCCGGGATCATGTA 1495

QY 181 CCGAAGTCCTGTGATCATCAGGCGCTGTCTCATCGCTTCGCGGTACCAAGTCCTT 240  
QY |  
Db 1494 CCGCAAGTCCTGTGATCATCAGGCGCTGTCTCATCGCTTCGCGGTACCAAGTCCTT 1435  
QY 241 CTGCTCCCAAGGAACTGAAGTGTGATCAGCTGTGCAACACCCCTTTGTAA 300  
QY |  
Db 1434 CTGCTCCCAAGGAACTGAAGTGTGATCAGCTGTGCAACACCCCTTTGTAA 1375  
QY 301 CGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTCGGCCCTCAGGCGCAGCGCTCCGAC 360  
QY |  
Db 1374 CGGCGCAAGGCGCAAGAAAGGGAAGTTCGCTCGGCCCTCAGGCGCAGCGCTCCGAC 1316  
QY 361 CACCATCCTGTGCTCAATTAAGCCCTTCTGCGGACACTGTGAAAGTGAAGAGATG 420  
QY |  
Db 1315 CACCATCCTGTGCTCAATTAAGCCCTTCTGCGGACACTGTGAAAGTGAAGAGATG 1256  
QY 421 CCAACCCCTCTGATGTTTCTTCCAGCCCTCCGCCCAACCCCAAGCTCCCTGAGTGA 480  
QY |  
Db 1255 CCAACCCCTCTGATGTTTCTTCCAGCCCTCCGCCCAACCCCAAGCTCCCTGAGTGA 1196  
QY 481 GTTTCCTTCTGGGTGCTCTTTTATTTGAGGAGCGGAGTCCGTGTTCTTTGTT 540  
QY |  
Db 1195 GTTTCCTTCTGGGTGCTCTTTTATTTGAGGAGCGGAGTCCGTGTTCTTTGTT 1136  
QY 541 CCGTGCATTAATTAAGAAAGCTCGGTAAGCAATTCGTAATTAATCAGCTGACTGAAT 600  
QY |  
Db 1135 CCGTGCATTAATTAAGAAAGCTCGGTAAGCAATTCGTAATTAATCAGCTGACTGAAT 1076  
QY 601 TTTTCAATGATCTTGAAGGAGAGGAGTGAAGTGAAGTCAACCCCAAGTCTGTGTAA 660  
QY |  
Db 1075 TTTTCAATGATCTTGAAGGAGAGGAGTGAAGTGAAGTCAACCCCAAGTCTGTGTAA 1016  
QY 661 CGAGAGCAAGGCGCAGGCTGGCAGAGTCACTCTTGAAGTCACTGAGTGGGCACTGCG 720  
QY |  
Db 1015 CGAGAGCAAGGCGCAGGCTGGCAGAGTCACTCTTGAAGTCACTGAGTGGGCACTGCG 956  
QY 721 TTTTGAAGGCTCCAGTGTCTCATTCATCCCTGATGAGGAGGATGTTGAGATGCA 780  
QY |  
Db 955 TTTTGAAGGCTCCAGTGTCTCATTCATCCCTGATGAGGAGGATGTTGAGATGCA 896  
QY 781 GTGAGATGACGTTTCTTAAGGCTGAGGCGCAAGTTCCTCAAGGCTCCCTGCTTG 840  
QY |  
Db 895 GTGAGATGACGTTTCTTAAGGCTGAGGCGCAAGTTCCTCAAGGCTCCCTGCTTG 836  
QY 841 ACATTAACCTTCATCTCTCTGAAACATTCCTGACAGCAAAATGCTGCTTCCGCG 900  
QY |  
Db 835 ACATTAACCTTCATCTCTCTGAAACATTCCTGACAGCAAAATGCTGCTTCCGCG 776  
QY 901 CTGAGTGGGCTCTAGTGAAGTCAATGAGTGGGACTTGAAGTGGGCTCGGCT 960  
QY |  
Db 775 CTGAGTGGGCTCTAGTGAAGTCAATGAGTGGGACTTGAAGTGGGCTCGGCT 716  
QY 961 CGCTCGAAGAGTGTGAAGAAATCTTCTGAGTCTCTTCAAGAGACATGCGCCG 1020  
QY |  
Db 715 CGCTCGAAGAGTGTGAAGAAATCTTCTGAGTCTCTTCAAGAGACATGCGCCG 656  
QY 1021 ACGCGAAGCAAGGCGCTGACAAAGCGGCGCTGCTGCTGAGTGGAGTGGCATGTA 1080  
QY |  
Db 655 ACGCGAAGCAAGGCGCTGACAAAGCGGCGCTGCTGCTGAGTGGAGTGGCATGTA 596  
QY 1081 CGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
QY |  
Db 595 CGGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537  
QY 1141 ACGAAGACCGCGCGAAGTGTGAGGAGACCGGTACAGAGCGGTTATATACCGAG 1200  
QY |  
Db 536 ACGAAGACCGCGCGAAGTGTGAGGAGACCGGTACAGAGCGGTTATATACCGAG 477  
QY 1201 CTGAGGTAGAAAAACGTCCTGAGAGAGGAGAGATCATGTACGCGCGAATAGAGAC 1280  
QY |  
Db 476 CTGAGGTAGAAAAACGTCCTGAGAGAGGAGAGATCATGTACGCGCGAATAGAGAC 417  
QY 1261 CTGCTCAGTGTGCTTGGGCTTGGCGCGACCATGATCTCCGAATCTGTTGGGATC 1320

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|||||
Db 416 CTCGTCAGTGTGCTTGGCCCGCAGCATGATCTCCGAAATCTGTTGGGCATC 357
Oy 1321 CAGCATAGGCGCAATGTACAAACATAGCCCTGGGACAGACAGGAGGAGAGAC 1380
Db 336 CAGCATAGGCGCAATGTACAAACATAGCCCTGGGACAGACAGGAGGAGAGAC 297
Oy 1381 AGAGAAAAGAAAACACAGCATGAGAACACAGTAATGAATAAACCTAAATATTTAG 1440
Db 296 AGAGAAAAGAAAACACAGCATGAGAACACAGTAATGAATAAACCTAAATATTTAG 237
Oy 1441 CCCCTCTGTTCTGTCTTACTGCGCAGGAAATGTAACCAATTTTCACTGTTGACCTTGA 1500
Db 236 CCCCTCTGTTCTGTCTTACTGCGCAGGAAATGTAACCAATTTTCACTGTTGACCTTGA 177
Oy 1501 CAGCTTCTTTGGCCAGCAAGAGAGAAATTAACACTGTTTCAACCCCGGGAGATTGG 1560
Db 176 CAGCTTCTTTGGCCAGCAAGAGAGAAATTAACACTGTTTCAACCCCGGGAGATTGG 117
Oy 1561 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 1600
Db 116 CTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 77

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RESULT 9  
AAF93845  
ID AAF93845 standard; cDNA; 1890 BP.

AAF93845:

23-MAY-2001 (first entry)

Human cDNA encoding a membrane or secretory protein clone PSEC0181.

Human: secretory protein; membrane protein; vaccine; gene therapy;  
rheumatoid arthritis; diabetes; ss.

Homo sapiens.

EP1067182-A2.

10-JAN-2001.

07-JUL-2000; 2000EP-0114090.

08-JUL-1999; 99JP-0194179.

11-JAN-2000; 2000JP-0118775.

02-MAY-2000; 2000JP-0183766.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

WPI: 2001-093989/11.

P-PSDB: AAB88418.

Nucleic acids encoding secretory proteins/membrane proteins, useful in  
gene therapy or as candidate target molecules in drug development -

Claim 1: SEQ ID 203; 609bp + CD ROM; English.

This invention relates to nucleic acid sequences AAF93744 - AAF93916

which encode human secretory or membrane proteins represented by

AAAB88317 - AAB88419. Included in the invention are primers

AA93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the

cDNA sequences of the invention. The invention also includes methods for

the production of antibodies directed against the proteins, and cDNA

sequences, which can be used in vaccines. The polynucleotide sequences

can be used in gene therapy. The polynucleotide sequences and the

proteins they encode may be used in the prevention, treatment and

diagnosis of diseases associated with inappropriate secretory

protein/membrane protein expression. The nucleic acids and complementary

sequences may also be used as DNA probes in diagnostic assays

CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
CC presence of similar nucleic acid sequences in samples. They may also be  
CC used to study the expression and function of secretory proteins/membrane  
CC polypeptides and their role in metabolism. The polypeptides may be used  
CC as antigens in the production of antibodies against them and in assays to  
CC identify modulators (agonists and antagonists) of expression and  
CC activity. The antibodies and antagonists may also be used as therapeutic  
CC agents to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of the  
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay  
CC (ELISA). Examples of diseases which may be treated include rheumatoid  
CC arthritis and diabetes.

Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other;

Query Match 95.7%; Score 1548.8; DB 22; Length 1890;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1594; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

Oy 1 GGCACATTTTGGCGATGTTCTTGGCTTCCAGGCTTGGCCGCAATCCAGTCAACA 60  
Db 294 GGCACATTTTGGCGATGTTCTTGGCTTCCAGGCTTGGCCGCAATCCAGTCAACA 353

Oy 61 GTGTGAAGAAATCCAGCTGAACAACGACTCTCTCCCGGAGTTCATGTGAATTGCAC 120  
Db 354 GTGTGAAGAAATCCAGCTGAACAACGACTCTCTCCCGGAGTTCATGTGAATTGCAC 413

Oy 121 GGTGAAGCTTCAAGACATGTCGTCAAGAAAGAGTGAAGAGCAAAAGTCCGGATCATGTA 180  
Db 414 GGTGAAGCTTCAAGACATGTCGTCAAGAAAGAGTGAAGAGCAAAAGTCCGGATCATGTA 473

Oy 181 CCGCAATCTCTGTCATCATCAGGCGCTCTCATCGCTGCGGGATCAGTCTT 240  
Db 474 CCGCAATCTCTGTCATCATCAGGCGCTCTCATCGCTGCGGGATCAGTCTT 533

Oy 241 CTGCTCCCGAGGAACTGAACTGATTCATGATGCTGCAACACCCCTTTGTAA 300  
Db 534 CTGCTCCCGAGGAACTGAACTGATTCATGATGCTGCAACACCCCTTTGTAA 593

Oy 301 CGGGCAAGGCGCCAAAGGAGGAAAGTTCGCTCGGCGCTCAAGGCGCTCGGCAAC 360  
Db 594 CGGGCAAGGCGCCAAAGGAGGAAAGTTCGCTCGGCGCTCAAGGCGCTCGGCAAC 653

Oy 361 CACCATCTGTTCTCAAAATTAAGCCCTTCTCGGACACATGCTGAAGTGAAGAGATG 420  
Db 654 CACCATCTGTTCTCAAAATTAAGCCCTTCTCGGACACATGCTGAAGTGAAGAGATG 711

Oy 421 CCACCCCTCTCGATGTTCTTCAGCCCTCGCCCAACCCCCACCTCCCTGAGTGA 480  
Db 712 CCACCCCTCTCGATGTTCTTCAGCCCTCGCCCAACCCCCACCTCCCTGAGTGA 771

Oy 481 GTTCTCTTGGGTCCTCTTATTCCTGGTGAAGAGGAGGAGTCCGTTCTTTTGT 540  
Db 772 GTTCTCTTGGGTCCTCTTATTCCTGGTGAAGAGGAGGAGTCCGTTCTTTTGT 831

Oy 541 CCTGCAAAATGAAGAGAGCTCGTAAGACATTCGTAATTAATTCAGCTGACTGAAT 600  
Db 832 CCTGCAAAATGAAGAGAGCTCGTAAGACATTCGTAATTAATTCAGCTGACTGAAT 891

Oy 601 TTTAGTATGTTACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATCTCTGTGAAC 660  
Db 892 TTTAGTATGTTACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATCTCTGTGAAC 951

Oy 661 CGGAGTCAAGGCGCGCTGAGAGTCAAGTCTTAAGACACTGAGAGTGGGATCGGCC 720  
Db 952 CGGAGTCAAGGCGCGCTGAGAGTCAAGTCTTAAGACACTGAGAGTGGGATCGGCC 1011

Oy 721 TTTTGAAGGCTCACTGTCATTCATCCATGATGGGGCATAGTTTGAAGTCAAGTCA 780  
Db 1012 TTTTGAAGGCTCACTGTCATTCATCCATGATGGGGCATAGTTTGAAGTCAAGTCA 1071

Oy 781 GTGAGAGTGAAGTCTTGAAGGCTGAAGGCGCATTCACATCAAGCTCCCTCGCTTG 840  
Db 1071 GTGAGAGTGAAGTCTTGAAGGCTGAAGGCGCATTCACATCAAGCTCCCTCGCTTG 1131

Db 1072 GTGAGAGTACGCTTTTCTTAGGGCTGAGAGGCCAGTCCCACTCAAGGCTCCCTCGCTTG 1131  
 QY 841 ACATTCAAACTTCATGCTCCTGAAAAACATCTCTGACAGCAAAATGGCTGGTTCCGGC 900  
 Db 1132 ACATTCAAACTTCATGCTCCTGAAAAACATCTCTGACAGCAAAATGGCTGGTTCCGGC 1191  
 QY 901 CTGAGTTGGGCTCTAGTGAATGAGACTCAATGACTGGGACTTAGACTGGGCTGGGCT 960  
 Db 1192 CTGAGTTGGGCTCTAGTGAATGAGACTCAATGACTGGGACTTAGACTGGGCTGGGCT 1251  
 QY 961 CGCTCTGAAAAATGCTTAAAGAAAATCTTCTCACTTCT-CTTTGACAGAGACTGGCGCCG 1019  
 Db 1252 CGCTCTGAAAAATGCTTAAAGAAAATCTTCTCACTTCTCGAGAGAGACTGGCGCCG 1311  
 QY 1020 GACGGCAAGAGACAGGGGGCTGCACAAAAGGGGGCTGTGGTGGTGGAGGGCCATGT 1079  
 Db 1312 GACGGCAAGAGACAGGGGGCTGCACAAAAGGGGGCTGTGGTGGTGGAGGGCCATGT 1371  
 QY 1080 ACGCGGAGGCGCTTCTCGTGGTGGCGTGTGCTGACAGCAGAGGCGGACAGCAGCCTTG 1139  
 Db 1372 ACGCGGAGGCGCTTCTCGTGGTGGCGTGTGCTGACAGCAGAGGCGGACAGCAGCCTTG 1430  
 QY 1140 CACGAACACCCCGCAAACTGCTGCGAGAGACCGCTGTACAGAGAGCGGGTGTATGACCGA 1199  
 Db 1431 CACGAACACCCCGCAAACTGCTGCGAGAGACCGCTGTACAGAGAGCGGGTGTATGACCGA 1490  
 QY 1200 GCTGAGGTGAAAAAGCTCCGAGAAAGGGAGAGAGATCAATGATCGGCCGCACTAGCA 1259  
 Db 1491 GCTGAGGTGAAAAAGCTCCGAGAAAGGGAGAGAGATCAATGATCGGCCGCACTAGCA 1550  
 QY 1260 CCTGCTCAGTGTGCTTGGGTTGGCGCAGCAGCAGTGTCTCCGATCTGGTTGGGCGAT 1319  
 Db 1551 CCTGCTCAGTGTGCTTGGGTTGGCGCAGCAGCAGTGTCTCCGATCTGGTTGGGCGAT 1610  
 QY 1320 CCAGCATAGCGGCATATGTCACACATACAGCCCTGGCAGACAGCAGCAGAGGAGAGA 1379  
 Db 1611 CCAGCATAGCGGCATATGTCACACATACAGCCCTGGCAGACAGCAGCAGAGGAGAGA 1670  
 QY 1380 CAGAGAAAAGAAAACACAGCATGAGAACACAGTAATGAATAAACATTAATATTTA 1439  
 Db 1671 CAGAGAAAAGAAAACACAGCATGAGAACACAGTAATGAATAAACATTAATATTTA 1730  
 QY 1440 GCCCCTCTGCTGTGCTTACTGCGCAGAGAAATGTACCAATTTTTCAGTTGGACTTG 1499  
 Db 1731 GCCCCTCTGCTGTGCTTACTGCGCAGAGAAATGTACCAATTTTTCAGTTGGACTTG 1790  
 QY 1500 ACAGCTCTCTTGGCCACAAGAGAGAGATTAACATCTGTTCAACCCGGGGAGTTG 1559  
 Db 1791 ACAGCTCTCTTGGCCACAAGAGAGAGATTAACATCTGTTCAACCCGGGGAGTTG 1850  
 QY 1560 GCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGT 1599  
 Db 1851 GCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGT 1890  
 RESULT 10  
 AB054231.  
 ID AB054231 standard; cDNA; 1608 BP.  
 XX  
 AC AB054231;  
 XX  
 DT 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.  
 XX  
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynecological; reproductive; chromosome 2q21-22;  
 KW gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US18569.  
 XX  
 PR 07-JUN-2000; 2000US-209467P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Birse CE, Rosen CA;  
 XX  
 DR WPI; 2002-147878/19.  
 XX  
 DR P-PSDB; ABP41154.  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
 PT ovarian cancer), immune disorders, cardiovascular disorders and  
 PT neurological diseases -  
 XX  
 PS Claim 1; SEQ ID NO 111; 2922pp; English.  
 XX  
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents cDNA encoding a human ovarian antigen of the  
 CC invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIFO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX  
 SQ Sequence 1608 BP; 402 A; 402 C; 417 G; 381 T; 6 other;  
 Query Match 86.2%; Score 1395; DB 24; Length 1608;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1428; Conservative 2; Mismatches 2; Indels 3; Gaps 3;  
 QY 166 TGGCGGATCATGTACCGCAAGTCTGTGCATCATGAGGCGCTGTCTGACGCTCTGC 225  
 Db 101 TCCAGAGATATGATGACGCAAGTCGTGTATATACAGGCGCTGTCTGACGCTCTGC 160  
 QY 226 CGGGTACCACTCTTGTGCTCCCGAGGAAAGTGAAGTCAAGTTGGATCAGCTGTGCA 285  
 Db 161 CGGGTACCACTCTTGTGCTCCCGAGGAAAGTGAAGTCAAGTTGGATCAGCTGTGCA 220

Qy	286	CACCCCTCTTTGTAAGGGGCGAAGGCCCAAGAAAAGGGAAGAACTTTCGCTCGGCCCTAG	345
Db	221	CACCCCTCTTTGTAGGGGCGAAGG-CGAAGAAAAGGGAATTTCTGCTCGGCCCTAG	279
Qy	346	GCGAGGGCTCCGACCAACATCTCTGTCTCAAAATTAAGCCCTCTTCTCGGCACACTGCTG	405
Db	280	G-CAGGGGCTCCGACCAACATCTCTGTCTCAAAATTAAGCCCTCTTCTCGGCACACTGCTG	338
Qy	406	AAGCTGAAGGAGATGCCACCCCTCTCGATTTGTTCTCACACCCTGGCCCAACCCCC	465
Db	339	AAGCTGAAGGAGATGCCACCCCTCTCGATTTGTTCTCACACCCTGGCCCAACCCCC	398
Qy	466	CACCTCCCTAGAGAGATTTCTTGTGGGTGTCCTTTTATCTGGGTAGGAGAGCGGAGTCC	525
Db	399	CACCTCCCTAGAGAGATTTCTTGTGGGTGTCCTTTTATCTGGGTAGGAGAGCGGAGTCC	458
Qy	526	GTCGTCCTTTTGTCTGTGCAAAATTAATGAAAGAGCTCGTAAAGCATTTCTGAATAAT	585
Db	459	GTCGTCCTTTTGTCTGTGCAAAATTAATGAAAGAGCTCGTAAAGCATTTCTGAATAAT	518
Qy	586	TGAGCCCTGATGAATTTTTCAGTATGTACTTTGAAGAGAGAGGTGGAGTGAAGTTCAACC	645
Db	519	TGAGCCCTGATGAATTTTTCAGTATGTACTTTGAAGAGAGAGGTGGAGTGAAGTTCAACC	578
Qy	646	CCATGTCGTGTAAACCGGAGTCAAAAGCCCAAGGCTGGAGAGTGAAGTCCTAGAAGTCACTG	705
Db	579	CCATGTCGTGTAAACCGGAGTCAAAAGCCCAAGGCTGGAGAGTGAAGTCCTAGAAGTCACTG	638
Qy	706	AGGTGGGCATCTGCCTTTTGTAAAGCCCTCAGTGTCCATTCATCCCTGATGGGGGACTA	765
Db	639	AGGTGGGCATCTGCCTTTTGTAAAGCCCTCAGTGTCCATTCATCCCTGATGGGGGACTA	698
Qy	766	GTTTGAAGACTGCAAGATGAGAGTGAACGTTTTCTTAAGGCTGGAGGGCCAGTTCCACTCA	825
Db	699	GTTTGAAGACTGCAAGATGAGAGTGAACGTTTTCTTAAGGCTGGAGGGCCAGTTCCACTCA	758
Qy	826	AGGCTCCCTGCTGATTAACATTAACACTCAATGCTCCGAAAGCAATTCCTGACAGAGAT	885
Db	759	AGGCTCCCTGCTGATTAACATTAACACTCAATGCTCCGAAAGCAATTCCTGACAGAGAT	818
Qy	886	TGGCTGTTTTGCGCGCTGAGTTGGGCTCTAGTACTCGAGATCAATTAAGTGGGACTTAG	945
Db	819	TGGCTGTTTTGCGCGCTGAGTTGGGCTCTAGTACTCGAGATCAATTAAGTGGGACTTAG	878
Qy	946	ACTGGGGCTTGCGGCTGCTCTGAAAAGTGCCTTAAGAAAATCTTCTCAGTTCCTCTTCAG	1005
Db	879	ACTGGGGCTTGCGGCTGCTCTGAAAAGTGCCTTAAGAAAATCTTCTCAGTTCCTCTTCAG	938
Qy	1006	AGGACTGGGCGCGGGAGCGGGAAGCAAGGCGCGCTGCACAAAGCGGGCGCTGTGGTGG	1065
Db	939	AGGACTGGGCGCGGGAGCGGGAAGCAAGGCGCGCTGCACAAAGCGGGCGCTGTGGTGG	998
Qy	1066	TGCGAGTTCGCGATTTAGCGCGAGCGCTTCTCGTGTGTGGCGTGTGCGACGCAAGGCGGC	1125
Db	999	TGCGAGTTCGCGATTTAGCGCGAGCGCTTCTCGTGTGTGGCGTGTGCGACGCAAGGCGGC	1058
Qy	1126	AGCAGACACCTTTGACGAACAACCCGCGAATTCGTCGAGAGACACCGTGTACAGAGC	1185
Db	1059	AGCAGACACCTTTGACGAACAACCCGCGAATTCGTCGAGAGACACCGTGTACAGAGC	1117
Qy	1186	GGGTGATGACGACGATGAGAGTGAAGAAAACGTCCTCGAGAAAGGAGAGAGATCATGTAC	1245
Db	1118	GGGTGATGACGACGATGAGAGTGAAGAAAACGTCCTCGAGAAAGGAGAGAGATCATGTAC	1177
Qy	1246	GCCCGGAAGTAGACCTCGTACGTCGTGTGGTTTTGGCGCGACGACATGATCCTCGGA	1305
Db	1178	GCCCGGAAGTAGACCTCGTACGTCGTGTGGTTTTGGCGCGACGACATGATCCTCGGA	1237
Qy	1306	ATCTGTTGGGCTACAGCATACGCGCAATGTACAAACATACGCTTGCGGAGACACAGA	1365
Db	1238	ATCTGTTGGGCTACAGCATACGCGCAATGTACAAACATACGCTTGCGGAGACACAGA	1297
Qy	1366	GCGAGAGGAGACAGAGAAAAGAAAACACAGCATGAGAACACATGAATTAATTAAT	1425

Db	1298	GCAGGAGGAGGACACAGAGAAAAAACAACACAGCTGGAACACGTAATTAATTAATAA	1357		
QY	1426	CCATTAATAATATTTAGCCCCCTCTTCTGCTTACTGCGCAGGAATGTACCAATTTT	1485		
Db	1358	CCATTAATAATATTTAGCCCCCTCTGCTGCTTACTGCGCAGGAATGTACCAATTTT	1417		
QY	1486	CAGTGTGGAGCTTGACAGCTCTTTTGGCCACAAGCAGAAGAAATTTAACTGTTTCA	1545		
Db	1418	CAGTGTGGAGCTTGACAGCTCTTTTGGCCACAAGCAGAAGAAATTTAACTGTTTCA	1477		
QY	1546	ACCGGGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTAAAGACAGTGA	1600		
Db	1478	ACCGGGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTAAAGACAGTGA	1532		
RESULT 11					
ABK33543	ABK33543 standard; cDNA; 1524 BP.				
XX	ABK33543:				
AC					
XX	08-MAY-2002 (first entry)				
DT					
XX	DE	cDNA encoding human PRO protein, Seq ID No 15.			
XX	XX				
XX	XX	Human; secreted protein; PRO; tumour; lung cancer; colon cancer;			
XX	XX	breast cancer; prostate tumour; rectal tumour; liver tumour;			
XX	XX	pericyte cell proliferation; chondrocyte cell proliferation;			
XX	XX	tumour necrosis factor-alpha; gene; ss.			
OS	Homo sapiens.				
XX	WO200208288-A2.				
PN					
XX	31-JAN-2002.				
PD					
XX	29-JUN-2001; 2001WO-US21066.				
PF					
XX	20-JUL-2000; 2000US-219556P.				
PR	25-JUL-2000; 2000US-220585P.				
PR	25-JUL-2000; 2000US-220605P.				
PR	25-JUL-2000; 2000US-220607P.				
PR	25-JUL-2000; 2000US-220624P.				
PR	25-JUL-2000; 2000US-220638P.				
PR	25-JUL-2000; 2000US-220664P.				
PR	25-JUL-2000; 2000US-220666P.				
PR	26-JUL-2000; 2000US-220893P.				
PR	28-JUL-2000; 2000WO-US20710.				
PR	23-AUG-2000; 2000WO-US23522.				
PR	24-AUG-2000; 2000WO-US23328.				
PR	15-SEP-2000; 2000US-000000P.				
PR	10-NOV-2000; 2000WO-US30873.				
PR	28-NOV-2000; 2000US-253646P.				
PR	01-DEC-2000; 2000WO-US32678.				
PR	20-DEC-2000; 2000US-0747259.				
PR	20-DEC-2000; 2000WO-US34956.				
PR	28-FEB-2001; 2001WO-US06520.				
PR	10-MAY-2001; 2001US-0854280.				
PR	25-MAY-2001; 2001WO-US17092.				
XX					
PA	(GETH ) GENENTECH INC.				
XX					
PI	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;				
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;				
XX	WPI; 2002-172001/22.				
XX	P-PSDB; AAU83559.				
XX					
XX	One hundred and twenty two nucleic acids encoding PRO polypeptides,				
XX	useful for treating a PRO related disorder and for diagnosing tumors				
XX	such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal				
XX	tumour or liver tumour -				



XX Claim 2; Figure 15; 359pp; English.  
 XX  
 CC The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encoding human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology. Including use as hybridisation probes,  
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
 CC PRO protein coding sequences of the invention.  
 XX  
 SO Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other:  
 Query Match 84.8%; Score 1373; DB 24; Length 1524;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 GGCACTTTTGGGATGCTGCTGCTCCAGGCTTTGGCGCAAAATCCAGTGTACCA 60  
 DB 141 GGGAACTTTTGGGATGCTGCTGCTCCAGGCTTTGGCGCAAAATCCAGTGTACCA 200  
 QY 61 GTGTGAAGATTTCCAGCTGACAGACGACTGCTCTCCCGAGTTTCATTGTGAATGAC 120  
 DB 201 GTGTGAAGATTTCCAGCTGACAGACGACTGCTCTCCCGAGTTTCATTGTGAATGAC 260  
 QY 121 GGTGAACGTTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTCCGGGATCATGTA 180  
 DB 261 GGTGAACGTTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTCCGGGATCATGTA 320  
 QY 181 CCGCAAGTCTGTGATCATGACAGCGGCTGTGTCATGCGCTGCGGGGTACAGCTCT 240  
 DB 321 CCGCAAGTCTGTGATCATGACAGCGGCTGTGTCATGCGCTGCGGGGTACAGCTCT 380  
 QY 241 CTGCTCCCGAGGAACTGACTGATTTGATCATGCTGTCGAACACCCCTCTTTGTA 300  
 DB 381 CTGCTCCCGAGGAACTGACTGATTTGATCATGCTGTCGAACACCCCTCTTTGTA 440  
 QY 301 CGGGCCAAAGGCCAAGAAAGGGGAAGTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 360  
 DB 441 CGGGCCAAAGGCCAAGAAAGGGGAAGTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 500  
 QY 361 CACCATCTGTTCTCCAAATTAAGCCCTTCTCGGACACTGCTGAAGCTGAAGAGATG 420  
 DB 501 CACCATCTGTTCTCCAAATTAAGCCCTTCTCGGACACTGCTGAAGCTGAAGAGATG 560  
 QY 421 CCAACCCCTCTGATGTTGTTTCCAGCCCTGCCCCCAACCCCTCCCTGAGTGA 480  
 DB 561 CCAACCCCTCTGATGTTGTTTCCAGCCCTGCCCCCAACCCCTCCCTGAGTGA 620  
 QY 481 GTTCTTTCGGGGTCTCTTTATTCGGGTAGGAGCGGGAGTCCGTTCTCTTTGTT 540  
 DB 621 GTTCTTTCGGGGTCTCTTTATTCGGGTAGGAGCGGGAGTCCGTTCTCTTTGTT 680  
 QY 541 CCTGTCAATATATGAAGAAGCTCGGTAAGCATCTGTAATTAATTCAGCCGACTGAAT 600  
 DB 681 CCTGTCAATATATGAAGAAGCTCGGTAAGCATCTGTAATTAATTCAGCCGACTGAAT 740  
 QY 601 TTTCACTATGTAAGAGAGAGAGAGTGAAGTTCACCCCATGCTGTGTAAAC 660  
 DB 741 TTTCACTATGTAAGAGAGAGAGTGAAGTTCACCCCATGCTGTGTAAAC 800  
 QY 661 CGGAGTCAGAGCGGCTGGCAGAGTCACTCTTGAAGTCACTGAAGTGGGCACTGCGC 720  
 DB 801 CGGAGTCAGAGCGGCTGGCAGAGTCACTCTTGAAGTCACTGAAGTGGGCACTGCGC 860

QY 721 TTTTGAAGCCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAGACTGCAGA 780  
 DB 861 TTTTGAAGCCTCCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAGACTGCAGA 920  
 QY 781 GTGAGAGTGAAGTCTTCTTAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCTTG 840  
 DB 921 GTGAGAGTGAAGTCTTCTTAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCTTG 980  
 QY 841 ACATTCAAACTTCAATGCTCTCGAAGAACCATTTCTGACAGCAAGATTGGCTGTGCGCC 900  
 DB 981 ACATTCAAACTTCAATGCTCTCGAAGAACCATTTCTGACAGCAAGATTGGCTGTGCGCC 1040  
 QY 901 CTGAGTTGGGCTTCAAGTACTCGAGCTCAATGACTGCGGACTTGAAGTGGGCTGCGCT 960  
 DB 1041 CTGAGTTGGGCTTCAAGTACTCGAGCTCAATGACTGCGGACTTGAAGTGGGCTGCGCT 1100  
 QY 961 CGCTCTGAAGAGTCTTAAGAAATCTTCTCAGTTCTCTTGCAGAGAGACTGGCGCGCG 1020  
 DB 1101 CGCTCTGAAGAGTCTTAAGAAATCTTCTCAGTTCTCTTGCAGAGAGACTGGCGCGCG 1160  
 QY 1021 ACGGAGAGAGCAAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGTGATGCGCATGTA 1080  
 DB 1161 ACGGAGAGAGCAAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGTGATGCGCATGTA 1220  
 QY 1081 CGCGAGGCGGCTTCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 DB 1221 CGCGAGGCGGCTTCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279  
 QY 1141 ACGAAGACCCGCGCAAACTGCTGCGAGAGACACCGTGTACAGAGAGCGGGTGTATGACGAG 1200  
 DB 1280 ACGAAGACCCGCGCAAACTGCTGCGAGAGACACCGTGTACAGAGAGCGGGTGTATGACGAG 1339  
 QY 1201 CTGAGTGAAGAAACGCTCTCGAAGAGGAGAGATCATGTATGCGCCCGGAAGTATGAGAC 1260  
 DB 1340 CTGAGTGAAGAAACGCTCTCGAAGAGGAGAGATCATGTATGCGCCCGGAAGTATGAGAC 1399  
 QY 1261 CTGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 DB 1400 CTGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459  
 QY 1321 CAGCATACGGCCAAATGTACAAATACAGCCCTGCGCAGACAGAGAGAGAGAGAC 1380  
 DB 1460 CAGCATACGGCCAAATGTACAAATACAGCCCTGCGCAGACAGAGAGAGAGAGAC 1519  
 QY 1381 AGAGA 1385  
 DB 1520 AGAGA 1524  
 RESULT 12  
 AAD18690/c  
 ID AAD18690 standard; cDNA; 2528 BP.  
 XX  
 AC AAD18690;  
 AC  
 AC  
 DT 18-DEC-2001 (first entry)  
 DT  
 XX  
 DE Human G protein coupled receptor (GPCR) 4941 cDNA.  
 XX  
 KW Human; cardiovascular; tumorigenic disorder; aberrant angiogenesis;  
 KW gene therapy; aberrant vascularisation; arteriosclerosis; ovarian cancer;  
 KW ischaemia/reperfusion injury; hypertension; arterial inflammation;  
 KW myoastasia; endothelial cell disorder; diabetic retinopathy; restenosis;  
 KW myocardial infarction; Grave's disease; G protein coupled receptor;  
 KW GPCR 4941; vasotropic; hypotensive; antiinflammatory; cytostatic;  
 KW antidiabetic; antipsoriatic; leukaemia; ss.  
 OS  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 42..1403  
 FT CDS  
 FT /\*tag= a



PT	/product="Human GPCR 4941"
FT	/note="The CDS is specifically claimed in claim 1 of
FT	the specification"
XX	
XX	
PN	WO200181634-A2.
XX	
PD	01-NOV-2001.
XX	
PF	25-APR-2001: 2001WO-US13788.
XX	
PR	26-APR-2000: 2000US-199908P.
PR	09-AUG-2000: 2000US-0635521.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Galvin KA, Rudolph-owen LA;
XX	
DR	WPI: 2001-611743/70.
DR	P-PSDB: AAEL1751.
XX	
PT	Identifying nucleic acids for the diagnosis and treatment of
PT	cardiovascular and tumorigenic disorders, comprises identifying G
PT	protein coupled receptor (GPCR)-4941 -
XX	
DS	Example 1; Fig 1; 118pp; English.

CC The present invention relates to method for identifying a nucleic acid  
CC molecule (G protein coupled receptor gene, GPCR 4941) associated with a  
CC cardiovascular or tumourigenic disorder. The method comprising contacting  
CC a sample containing a nucleic acid molecule with a hybridisation probe or  
CC amplification primers and detecting the presence. The invention is used  
CC in gene therapy. The method of the invention is used for identifying  
CC nucleic acids or polypeptides associated with a cardiovascular or  
CC tumourigenic disorder such as aberrant angiogenesis, aberrant  
CC vascularisation, atherosclerosis, or ovarian cancer, ischemia/  
CC reperfusion injury, hypertension, restenosis, arterial inflammation,  
CC endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial  
CC infarction, Grave's disease and leukæmia. The methods can also detect  
CC mRNA or genomic DNA in a sample. The present sequence is G protein  
CC coupled receptor (GPCR) 4941 cDNA.  
XX  
50 Sequence 2528 BP, 516 A; 766 C; 677 G; 567 T; 2 other:

	Query Match	80.9%	Score 1310.4;	DB 22;	Length 2528;
	Best Local Similarity	99.5%;	Pred. No. 0;		
	Matches 1325; Conservative	0;	Mismatches	6; Indels	1; Gaps
Oy	29	CCAGGCTTTGGCGCTCAATCCAGTGTACAGTGTCFACAGTGAAGAATTCCAGGTGAACAACGC	88		
Db	2219	CAGGCTTTGGCGCTCAATCCAGTGTACAGTGTACAGTGAAGAATTCCAGGTGAACAACGC	2160		
Oy	89	TGCTCCTCCCCCGAGTTGATTTGTGAATTGTGCAGGTGAACGTTCAAGACATGTGTGAGAA	148		
Db	2159	TGCTCCTCCCCCGAGTTGATTTGTGAATTGTGCAGGTGAACGTTCAAGACATGTGTGAGAA	2100		
Oy	149	GAGTGATGTGAGAACAAAGTTCGCGGATCATGTACCAGTAECTGTGTGCATCATCAGCGCC	208		
Db	2099	GAAAGTAGTAGAACAAGTTCGCGGATCATGTACCAGTAECTGTGTGCATCATCAGCGGCC	2040		
Oy	209	TGTCATACGCCCTTGCGCGGGTACAGTCCCTTGCTCCCGAGGGGAAATGTAACATCAGTT	268		
Db	2039	TGTCATACGCCCTTGCGCGGGTACAGTCCCTTGCTCCCGAGGGGAAATGTAACATCAGTT	1980		
Oy	269	TGCATCACGTGTGTGCACACCCCCTTTTGTAAACGGGGCCAAAGGCCCAAGAAAAGGGAAAT	328		
Db	1979	TGCATCACGTGTGTGCACACCCCCTTTTGTAAACGGGGCCAAAGGCCCAAGAAAAGGGAAAT	1920		
Oy	339	TCTGCTCGGGCCCTCAGGCGCAGGCTCCGACACCAATCTGTCTTCTCAATAATAGCCCTC	388		
Db	1919	TCTGCTCGGGCCCTCAGGCGCAGGCTCCGACACCAATCTGTCTTCTCAATAATAGCCCTC	1860		
Oy	389	TTTCTGGCACAATGCTGGAAGCTGGAAGAGATGCCACCCCTCTGATTTGTTCTTCACG	448		

Db	1859	TTTTCGGACACGTGCTCAACCTGTAAGAGACATGGCACCACCCTCTCGATGTTGTTCTTCACGC	1800
Qy	449	CCTCGCCCCCAACCCCCCACCCTCCCTGAGTAGTTCCTTCGCGGTCCCTTTATTTCTCG	508
Db	1799	CCCTGCCCCCAACCCCCCACCCTCCCTGAGTAGTTCCTTCGCGGTCCCTTTATTTCTCG	1740
Qy	509	GTAGGAGACGGGAGTCCGCTGTTCTCTTTTGTTCCTGTGAAATATATGAAAGACCTCGGTA	568
Db	1739	GTAGGAGACGGGAGTCCGCTGTTCTCTTTTGTTCCTGTGAAATATATGAAAGACCTCGGTA	1680
Qy	569	AAGCATTTCTGAATTAATTCAGCCGACGTGAATTTTATATGTACTTGAAGAGAGAGT	628
Db	1679	AAGCATTTCTGAATTAATTCAGCTTGAATTTTATAGTATGTACTTGAAGAGAGAGT	1620
Qy	629	GGAGTGAAGTTCACCCCCATGTCGTGTATACCGGAGTCAAGGCCAGGCTGGACAGTCA	688
Db	1619	GGAGTGAAGTTCACCCCCATGTCGTGTATACCGGAGTCAAGGCCAGGCTGGACAGTCA	1560
Qy	689	GTCTTTAGAGTCACTGAGGTGGGCACTTGCCCTTTTGTAAAGCCTCCAGTGTCCATTCCA	748
Db	1559	GTCTTTAAGTCACTGAGGTGGGCACTTGCCCTTTTGTAAAGCCTCCAGTGTCCATTCCA	1500
Qy	749	TCCCGATGGGGGGATGATGTTTGAGACTGCAGACGTAGAGTGAAGCTTTTCTTAGGGCTGGA	808
Db	1499	TCCCGATGGGGGGATGATGTTTGAGACTGCAGAGTGAAGTGAAGCTTTTCTTAGGGCTGGA	1440
Qy	809	GGGCGCAGTTCCTCACTCAAGGCTCCCTCGCTGTGACATTCACAACTTCATGCTCCTGAAAC	868
Db	1439	GGGCGCAGTTCCTCACTCAAGGCTCCCTCGCTGTGACATTCACAACTTCATGCTCCTGAAAC	1380
Qy	869	ATTCTCTGCACAGCAATTTGGCTGGTTTCGCGCTGAGTTGGGCTCTAGTACTGAGACT	928
Db	1379	ATTCTCTGCACAGCAATTTGGCTGGTTTCGCGCTGAGTTGGGCTCTAGTACTGAGACT	1320
Qy	929	CAATACACGGGACCTTAACACGTGGGCTCGCTCGCTCAATAAAGCTTAAGCAAAATCTT	988
Db	1319	CAATACACGGGACCTTAACACGTGGGCTCGCTCGCTCAATAAAGCTTAAGCAAAATCTT	1260
Qy	989	CTCACTTCTCCTTCAGAGGACTGGCCGCGGAGCGGAAGAGCAACGGGCGCTGCACAAA	1048
Db	1259	CTCACTTCTCCTTCAGAGGACTGGCCGCGGAGCGGAAGAGCAACGGGCGCTGCACAAA	1200
Qy	1049	GGGGGCGCTGTGCGTGTGTGAGTGGCAGTACGCGCAGGCGCTTCCTGCTGGTGGCGTG	1108
Db	1199	GGGGGCGCTGTGCGTGTGTGAGTGGCAGTACGCGCAGGCGCTTCCTGCTGGTGGCGTG	1140
Qy	1109	CTGCAGCGCACAGGGGCGCACAGACACACTTGCACGAAACCCGCGGAACCTCTCGAGG	1168
Db	1139	CTGCAGCGCACAGGGGCGCACAGACACACTTGCACGAAACCCGCGGAACCTCTCGAGG	1081
Qy	1169	ACACGCTTAAAGAGAGCGGGGTGATGCCAGGTGAAGTGAAGAAAAACGCTCCGAGAAG	1228
Db	1089	ACACGCTTAAAGAGAGCGGGGTGATGCCAGGTGAAGTGAAGAAAAACGCTCCGAGAAG	1021
Qy	1229	GGAGGAGGATCATGTACGCCCGGAAGTAGGACCTGCTCCAGTGTGCTTTGGGTTGGCCG	1288
Db	1020	GGAGGAGGATCATGTACGCCCGGAAGTAGGACCTGCTCCAGTGTGCTTTGGGTTGGCCG	961
Qy	1289	CAGGCATGATCTCTCCGAATCTGCTGGGACTCCAGGATACGGGCAATGTCAACAATCA	1348
Db	960	CAGGCATGATCTCTCCGAATCTGCTGGGACTCCAGGATACGGGCAATGTCAACAATCA	901
Qy	1349	GCCTTGGGCGAGA 1360	
Db	900	GCCTTGGGCGAGA 889	
RESULT 13			
ABT03280			
ID	ABT03280	standard; cDNA; 625 BP.	
AC	ABT03280;		
XX			

RESULT 13	
ABT03280	
ID	ABT03280 standard; cDNA; 625 BP.
XX	
AC	ABT03280;
XX	

DT 05-SEP-2002 (first entry)  
 XX  
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 210.  
 XX  
 KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
 KW cytostatic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200239885-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PE 13-NOV-2001; 2001WO-US45395.  
 XX  
 PR 14-NOV-2000; 2000US-0713550.  
 PR 03-APR-2001; 2001US-0825294.  
 PR 02-OCT-2001; 2001US-0970966.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA.  
 XX  
 DR WPI; 2002-500186/53.  
 XX  
 PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
 PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
 PT  
 XX  
 PS Claim 2: Page 194; 197pp; English.  
 XX  
 CC The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.  
 CC  
 SQ Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;  
 Query Match 37 98; Score 613; DB 24; Length 625;  
 Best Local Similarity 99.78; Pred. No. 4,6e-164;  
 Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 OY 992 AGTTCTCTTGAGAGAGACTGGCGCGGAGCGGAGAGACAGAGCGGCTGCACAAAGC 1051  
 DB 1 AGTTCTCTTGAGAGAGACTGGCGCGGAGCGGAGAGACAGAGCGGCTGCACAAAGC 60  
 OY 1052 GCGGCTGTCGCTGAGTGGAGTGGCATGTACGGCAGGCGCTTCTGCTGTTGGCTGCTG 1111  
 DB 61 GCGGCTGTCGCTGAGTGGAGTGGCATGTACGGCAGGCGCTTCTGCTGTTGGCTGCTG 120  
 OY 1112 CAGCGACAGCGCGGAGAGACAGCCTTGACAGACACCAGCGGAGAACTGCTCGAGGACA 1171  
 DB 121 CAGCGACAGCGCGGAGAGACAGCCTTGACAGACACCAGCGGAGAACTGCTCGAGGACA 179  
 OY 1172 CCGTGACAGAGCGGCTGATGACCGAGCTGAGGTAGAAACGCTCCGAGAGGGA 1231  
 DB 180 CCGTGACAGAGCGGCTGATGACCGAGCTGAGGTAGAAACGCTCCGAGAGGGA 239  
 OY 1232 GAGAGATCATGTACGCCCGGAAAGTAGAGACTGTCCAGTCTGTTGGGTTGGCCGAG 1291  
 DB 240 GAGAGATCATGTACGCCCGGAAAGTAGAGACTGTCCAGTCTGTTGGGTTGGCCGAG 299  
 OY 1292 CCATGATCTCTCGGAATCTGTTGGGCTATCCAGATACGGCCCAATTCACACATCAGCC 1351  
 DB 300 CCATGATCTCTCGGAATCTGTTGGGCTATCCAGATACGGCCCAATTCACACATCAGCC 359  
 OY 1352 CTGGCGAGACAG 1411  
 DB 360 CTGGCGAGACAG 419  
 OY 1412 GTAATGAAATAAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1471

DB 420 GTAATGAAATAAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 479  
 OY 1472 TGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTTTCCAGACAGAGAGATT 1531  
 DB 480 TGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTTTCCAGACAGAGAGATT 539  
 OY 1532 TAACACGTGTTCAAAACCGGGGGAGTTGGCTGTAAAGAAACAGCATTAATGCTTTA 1591  
 DB 540 TAACACGTGTTCAAAACCGGGGGAGTTGGCTGTAAAGAAACAGCATTAATGCTTTA 599  
 OY 1592 GACAGGTGTAATAAAAAAAAAAAAAA 1617  
 DB 600 GACAGGTGTAATAAAAAAAAAAAAAA 625  
 RESULT 14  
 ABLA0348  
 ID ABLA0348 standard; cDNA; 625 BP.  
 XX  
 AC ABLA0348;  
 XX  
 DT 28-JUN-2002 (first entry)  
 XX  
 DE Ovarian carcinoma O1034C EST clone nucleotide sequence.  
 XX  
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KW expressed sequence tag; EST; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002004491-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 03-APR-2001; 2001US-0825294.  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PA (XUJ/) XU J.  
 PA (STOLK/) STOLK J A.  
 PA (ALGAE/) ALGAE P A.  
 PA (FLING/) FLING S P.  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 XX  
 DR WPI; 2002-171027/22.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 PT prevention and/or treatment of cancer, especially ovarian cancer -  
 XX  
 PS Claim 1a: Page 125; 131pp; English.  
 XX  
 CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma O1034C EST clone nucleotide  
 CC sequence.



992

QY 1472 TGGTACCAATTTTTCAGTGTGGACTTGAACGCTTCTTTGGCACAAGCAGAGAAATT 1531  
 |||||  
 DB 480 TGGTACCAATTTTTCAGTGTGGACTTGAACGCTTCTTTGGCACAAGCAGAGAAATT 539  
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 QY 1532 TAACACTGTTTCAACCCGGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 1591  
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 DB 540 TAACACTGTTTCAACCCGGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 599  
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 QY 1592 GACAGTGTAAAAA 1617  
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 DB 600 GACAGTGTAAAAA 625  
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

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2: /cgn2\_6/pdata/1/lna/5B.COMB.seq:\*  
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4: /cgn2\_6/pdata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/pdata/1/lna/PCRTUS.COMB.seq:\*  
6: /cgn2\_6/pdata/1/lna/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.4	3.1	7218	1	US-08-232-463-14
2	50	3.1	1872	1	US-08-153-848-39
3	50	3.1	1872	3	US-09-299-843A-39
4	50	3.1	1872	4	US-09-088-337B-39
5	50	3.1	1872	5	PCR-US93-11153-39
6	48.2	3.0	7218	1	US-08-232-463-14
7	46	2.8	289	4	US-09-007-005-17
8	46	2.8	289	4	US-09-244-796-17
9	44	2.7	1176	4	US-09-200-090-3
10	44	2.7	1342	3	US-08-832-399-1
11	43	2.7	1342	4	US-09-372-498-1
12	43	2.7	1575	3	US-08-858-876A-1
13	43	2.7	1575	4	US-09-472-880-1
14	41.4	2.6	1233	4	US-09-200-090-1
15	39	2.4	6379	1	US-08-499-215-1
16	38	2.3	1417	4	US-09-199-737-3
17	38	2.3	1417	4	US-09-058-333A-3
18	37.2	2.3	1951	4	US-08-922-865-1
19	37.2	2.3	1951	4	US-09-510-949-1
20	36	2.2	2205	4	US-08-687-590-59
21	35.6	2.2	1600	4	US-09-029-027B-1
22	35.4	2.2	1063	4	US-09-077-675A-1
23	35.2	2.2	735	4	US-09-003-287-7
24	35.2	2.2	1535	4	US-09-668-680-12
25	35	2.2	1137	3	US-09-082-088-1
26	35	2.2	1137	4	US-09-546-117-1
27	35	2.2	1555	4	US-08-809-802-11

28	34.8	2.1	1210	4	US-09-443-041A-29	Sequence 29, Appl
29	34.8	2.1	3946	3	US-09-083-351-1	Sequence 1, Appl
30	34.8	2.1	3946	4	US-09-083-352-1	Sequence 1, Appl
31	34.6	2.1	1164	4	US-08-993-088A-6	Sequence 6, Appl
32	34.6	2.1	1164	4	US-08-993-424B-6	Sequence 6, Appl
33	34.6	2.1	3390	4	US-08-993-088A-5	Sequence 5, Appl
34	34.6	2.1	3390	4	US-08-993-424B-5	Sequence 5, Appl
35	34.4	2.1	924	4	US-08-775-882-3	Sequence 3, Appl
36	34.4	2.1	1024	3	US-08-411-607A-1	Sequence 1, Appl
37	34.4	2.1	1122	2	US-08-927-433-2	Sequence 2, Appl
38	34.4	2.1	1201	4	US-08-276-882-5	Sequence 5, Appl
39	34.4	2.1	1201	4	US-08-276-600-1	Sequence 1, Appl
40	34.2	2.1	6755	3	US-08-931-999-4	Sequence 4, Appl
41	34.2	2.1	15378	3	US-08-785-420-1	Sequence 1, Appl
42	34	2.1	1151	1	US-07-704-288C-2	Sequence 2, Appl
43	34	2.1	1151	1	US-08-093-372-1	Sequence 1, Appl
44	34	2.1	1151	1	US-08-379-259-2	Sequence 1, Appl
45	34	2.1	1248	2	US-08-897-340-5	Sequence 5, Appl

#### ALIGNMENTS

RESULT 1  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEFFELINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)863-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-F1s  
US-08-232-463-14  
Query Match 3.1%; Score 50.4; DB 1; Length 7218;

Best Local Similarity 2.4%; Pred. No. 0.00032;  
Matches 9; Conservative 221; Mismatches 152; Indels 0; Gaps 0;

Oy	1170	GGGATGACGTAGCCCAAGCTCCTGGCATATTCAGCGGCCTGACTAATGCCCTTGTCCGGG	229
Dd	1062	GGGATTT	1121
Oy	230	TACCAgTCCTTGCTGCTCCcAgGAAAcTGmACTAgTTTGATcAGCTGTGAACAACC	289
Dd	1122	TT	1181
Oy	280	CCTCTTTGTATACGGGCCAAGGCCAGAATAAGGGAGTTTGCTCGGccCTCAGGCCA	349
Dd	1182	TT	1241
Oy	350	GGGCTCCGACACACACTCTGTCTTCATTGAATTAAGCcCTCTcMGCCAACGTGTGAAGC	409
Dd	1242	TT	1301
Oy	410	TGAAGAGATGcCACcccCTCTGATGTGTTCTTCAGCcCTCGcCCCAACccccCAC	469
Dd	1302	TT	1361
Oy	470	TCCCTGAgtATtTCTTCTTGggTGtcCTTTAtTTCTGgcTLnGGAGcGGAGTCcGTGT	529
Dd	1362	TT	1421
Oy	530	TCTCTTTTGTCCTGTGCAAAAT	551
Dd	1422	TTTTTTTTTTTTTTTTTTTT	1443

```

RESULT 2
US-08-153-848-39/C
Sequence 39, Application US/08153848
Patent No. 575804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellbart, Vicki L.
TITLE OF INVENTION: No. 575804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 202..1341
;
US-08-153-848-39

```

Query Match	3.1%;	Score 50;	DB 1;	Length 1872;
Best Local Similarity	52.4%;	Pred. No. 0.00019;		
Matches 110; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

QY	1143	GAAACACCCGGCGAAACAGCTGCTGCAGAGACACACCGTGTACAGAGACCGGGGTGTATACCCGACCT	1202
Db	1161	GCAAGCCTTGGGGGGAAGCGGGGGGTTCGAAAAAGGATAGAGAAAGGGGTTTGAAGCACTGTT	11020
QY	1203	GAGGTAGAAAAACGTCCTCCAGAGAAGGGGAGAGAGATCATGTATAGCCCGCGAATAGAGACCT	12623
Db	1101	GACGTACTGATGCAGGTGCAGTAGTGGGGAAGATGTCTCATGAGGAAGAGGTCAAAAGTCA	1042
QY	1263	CGTCCATCTGCTGCTTGGGTTTGGCCCGCACCATGATCCTTCCCAATCTGGTTGGGATCA	13222
Db	1041	GGGCGCAATGCAAGAGCGTGTCCACGATGTACAGACCGCTTTCACACAGGTGGTAGGGGATCA	982
QY	1323	GCATACGGCCATGTCTCAACATCATCAGGCC	1352
Db	981	GCACAGGGCAAGGTCAACCAACGCAACCCAC	952

RESULT 3  
US-09-299-843A-39/C  
Sequence 39, Application US/09299843A  
Patent No. 6107475  
GENERAL INFORMATION:  
APPLICANT: Godtska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
City: Chicago  
STATE: Illinois  
COUNTRY: USA  
Zip: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,843A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/088,337  
FILING DATE: 01-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jill E. Uhl  
REGISTRATION NUMBER: 43, 213  
REFERENCE/DOCKET NUMBER: 27866/32059B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448

```

TELEX:
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 202..1341
US-09-299-843A-39

```

```

Query Match 3.1% Score 50; DB 3; Length 1872;
Best Local Similarity 52.4%; Pred. No. 0.00019;
Matches 110; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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```

QY 1143 GAAACCCCGCCGAACTGCTGCGAGAGACCGCTGATGACCGAGCT 1202
DB 1161 GCAGGCTGCGGGAAGGGGGGTGGAAGGATGAGGAGGCTGTT 1102
QY 1203 GAGGTAGAAAACCTCTCCGAGAGGAGGAGATGATGACCGAGT 1262
DB 1101 GAGGTAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGTCA 1042
QY 1263 GGTCCAGTCTGCTTGGGTTGGCCGAGCAGATGATCCTCGAATGTTGGGATCCA 1322
DB 1041 GGGCCAGTGCAGCAGGCTGCCAGCATGTACAGCTTTCACACAGGTGTAGGCGATCCA 982
QY 1323 GCATACGGCCATGTACACATACAGCC 1352
DB 981 GCACAGGGCAAGGTACACACAGCACCAC 952

```

RESULT 4

US-09-088-337B-39/c

Sequence 39, Application US/09088337B

Patent No. 6348574

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald  
Gray, Patrick W.  
Schweikart, Vicki L.  
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/088.337B

FILING DATE: 01-Jun-1998

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848

FILING DATE: 17-Nov-1993

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-Nov-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 6348574and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

```

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 202..1341
US-09-088-337B-39

```

```

Query Match 3.1% Score 50; DB 4; Length 1872;
Best Local Similarity 52.4%; Pred. No. 0.00019;
Matches 110; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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QY 1143 GAAACCCCGCCGAACTGCTGCGAGAGACCGCTGATGACCGAGCT 1202
DB 1161 GCAGGCTGCGGGAAGGGGGGTGGAAGGATGAGGAGGCTGTT 1102
QY 1203 GAGGTAGAAAACCTCTCCGAGAGGAGGAGATGATGACCGAGT 1262
DB 1101 GAGGTAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGTCA 1042
QY 1263 GGTCCAGTCTGCTTGGGTTGGCCGAGCAGATGATCCTCGAATGTTGGGATCCA 1322
DB 1041 GGGCCAGTGCAGCAGGCTGCCAGCATGTACAGCTTTCACACAGGTGTAGGCGATCCA 982
QY 1323 GCATACGGCCATGTACACATACAGCC 1352
DB 981 GCACAGGGCAAGGTACACACAGCACCAC 952

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RESULT 5

PCT-US93-11153-39/c

Sequence 39, Application PC/TUS9311153

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald  
Gray, Patrick W.  
Schweikart, Vicki L.  
TITLE OF INVENTION: Novel Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11153

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-Nov-1992

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 39:

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:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 1872 base pairs
:      TYPE: nucleic acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:      MOLECULE TYPE: DNA (genomic)
:      FEATURE:
:      NAME/KEY: CDS
:      LOCATION: 202..1341
:      PCT-US93-11153-39

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; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PT29pt-fls
US-08-232-463-14

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FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: King, William T  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: GH50020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5515  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1342 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-832-399-1

Query Match 2.7%; Score 43; DB 3; Length 1342;  
Best Local Similarity 50.2%; Pred. No. 0.017;  
Matches 106; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1136 CTTGCACGAAACCCCGGAAATGCTGGAGAGACACCGCTGACAGAGCGGGTTGATGA 1195  
DB 893 CTTCCAGGAGAGATTTTCTGAGAGAGAGACACGCGCTGTGAGAGAGAGAGTACAG 834  
QY 1196 CCGAGCTGAGTAGAAGAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGAAGT 1255  
DB 833 CTGAGCTGAGTAGAAGAAAGTGTGTGTCACCATGTAGAGATGTAGAAATTTGTACA 774  
QY 1256 AGGACCTGCTCAGTGTGCTGGTTTGGCCGACCATGATCCCTCGAATCTGGTTGG 1315  
DB 773 GTGGGTGATGTCACGCGCTCATGACGTAGAGATGAGCTTGGCGGATGTACG 714  
QY 1316 GCATCCAGCATACGGCCATGTGCAACAAT 1346  
DB 713 GCAGCCAGCATGACATATGACCAAGT 683

RESULT 11  
US-09-372-498-1/c  
Sequence 1, Application US/09372498  
Patent No. 6166182  
GENERAL INFORMATION:  
APPLICANT: Derek J. Bergsma  
TITLE OF INVENTION: NOVEL HUMAN NEUTROPHIL RECEPTOR TYPE 2  
FILE REFERENCE: GH-50020-1  
CURRENT APPLICATION NUMBER: US/09/372,498  
CURRENT FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: 08/832,399  
PRIOR FILING DATE: 1997-04-02  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 1  
LENGTH: 1342  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
US-09-372-498-1

Query Match 2.7%; Score 43; DB 4; Length 1342;  
Best Local Similarity 50.2%; Pred. No. 0.017;  
Matches 106; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1136 CTTGCACGAAACCCCGGAAATGCTGGAGAGACACCGCTGACAGAGCGGGTTGATGA 1195  
DB 893 CTTCCAGGAGAGATTTTCTGAGAGAGAGACACGCGCTGTGAGAGAGAGAGTACAG 834  
QY 1196 CCGAGCTGAGTAGAAGAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGAAGT 1255  
DB 833 CTGAGCTGAGTAGAAGAAAGTGTGTGTCACCATGTAGAGATGTAGAAATTTGTACA 774

QY 1256 AGGACCTGCTCAGTGTGCTGGTTTGGCCGACCATGATCCCTCGAATCTGGTTGG 1315  
DB 773 GTGGGTGATGTCACGCGCTCATGACGTAGAGATGTAGAGATGTAGAAATTTGTACA 714  
QY 1316 GCATCCAGCATACGGCCATGTGCAACAAT 1346  
DB 713 GCAGCCAGCATGACATATGACCAAGT 683

RESULT 12  
US-08-858-876A-1/c  
Sequence 1, Application US/08858876A  
Patent No. 6022856  
GENERAL INFORMATION:  
APPLICANT: Daniel CAPUT  
APPLICANT: Pascale CHALON  
APPLICANT: Pascual FERRARA  
APPLICANT: VITA NATALIO  
TITLE OF INVENTION: Type 2 Neurotensin Receptor  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC  
STREET: 400 Seventh Street  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/858,876A  
FILING DATE: 19-SEP-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR 9723204  
FILING DATE: 17-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,049  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1575 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 37..1266  
US-08-858-876A-1

Query Match 2.7%; Score 43; DB 3; Length 1575;  
Best Local Similarity 50.2%; Pred. No. 0.018;  
Matches 106; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1136 CTTGCACGAAACCCCGGAAATGCTGGAGAGACACCGCTGACAGAGCGGGTTGATGA 1195  
DB 1150 CTTCCAGGAGAGATTTTCTGAGAGAGAGACACGCGCTGTGAGAGAGAGAGTACAG 1091  
QY 1196 CCGAGCTGAGTAGAAGAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGAAGT 1255  
DB 1090 CTGAGCTGAGTAGAAGAAAGTGTGTGTCACCATGTAGAGATGTAGAAATTTGTACA 1031  
QY 1256 AGGACCTGCTCAGTGTGCTGGTTTGGCCGACCATGATCTCCGAATCTGGTTGG 1315  
DB 1030 GTGGGTGATGTCACGCGCTCATGAGTACGTAGAGATGAGAGCTGCGGATGTACG 971



ok

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; STRAIN: No. 561204ardla corallina B-276 (FERM P-4094; FERM
; STRAIN: BP-5124; ATCC 31338)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 910..1935
; OTHER INFORMATION: /product= "amoA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1935..2285
; OTHER INFORMATION: /product= "amoB"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2300..3802
; OTHER INFORMATION: /product= "amoc"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3805..4830
; OTHER INFORMATION: /product= "amod"
;
US-08-499-215-1
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Query Match          2.4%; Score 39; DB 1; Length 6379;
Best Local Similarity 49.8%; Pred. No. 0.59;
Matches 125; Conservative 0; Mismatches 125; Indels 1; Gaps 1;
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QY 1049 GCGGGCGCTGTGCGTGTGAGTGCATGTACGCGCAGCGGCTCTCGTGTGGCGTG 1108
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1473 GCGGGCGCGCGCGTGTGCGTGTGAGTGCATGTACGCGCAGCGGCTCTCGTGTGGCGTG 1414
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 1109 CTGCAGCGCAGCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1168
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1413 GTCTGTGAGCAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1355
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 1169 ACACCGTGTACAGAGCGGCTGTATGACGAGCTGAGGTAGAAAAAGCTCTCGAGAGAG 1228
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1354 CGGACATGCGCTGTGCGCAGCGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGATG 1295
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 1229 GGAGAGAGATCATGTACGCGCGGAGAGTAGACCTCGTCCAGTGTGCTTGGGTTGGCGG 1288
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1294 GCCAGCGCGGCTGAGACCTGTGCGAGAGATCTTGTGCGACCATGATGGCGTGTGCGCGCG 1235
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 1289 CAGCCATGATC 1299
      |||||  |||
DB 1234 ACCECATGTGTC 1224
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Search completed: November 7, 2002, 15:58:56
Job time : 97.6676 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 13:45:13 : Search time 70.3601 Seconds  
(without alignments)  
8163.686 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619

Sequence: 1 ggcacatttgcggtatgtt.....aaaaaaaaaaaaaaaaa 1619

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Database : Published.Applications\_NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1606.2	99.2	1897	10	US-09-825-294-214
4	613	37.9	625	10	US-09-825-294-210
5	613	37.9	625	10	US-09-825-294-208
6	497.6	30.7	1362	10	US-09-825-294-208
7	424.2	26.2	558	10	US-09-825-294-210
8	396.4	24.5	409	10	US-09-825-294-212
9	388.4	24.0	1010	10	US-09-825-294-212
10	377.4	23.3	430	10	US-09-825-294-212
11	365.4	22.6	369	10	US-09-825-294-212
12	362	22.4	373	10	US-09-825-294-212
13	362	22.4	396	10	US-09-825-294-212
14	354	21.9	390	10	US-09-825-294-212
15	330.8	20.4	381	10	US-09-825-294-212
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17	197.8	12.2	480	10	US-09-825-294-212
18	171.2	10.6	201	10	US-09-825-294-212
19	50	3.1	1464	10	US-09-149-045-1

C	20	40	2.5	2036	10	US-09-866-582-17	Sequence 17, App1
C	21	40	2.5	32177	10	US-09-764-877-3251	Sequence 3251, Ap
C	22	40	2.5	32207	10	US-09-764-877-3250	Sequence 3250, Ap
C	23	39.6	2.4	332	10	US-09-867-701-8973	Sequence 8973, Ap
C	24	37.2	2.3	1743	10	US-09-925-301-541	Sequence 541, App
C	25	36.8	2.3	488	10	US-09-924-035A-347	Sequence 347, App
C	26	36.8	2.3	628	10	US-09-770-149-714	Sequence 147, App
C	27	36	2.2	371	10	US-09-969-347-117	Sequence 117, App
C	28	36	2.2	3977	10	US-09-764-869-1999	Sequence 1999, Ap
C	29	36	2.2	3977	10	US-09-764-869-1999	Sequence 2001, Ap
C	30	35.8	2.2	21860	10	US-09-764-877-3803	Sequence 3803, Ap
C	31	35.4	2.2	3007	10	US-09-795-006A-148	Sequence 148, App
C	32	35	2.2	1137	12	US-10-037-616-3	Sequence 3, App11
C	33	34.8	2.1	466	10	US-09-920-300A-1456	Sequence 1456, Ap
C	34	34.8	2.1	466	12	US-10-033-5528-1456	Sequence 1456, Ap
C	35	34.8	2.1	495	10	US-09-998-598-1084	Sequence 1084, Ap
C	36	34.8	2.1	503	10	US-09-998-598-1030	Sequence 1030, Ap
C	37	34.8	2.1	582	10	US-09-998-598-309	Sequence 309, App
C	38	34.8	2.1	597	10	US-09-777-551B-41	Sequence 589, App
C	39	34.8	2.1	624	10	US-09-804-551B-41	Sequence 41, App1
C	40	34.8	2.1	1619	10	US-09-925-300-746	Sequence 746, App
C	41	34.8	2.1	30352	10	US-09-764-869-1768	Sequence 1768, Ap
C	42	34.6	2.1	227	10	US-09-880-107-2870	Sequence 2870, Ap
C	43	34.6	2.1	396	10	US-09-825-294-25	Sequence 25, App1
C	44	34.6	2.1	425	10	US-09-960-352-1711	Sequence 1711, Ap
C	45	34.6	2.1	1368	10	US-09-834-975-825	Sequence 825, App

#### ALIGNMENTS

RESULT 1  
US-09-825-294-205  
Sequence 205, Application US/09825294  
Patent No. US20020004491A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Algate, Paul A.  
APPLICANT: Filing, Steven P.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C5  
CURRENT APPLICATION NUMBER: US/09/825,294  
CURRENT FILING DATE: 2001-04-03  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 205  
LENGTH: 1619  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-825-294-205

Query Match	100.0%	Score 1619:	DB 10:	Length 1619:
Best Local Similarity	100.0%	Pred. No. 0:		
Matches 1619:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
Oy	1	GGCACTTTGGGATGTTCTTCAGCTTCCAGCTTGGCGTGAATCCAGTCTCA	60	
Db	1	GGCACTTTGGGATGTTCTTCAGCTTCCAGCTTGGCGTGAATCCAGTCTCA	60	
Oy	61	GTGTGAAGTAATCCAGTGAACAAGCAAGTCTCCCGAGTTCATTTGAATTCAC	120	
Db	61	GTGTGAAGTAATCCAGTGAACAAGCAAGTCTCCCGAGTTCATTTGAATTCAC	120	
Oy	121	GGTGAAGCTTAAGACATGTCTCAAGAAAGATGATGAGCAAGTCCCGGATCATGTA	180	
Db	121	GGTGAAGCTTAAGACATGTCTCAAGAAAGATGATGAGCAAGTCCCGGATCATGTA	180	
Oy	181	CCGCAAGCTCTGTGATCATGACGGCGCTGTCATGCGCTCCGAGTACCAAGTCTT	240	
Db	181	CCGCAAGCTCTGTGATCATGACGGCGCTGTCATGCGCTCCGAGTACCAAGTCTT	240	

QY	241	CTGCTCCCAAGGAAACGTAAC	TGAGTTGGATGACGCTGCAACACCCCTCTTTGTAA	300
Db	241	CTGCTCCCAAGGAAACGTAAC	TGAGTTGGATGACGCTGCAACACCCCTCTTTGTAA	300
QY	301	CGGGCCAAAGGCCCCAAGAAAA	GGGGGAAGTTCTGCGCTCGGCCCTCGAGGCACAGGGCTCCGCAC	360
Db	301	CGGGCCAAAGGCCCCAAGAAAA	GGGGGAAGTTCTGCGCTCGGCCCTCGAGGCACAGGGCTCCGCAC	360
QY	361	CACCAATCCGTTCCCAAAATTA	TAGCCCTCTTTCGCGCACACTGCTGAAGCTGAAGAGATG	420
Db	361	CACCAATCCGTTCCCAAAATTA	TAGCCCTCTTTCGCGCACACTGCTGAAGCTGAAGAGATG	420
QY	421	CCACCCCTCCCGCATGTTGTTCT	TCCAGCCCTCGGCCCAACCCCCACCCCTCCGAGTGA	480
Db	421	CCACCCCTCCCGCATGTTGTTCT	TCCAGCCCTCGGCCCAACCCCCACCCCTCCGAGTGA	480
QY	481	GTTTCTCTTGCGGTGTCCTTTTA	TTCCTGGGTAGGAGCGGGAGTCCGTTCTCTTTGTT	540
Db	481	GTTTCTCTTGCGGTGTCCTTTTA	TTCCTGGGTAGGAGCGGGAGTCCGTTCTCTTTGTT	540
QY	541	CCGTGTCGAATTAATAAAGAGCT	CGGTAACACTTCGAATTAATTAGCTGACAGAT	600
Db	541	CCGTGTCGAATTAATAAAGAGCT	CGGTAACACTTCGAATTAATTAGCTGACAGAT	600
QY	601	TTTTCACTATGTACTTTGAAGA	AGAGAGTGAGTGAAGATTACCCCCATGCTGTGTAA	660
Db	601	TTTTCACTATGTACTTTGAAGA	AGAGAGTGAGTGAAGATTACCCCCATGCTGTGTAA	660
QY	661	CGAGTCGAAGGCGCAGGCTGGG	AGAGTCAGTCTTAAGAAATCACMGAGTGGCATATGGC	720
Db	661	CGAGTCGAAGGCGCAGGCTGGG	AGAGTCAGTCTTAAGAAATCACMGAGTGGCATATGGC	720
QY	721	TTTTTGAAGCCCTCAAGTGCAT	TTCATCCCTGATGGGGGCATAGTTTGACTGAC	780
Db	721	TTTTTGAAGCCCTCAAGTGCAT	TTCATCCCTGATGGGGGCATAGTTTGACTGAC	780
QY	781	GTGAGAAGTACGATTTTCTTAG	GGGTGGAGGGCCAGTCCCACTCAAGGCTCCCTGGCTTG	840
Db	781	GTGAGAAGTACGATTTTCTTAG	GGGTGGAGGGCCAGTCCCACTCAAGGCTCCCTGGCTTG	840
QY	841	ACATTCAAACTTCATGCTCTG	AAACCATTTCTCGCAGCAGAAATGGCTGGTTGCGC	900
Db	841	ACATTCAAACTTCATGCTCTG	AAACCATTTCTCGCAGCAGAAATGGCTGGTTGCGC	900
QY	901	CTGAGTTGGGCTCTAAGTAC	TGAGACTCAATAGCTGGACTTAAAGACTGGGGCTGGGCT	960
Db	901	CTGAGTTGGGCTCTAAGTAC	TGAGACTCAATAGCTGGACTTAAAGACTGGGGCTGGGCT	960
QY	961	CGCTCTGAAAAGTCTTAAG	AAAAATCTTTCACATTTCTCTTGACAGAGACTGGCGCGGG	1020
Db	961	CGCTCTGAAAAGTCTTAAG	AAAAATCTTTCACATTTCTCTTGACAGAGACTGGCGCGGG	1020
QY	1021	ACGCGAAGACGACGGGCGCTG	CACAAGCGGGCGCTGTGCGGTGGTGAAGTCGCATGTA	1080
Db	1021	ACGCGAAGACGACGGGCGCTG	CACAAGCGGGCGCTGTGCGGTGGTGAAGTCGCATGTA	1080
QY	1081	CGCGAGGCGGCTTCTCGGGT	TGGCGGTGACAGCAAGGGGGAGCACAACACTTGGC	1140
Db	1081	CGCGAGGCGGCTTCTCGGGT	TGGCGGTGACAGCAAGGGGGAGCACAACACTTGGC	1140
QY	1141	ACGAACACCGCGCGAAACTCT	CTCGAGAGCACCGTGTACAGAGAGCGGGTTGATGACAG	1200
Db	1141	ACGAACACCGCGCGAAACTCT	CTCGAGAGCACCGTGTACAGAGAGCGGGTTGATGACAG	1200
QY	1201	CTGAGGTGAAGAAACGTTCTC	CGAAGGGAGAGAGATCATGTAGCCCGGAAGTAGAGAC	1260
Db	1201	CTGAGGTGAAGAAACGTTCTC	CGAAGGGAGAGAGATCATGTAGCCCGGAAGTAGAGAC	1260
QY	1261	CTGCTCCAGTGTGCTTTGGG	TTTGGCGCAGCCATATCTCTCGAATCTGGTTGGGCAATC	1320
Db	1261	CTGCTCCAGTGTGCTTTGGG	TTTGGCGCAGCCATATCTCTCGAATCTGGTTGGGCAATC	1320
QY	1321	CAGGATACGGCCATGTCTACA	ACAATACGCCCTGGGCGAGACACGAGACAGGAGAGAGAC	1380

Db	1321	CAGCATACGGCCATGTCACAAACATTCAGCCCTGGGCAGACACGAGCAGGAGGAGAAC	1380
QY	1381	AGAGAAAAAGAAAAACACAGCATGAGAAACACATTAATGAAATTAACATTAATTTTAG	1440
Db	1381	AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAATGATTAACCATTAATATTTTAG	1440
QY	1441	CCCCCTGCTTCTGCTTCTACTGSCCAGGAATGTACCAATTTTTCACTGTTGACACTGA	1500
Db	1441	CCCCCTGCTTCTGCTTCTACTGSCCAGGAATGTACCAATTTTTCACTGTTGACACTGA	1500
QY	1501	CAGCTTCTTTTGGCACAGCAGCAGAGAAATTTACACTTTTCAAAACCCGGGGAGTTGG	1560
Db	1501	CAGCTTCTTTTGGCCACAAGCAGAGAAATTTAACACCTTTCAAAACCCGGGGAGTTGG	1560
QY	1561	CTGTGTTAAAGAAAGACCAATTAATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAA	1619
Db	1561	CTGTGTTAAAGAAAGACCAATTAATGCTTTTAGCAGCTGTAAAAAAAAAAAAAAAAAA	1619

Query	Match	Best Local Similarity	Score 1619;	DB 10;	Length 1619;			
Matches 1619;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
US-09-825-294-211	2							
Sequence 211, Application US/09825294								
Patient No. US2002004491A1								
GENERAL INFORMATION:								
APPLICANT: Xu, Jiangchun								
APPLICANT: Stolk, John A.								
APPLICANT: Algate, Paul A.								
APPLICANT: Ping, Steven P.								
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE								
FILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER								
FILE REFERENCE: 210121.4845								
CURRENT APPLICATION NUMBER: US/09/825,294								
CURRENT FILING DATE: 2001-04-03								
NUMBER OF SEQ. ID NOS: 215								
SOFTWARE: FASTSEQ for Windows Version 3.0								
SEQ ID NO 211								
LENGTH: 1619								
TYPE: DNA								
ORGANISM: Homo sapiens								
US-09-825-294-211								
Query Match		100.0%;	Score 1619;	DB 10;	Length 1619;			
Best Local Similarity		100.0%;	Pred. No. 0;					
Matches 1619;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY 1	GGCAACTTTTTCGCGGATTTCTTCTCTTCACAGCTTTGCGCTGCACAAATTCAGTCTACCA	60						
DB 1	GGCAACTTTTTCGCGGATTTCTTCTCTTCACAGCTTTGCGCTGCACAAATTCAGTCTACCA	60						
QY 61	GTTGGAAGATTCACAGCTGATCAACAGAGCTGCTCCCGGAGTTCAATTTGTAATTCAC	120						
DB 61	GTTGGAAGATTCACAGCTGATCAACAGAGCTGCTCCCGGAGTTCAATTTGTAATTCAC	120						
QY 121	GGTGAACGTTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA	180						
DB 121	GGTGAACGTTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA	180						
QY 181	CGCGAAGTCTTGATCATCATCAGCGGCTGTCTCATCGCTTCGCGGGTACCAAGTCTT	240						
DB 181	CGCGAAGTCTTGATCATCATCAGCGGCTGTCTCATCGCTTCGCGGGTACCAAGTCTT	240						
QY 241	CTGCTCCCAAGGAAACAGTCACTAGTTTGATCAGTGTGCAACACCCCTTTTGTAA	300						
DB 241	CTGCTCCCAAGGAAACAGTCACTAGTTTGATCAGTGTGCAACACCCCTTTTGTAA	300						
QY 301	CGGCGCCAAAGCCCAAGAAAGGGGAGTTCTGCTCGGCTTCAGGCGCAAGGCTCCGAC	360						
DB 301	CGGCGCCAAAGCCCAAGAAAGGGGAGTTCTGCTCGGCTTCAGGCGCAAGGCTCCGAC	360						
QY 361	CACACTCTCTTCTTCAAAATTAAGCCCTTCTTGCGGACACTGCTGAAGTGAAGAGATG	420						
DB 361	CACACTCTCTTCTTCAAAATTAAGCCCTTCTTGCGGACACTGCTGAAGTGAAGAGATG	420						

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QY 421 CACACCCCTCTGCATTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 480
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DB 421 CCACCCCTCTGCATTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 480
QY 481 GTTCTCTGCGGTCTTTTATCTGGGTAGGAGCGGGAGTCCGTCTCTTTGTT 540
    |||||
DB 481 GTTCTCTGCGGTCTTTTATCTGGGTAGGAGCGGGAGTCCGTCTCTTTGTT 540
QY 541 CCGTGCATATATGAAGAGCTCGGTAAAGCATCTGATTAATTCACCCGACTGAT 600
    |||||
DB 541 CCGTGCATATATGAAGAGCTCGGTAAAGCATCTGATTAATTCACCCGACTGAT 600
QY 601 TTTCACTATGACTTGAAGAGAGAGGTGAGTGAAGTTCAACCCCACTGCTGTGAAC 660
    |||||
DB 601 TTTCACTATGACTTGAAGAGAGAGGTGAGTGAAGTTCAACCCCACTGCTGTGAAC 660
QY 661 CGAGAGCAAGGCGGCTGGCAGAGTCACTCTTGAAGTCACTGAGGTGGCACTGCC 720
    |||||
DB 661 CGAGAGCAAGGCGGCTGGCAGAGTCACTCTTGAAGTCACTGAGGTGGCACTGCC 720
QY 721 TTTTGAAGCCTCCAGTTCATTCATCCCTGATGGGGGATAGTTGAGACTGACGA 780
    |||||
DB 721 TTTTGAAGCCTCCAGTTCATTCATCCCTGATGGGGGATAGTTGAGACTGACGA 780
QY 781 GTGAGAGTACCTTTTCTTAGGGCTGAGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 840
    |||||
DB 781 GTGAGAGTACCTTTTCTTAGGGCTGAGAGGCGCAGTCCCACTCAAGGCTCCCTGCTTG 840
QY 841 ACATTCAAACTTCATGCTCCGTAAGAAACATTTCTGACAGAGATTTGGTGGTTCGGCC 900
    |||||
DB 841 ACATTCAAACTTCATGCTCCGTAAGAAACATTTCTGACAGAGATTTGGTGGTTCGGCC 900
QY 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTAGACTGGGCTCGGCT 960
    |||||
DB 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTAGACTGGGCTCGGCT 960
QY 961 CGCTCTGAAAAGTCTTAAAGAAATCTTCTCAGTTCTCTTTCAGAGAGACTGGCCGGG 1020
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DB 961 CGCTCTGAAAAGTCTTAAAGAAATCTTCTCAGTTCTCTTTCAGAGAGACTGGCCGGG 1020
QY 1021 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCGTGGTGGAGTGGCATGTA 1080
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DB 1021 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCGTGGTGGAGTGGCATGTA 1080
QY 1081 CGCGAGGCGCTTCTGTTGGTGGCTGCTGAGCGAGCAGCGGCGAGCAGACACTTGC 1140
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DB 1081 CGCGAGGCGCTTCTGTTGGTGGCTGCTGAGCGAGCAGCGGCGAGCAGACACTTGC 1140
QY 1141 ACGAACCACCGCGGAAACTGCTGCGAGAGACACCTGTACAGAGAGCGGTTGATGACCGAG 1200
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DB 1141 ACGAACCACCGCGGAAACTGCTGCGAGAGACACCTGTACAGAGAGCGGTTGATGACCGAG 1200
QY 1201 CTGAGGTAGAAAAAGTCTCCGAGAAAGGAGAGGATCATGTCGCCGGAAGTAGAGAC 1260
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DB 1201 CTGAGGTAGAAAAAGTCTCCGAGAAAGGAGAGGATCATGTCGCCGGAAGTAGAGAC 1260
QY 1261 CTGCTGTCAGTGTCTGTTGGGTTGGCGCGAGCATGATCTCCGATCTGGTTGGGATC 1320
    |||||
DB 1261 CTGCTGTCAGTGTCTGTTGGGTTGGCGCGAGCATGATCTCCGATCTGGTTGGGATC 1320
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DB 1321 CAGCATAGGCGCAATGTCAACAATCAAGCCCTGGGAGACACGAGCAGGAGGAGAGAC 1380
QY 1381 AGAGAAAAAGAAACACAGCATGAGAAACACAGTAATATTAATTAATTTAG 1440
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DB 1381 AGAGAAAAAGAAACACAGCATGAGAAACACAGTAATATTAATTAATTTAG 1440
QY 1441 CCCCCTCTGTTCTGCTTACTGAGGAGAGAAATGTCACAAATTTTCACTGTTGACTTGA 1500
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DB 1441 CCCCCTCTGTTCTGCTTACTGAGGAGAGAAATGTCACAAATTTTCACTGTTGACTTGA 1500

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QY 1501 CAGCTTCTTTGCCACAGCAAGAGAGATTTAACACTGTTCAACCCGGGGAGTTGG 1560
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QY 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619
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DB 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAAGAAAAA 1619

RESULT 3
US-09-825-294-214
: Sequence 214, Application us/09825294
: Patent No. US20020004491A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825,294
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1897)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

Query Match          99.2%; Score 1606.2; DB 10; Length 1897;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGCACATTTTGGCGGATTTGTTCTGCTTCCAGGCTTGGCGCTGCAATTCAGTCAACA 60
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DB 280 GGCACATTTTGGCGGATTTGTTCTGCTTCCAGGCTTGGCGCTGCAATTCAGTCAACA 339
QY 61 GTGTGAAGAAATTCAGCTGAACAAGCACTGCTCCCGGAGTCAATGTAATGAC 120
    |||||
DB 340 GTGTGAAGAAATTCAGCTGAACAAGCACTGCTCCCGGAGTCAATGTAATGAC 399
QY 121 GGTGAACGTTCAAGACATGTGTGCAAGAAAGATGATGAGCAAAAGTGCAGGATCATGTA 180
    |||||
DB 400 GGTGAACGTTCAAGACATGTGTGCAAGAAAGATGATGAGCAAAAGTGCAGGATCATGTA 459
QY 181 CCGGAATGCTGTGCAATCATCAGAGGCGCTGTCTCATGCTGTGCGGGATACAGTCTT 240
    |||||
DB 460 CCGGAATGCTGTGCAATCATCAGAGGCGCTGTCTCATGCTGTGCGGGATACAGTCTT 519
QY 241 CTGCTCCCGAGGAAATGCAATCAGTTTGCATCAGCTGCTGCAACACCCCTTTGTGA 300
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DB 520 CTGCTCCCGAGGAAATGCAATCAGTTTGCATCAGCTGCTGCAACACCCCTTTGTGA 579
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAGTGTGCTGCGGCGCTGAGGCCAGGCTCCGAC 360
    |||||
DB 580 CGGGCCAAAGGCCCAAGAAAGGGAGTGTGCTGCGGCGCTGAGGCCAGGCTCCGAC 639
QY 361 CACCATCTGCTGCTCAATTAAGCCCTTCTGGGACACATGCTGGAAGGAGAGAG 420
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DB 640 CACCATCTGCTGCTCAATTAAGCCCTTCTGGGACACATGCTGGAAGGAGAGAG 699
QY 421 CCACCCCTCTCGCATTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 480
    |||||
DB 700 CCACCCCTCTCGCATTTCTTCCAGCCCTGCCCCCAACCCCACTCCCTGAGTGA 759
QY 481 GTTCTCTGCGGTCTTTTATCTGGGTAGGAGCGGGAGTCCGTCTCTTTGTT 540
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Db 760 GTTCTGCTGGGTGCTCTTTATTTCTGGGTAGGAGCGGAGCTCCCTCTCTTTGTT 819
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Db 820 CCTGTGCAAAATTAAGAAAGAGCTGGTAAAGCATTTGGAATAAATTCAGCCTGACTGAAT 879
Qy 601 TTTTCACTATGTAAGTGAAGAAAGAGGTGAGTGAATTCACCCCATGTCGTGTATAC 660
Db 880 TTTTCACTATGTAAGTGAAGAAAGAGGTGAGTGAATTCACCCCATGTCGTGTATAC 939
Qy 661 CGGAGTCAAGCGGAGGAGTGGAGAGTCACTAGTCTTGAAGTCACTAGAGTGGGCACTTCC 720
Db 940 CGGAGTCAAGCGGAGGAGTGGAGAGTCACTAGTCTTGAAGTCACTAGAGTGGGCACTTCC 999
Qy 721 TTTTGAAGGCTCCAGTGTCTCATTCCTGATGGGGGCAATGTTGAGACTGCAGA 780
Db 1000 TTTTGAAGGCTCCAGTGTCTCATTCCTGATGGGGGCAATGTTGAGACTGCAGA 1059
Qy 781 GTGAGAGTGAAGTCTTCTTGAAGGCTGGAGGGGAGTCCCACTCAAGGCTCCCTGGCTTG 840
Db 1060 GTGAGAGTGAAGTCTTCTTGAAGGCTGGAGGGGAGTCCCACTCAAGGCTCCCTGGCTTG 1119
Qy 841 ACATTTCAAACTTCATGCTCTCTGAAAAACCATTCCTCTGACAGAGAAATTTGGCTGTTCCGCG 900
Db 1120 ACATTTCAAACTTCATGCTCTCTGAAAAACCATTCCTCTGACAGAGAAATTTGGCTGTTCCGCG 1179
Qy 901 CTGAGTGGGCTCTTACTGACTGAGACTCATGACTGGGACTTGAAGTGGGGCTTGGCCT 960
Db 1180 CTGAGTGGGCTCTTACTGACTGAGACTCATGACTGGGACTTGAAGTGGGGCTTGGCCT 1239
Qy 961 GCCTGTGAAAAATGCTTAAAGAAATCTTCTGATCTCTCTTGCAGAGAGACTGGGCGCGG 1020
Db 1240 GCCTGTGAAAAATGCTTAAAGAAATCTTCTGATCTCTCTTGCAGAGAGACTGGGCGCGG 1299
Qy 1021 ACGCGAAGAGCAAGCGGCGCTGCACAAAGCGGCGCTGTGGTGTGAGATGCGCATGTA 1080
Db 1300 ACGCGAAGAGCAAGCGGCGCTGCACAAAGCGGCGCTGTGGTGTGAGATGCGCATGTA 1359
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Db 1360 CGCGCAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
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Db 1419 ACGAACAACCGCGCGGAACTGCTGCGAGACACCTGTACAGAGAGCGGGTGTGACCGAG 1478
Qy 1201 CTGAGGTAGAAAAAGCTCTCCGAGAGAGGAGAGATCATGTATACCCCGGAATGAGAC 1260
Db 1479 CTGAGGTAGAAAAAGCTCTCCGAGAGAGGAGAGATCATGTATACCCCGGAATGAGAC 1538
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Db 1539 CTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1598
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Db 1599 CAGCATACGCGCAATGTCAACAACATCAAGCCTTGGGAGACACGAGAGAGAGAGAC 1658
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Qy 1441 CCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Db 1719 CCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1778
Qy 1501 CAGCTTCTTTTGCACAAAGAGAGATTTAACACTTTTCAAAACCGGCGGAGTTGG 1560
Db 1779 CAGCTTCTTTTGCACAAAGAGAGATTTAACACTTTTCAAAACCGGCGGAGTTGG 1838
Qy 1561 CTGTGTAAAGAAAGCAATTAATGCTTTAGACAGTGTAAAAAAGAGAGAGAGAGAGAGAG 1619
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RESULT 4
US-09-825-294-210
; Sequence 210, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(625)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210

Query Match 37.9%; Score 613; DB 10; Length 625;
Best Local Similarity 99.7%; Pred. No. 2,2e-164;
Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 1 AGTCTCTCTTGCAGAGAGACTGGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Qy 1052 GGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
Db 61 GGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 1112 CAGGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1171
Db 121 CAGGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
Qy 1172 CCGTGTACAGAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1231
Db 180 CCGTGTACAGAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239
Qy 1232 GGAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGCTGCTGCTGCTGCTGCTG 1291
Db 240 GGAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGCTGCTGCTGCTGCTGCTG 299
Qy 1292 CCATGATCTCTCCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1351
Db 300 CCATGATCTCTCCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359
Qy 1352 CTGGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
Db 360 CTGGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Qy 1412 GTAATGATTAATAACATTAATAATTTAGCCCTCTGCTGCTGCTGCTGCTGCTGCTG 1471
Db 420 GTAATGATTAATAACATTAATAATTTAGCCCTCTGCTGCTGCTGCTGCTGCTGCTG 479
Qy 1472 TGGTACCAATTTTCACTGTTGGACTGACAGCTTCTTTTCCACAAGCAGAGAGATTT 1531
Db 480 TGGTACCAATTTTCACTGTTGGACTGACAGCTTCTTTTCCACAAGCAGAGAGATTT 539
Qy 1532 TAAACATGTTTCAAAACCGGCGGAGTTGGCTGTGTAAAGAAAGAGAGAGAGAGAGAG 1591
Db 540 TAAACATGTTTCAAAACCGGCGGAGTTGGCTGTGTAAAGAAAGAGAGAGAGAGAGAG 599
Qy 1592 GACAGTGTAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1617

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Db 600 GACACTGNAAAAAAAAAAAAAAAAAAAA 625

## RESULT 5

US-09-867-701-10876  
Sequence 10876, Application US/09867701

Patent No. US2002013237A1

GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10876

LENGTH: 625

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 607

OTHER INFORMATION: n = A,T,C or G

US-09-867-701-10876

Query Match

Best Local Similarity 37.9%; Score 613; DB 10; Length 625;

Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 992 AGTTCTCTTGCAGAGACTGGGCGGGAAGAGACAGAGGCGCTGACAAAGCG 1051

1 AGTTCTCTTGCAGAGACTGGGCGGGAAGAGACAGAGGCGCTGACAAAGCG 60

Db 1052 GGGCGTGTGGTGGTGGATGGCATGTACGGCAGCGCTTCTCGTGGTGGCGTGTG 1111

61 GGGCGTGTGGTGGTGGATGGCATGTACGGCAGCGCTTCTCGTGGTGGCGTGTG 120

Db 1112 CAGCGACAGCGCGGACAGACAGACCTTGACAGAACCGCGGAACTCTCGAGAGACA 1171

121 CAGCGACAGCGCGGACAGACAGACCTTGACAGAACCGCGGAACTCTCGAGAGACA 179

Db 1172 CCGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCGAAGAGGGA 1231

180 CCGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCGAAGAGGGA 239

Db 1232 GGAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGCTGGTGGCGCGAG 1291

240 GGAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGCTGGTGGCGCGAG 299

Db 1292 CCATGATCTCTCGGATCTGTTGGGATCCAGATACGCCCAATGTACACAAATCAGCC 1351

300 CCATGATCTCTCGGATCTGTTGGGATCCAGATACGCCCAATGTACACAAATCAGCC 359

Db 1352 CTGGGACAGACAG 1411

360 CTGGGACAGACAG 419

Db 1412 GTAAATGAATAAACCATTAATTTAGCCCTCTGTTCTGTTCTGTTCTGTTCTGTTCT 1471

420 GTAAATGAATAAACCATTAATTTAGCCCTCTGTTCTGTTCTGTTCTGTTCTGTTCT 479

Db 1472 TGGTACCAATTTTTCAGTGTGAGCTTGACAGCTTTTTCACACAGACAGAGAAAT 1531

480 TGGTACCAATTTTTCAGTGTGAGCTTGACAGCTTTTTCACACAGACAGAGAAAT 539

Db 1532 TAAACACTGTTTCAAAACCGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 1591

540 TAAACACTGTTTCAAAACCGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 599

Qy 1592 GACACTGTAAAAAAG 1617

Db 600 GACACTGNAAAAAAAAAAAAAAAAAAAA 625

## RESULT 6

US-09-825-294-208/C

Sequence 208, Application US/09825294

Patent No. US20020004491A1

GENERAL INFORMATION:

APPLICANT: Xu, Jlangchun

APPLICANT: Stolk, John A.

APPLICANT: Aglate, Paul A.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C5

CURRENT APPLICATION NUMBER: US/09/825,294

NUMBER OF SEQ ID NOS: 215

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 208

LENGTH: 1362

TYPE: DNA

ORGANISM: Homo sapiens

US-09-825-294-208

Query Match

Best Local Similarity 30.7%; Score 497.6; DB 10; Length 1362;

Matches 511; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 845 TCAACTCTCATGCTCTGAAAAACATCTCTGACAGCAAGATTTGGCTGTGCGGCTGA 904

1362 TCAACTCTCATGCTCTGAAAAACATCTCTGACAGCAAGATTTGGCTGTGCGGCTGA 1303

Db 905 GTTGGCTCTAGTGTGCTGAGACTGACATGAGACTGAGACTGAGACTGAGACTGAG 964

1302 GTTGGCTCTAGTGTGCTGAGACTGACATGAGACTGAGACTGAGACTGAGACTGAG 1243

Db 965 CTGAAAATGCTTAAAGAAATCTTCTGAGTCTCTCTGACAGAGACAGTGGCGGAGCG 1024

1242 CTGAAAATGCTTAAAGAAATCTTCTGAGTCTCTCTGACAGAGACAGTGGCGGAGCG 1183

Db 1025 GAAAGCAACAGCGGCTGACAAAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1084

1182 GAAAGCAACAGCGGCTGACAAAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123

Db 1085 CAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1144

1122 CAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064

Db 1145 ACACCGCGGAAACGCTGCGAGAGACACCGTGTACAGAGAGCGGCTGCTGCTGCTG 1204

1063 ACACCGCGGAAACGCTGCGAGAGACACCGTGTACAGAGAGCGGCTGCTGCTGCTG 1004

Db 1205 GGTAGAAAAGAGTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264

1003 GGTAGAAAAGAGTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 944

Db 1265 TCCAGCTGCTTGGGTTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1324

943 TCCAGCTGCTTGGGTTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 884

Qy 1325 ATACGCGCAATGTACACACATCAGCCCTGGCGAGA 1360

883 ATACGCGCAATGTACACACATCAGCCCTGGCGAGA 848

RESULT 7

US-09-867-701-2375

Sequence 2375, Application US/09867701

Patent No. US2002013237A1

GENERAL INFORMATION:



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Db 227 GGGAACTTTTGGGAGTTTCTTCTTCCAGGGCTTTGCGTCAAAATCCAGTGTACC 286
OY 60 AGGTGAAGAAATTCAGTGAACAGACAGTGGCTCCCGCCAGTCAATGTGAATGGA 119
Db 287 AGGTGAAGAAATTCAGTGAACAGACAGTGGCTCCCGCCAGTCAATGTGAATGGA 346
OY 120 CGGTGAAGTTCAGACATGTGTCAAGAAAGTGAAGTGAAGTGGCGGATCATGT 179
Db 347 CGGTGAAGTTCAGACATGTGTCAAGAAAGTGAAGTGAAGTGGCGGATCATGT 406
OY 180 ACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTGCGGGATCAAGTCT 239
Db 407 ACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTGCGGGATCAAGTCT 466
OY 240 TCTGCTCCCGAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 299
Db 467 TCTGCTCCCGAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 526
OY 300 A-CGGGCAAGGCGCAAGAAAGGGAAGTGTGCTCGGCTCGGCTCGGCTCGGCTCGG 358
Db 527 ACCGCGCAAGGCGCAAGAAAGGGAAGTGTGCTCGGCTCGGCTCGGCTCGGCTCGG 586
OY 359 ACCACCATCTGTCTCTCAATTA--GCCCTCTTCTCGGCACTGCTGA--GCTGA 413
Db 587 ACCACCATCTGTCTCTCAATTAAGCCCTACTTCTCGGCACTGCTGAAGCTTGAAG 646
OY 414 GGAGATGCCACCCCTCTGCAATTTCTTCCAGCCCTCGGCGCCACCCCGCTCC 473
Db 647 GGAGAGGACACCCACTCTGCAATTTCTTCCAGCCCTCGGCGCCACCCCGCTCC 705
OY 474 TGAGTGAATTTCTTCTGCTGTC 497
Db 706 TGAGAGAGCAGCCCGCAGGAGACC 729

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RESULT 10
US-09-867-701-4251
; Sequence 4251, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4251
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-4251

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Query Match 23.3%; Score 377.4; DB 10; Length 430;
Best Local Similarity 96.3%; Pred. No. 1.5e-97;
Matches 419; Conservative 0; Mismatches 11; Indels 5; Gaps 3;
OY 245 TCCCGAGGAAATGCAATGATTTGATCAGCTGTGCAACACCCCTTTTGAACGG 304
Db 1 TCCCGAGGAAATGCAATGATTTGATCAGCTGTGCAACACCCCTTTTGAACGG 60
OY 305 CCAAGGCCCAAGAAAGGGAAGTGTGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 364
Db 61 CAAAG--CAAGAAAGGGAAGTGTGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 116
OY 365 ATCTGTTCTCTCAATTAAGTCTTCTGCGACACTGTGAAGTGAAGATGCGAC 424
Db 117 ATCTGTTCTCTCAATTAAGTCTTCTGCGACACTGTGAAGTGAAGATGCGCTC 176

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OY 425 CCCCTCTGATTTGTTCTTCCAGCCCTGCGCCCAACCCCGCCACCTGCTGAGTGT 484
Db 177 CCCGT-CTGCAATGTCTTCCAGCCCTGCGCCCAACCCCGCCACCTGCTGAGTGT 235
OY 485 CTTCTGGGTGTCTTTTATTTCTGAGGAGCGGAGTCCGTTCTTTTGTCTCG 544
Db 236 CTTCTGGGTGTCTTTTATTTCTGAGGAGCGGAGTCCGTTCTTTTGTCTCG 295
OY 545 TGCAATATATGAAGAGCTCGGTAAAGATTTCTGAATTAATTCAGCTGATTAATTC 604
Db 236 TGCAATATATGAAGAGCTCGGTAAAGATTTCTGAATTAATTCAGCTGATTAATTC 355
OY 605 AGTATGACTTGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 664
Db 356 AGTATGACTTGAAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 415
OY 665 GTCAAGGCCAGGCTG 679
Db 416 GTCAAGGCCAGGCTG 430

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RESULT 11
US-09-825-294-199
; Sequence 199, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Flinn, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.4845
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

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Query Match 22.6%; Score 365.4; DB 10; Length 369;
Best Local Similarity 99.2%; Pred. No. 3.6e-94;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GGCAACTTTTGGCGATTTGTTCTTCCAGGCTTTGCGCTGCAAAATCCAGTCAACA 60
Db 1 GGCAACTTTTGGCGATTTGTTCTTCCAGGCTTTGCGCTGCAAAATCCAGTCAACA 60
OY 61 GTGTGAAGATTTCCAGTGAACAGACGACTGCTCCCGAGTTCATTTGATTCAC 120
Db 61 GTGTGAAGATTTCCAGTGAACAGACGACTGCTCCCGAGTTCATTTGATTCAC 120
OY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGTGAAGTGAAGTGAAGTGAAGTGA 180
Db 121 GGTGAAGCTTCAAGACATGTGTGTCAAGAAAGTGAAGTGAAGTGAAGTGAAGTGA 180
OY 181 CCGGAAGTCTGTGATCATCATCAGGCGCTGTCTATGCGCTTCCGCGGATCAAGTCTT 240
Db 181 CCGGAAGTCTGTGATCATCATCAGGCGCTGTCTATGCGCTTCCGCGGATCAAGTCTT 240
OY 241 CTGCTCCCAAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
Db 241 CTGCTCCCAAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
OY 301 CGGCGCAAGGCCCAAGAAAGGGAAGTGTGCTGCGCTCGGCTCGGCTCGGCTCGG 360

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Db 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTCTGCTCGCCCTCANGCCATGGCTCCGAC 360  
 QY 361 CACCATCT 369  
 Db 361 CACCATCT 369

# RESULT 12

US-09-867-701-1516/C  
 ; Sequence 1516, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1516  
 ; LENGTH: 373  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-867-701-1516

Query Match 22.4%; Score 362; DB 10; Length 373;  
 Best Local Similarity 99.7%; Pred. No. 3.3e-93;  
 Matches 373; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1226 AGGGGAGAGATCATGTACGGCCGGAAGTAGACCTGTCAGTCAGTCGCTGGTTGG 1285  
 Db 373 AGGGGAGAGATCATGTACGGCCGGAAGTAGACCTGTCAGTCAGTCGCTGGTTGG 315  
 QY 1286 CGGACGATCATGTCTCCGAATCTGCTGGCATCCAGCATAGGCGCAATGTACAGAA 1345  
 Db 314 CGGACGATCATGTCTCCGAATCTGCTGGCATCCAGCATAGGCGCAATGTACAGAA 255  
 QY 1346 TCAGCCCTGGGACAGCAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1405  
 Db 254 TCAGCCCTGGGACAGCAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195  
 QY 1406 AACACAGTAATGAATAAACCAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCT 1465  
 Db 194 AACACAGTAATGAATAAACCAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCT 135  
 QY 1466 AGGAATGTACCAATTTTTCAGTGTGACCTTGACAGCTTTTGGCACAAGCAGAG 1525  
 Db 134 AGGAATGTACCAATTTTTCAGTGTGACCTTGACAGCTTTTGGCACAAGCAGAG 75  
 QY 1526 AGAATTTACAGCTTTCACACCGGGGAGTTGGCTGTGTAAGAAAGACCAATTAAT 1585  
 Db 74 AGAATTTACAGCTTTCACACCGGGGAGTTGGCTGTGTAAGAAAGACCAATTAAT 15  
 QY 1586 GCTTTAGACAGTGT 1599  
 Db 14 GCTTTAGACAGTGT 1

# RESULT 13

US-09-825-294-9  
 ; Sequence 9, Application US/09825294  
 ; Patent No. US20020004491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Fling, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C5

; CURRENT APPLICATION NUMBER: US/09/825,294  
 ; CURRENT FILING DATE: 2001-04-03  
 ; NUMBER OF SEQ ID NOS: 215  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 396  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(396)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-825-294-9

Query Match 22.4%; Score 362; DB 10; Length 396;  
 Best Local Similarity 97.7%; Pred. No. 3.5e-93;  
 Matches 377; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 GGCACCTTTTGGCGATTTCTTGTCTTCAGGCTTTCGCTGCAATCCAGTGTACCA 60  
 Db 11 GGCACCTTTTGGCGATTTCTTGTCTTCAGGCTTTCGCTGCAATCCAGTGTACCA 70  
 QY 61 GTGTGAAGATTCAGCTGAACAACGACCTCTCTCCCGAGTTTGTGAATTGAC 120  
 Db 71 GTGTGAAGATTCAGCTGAACAACGACCTCTCTCCCGAGTTTGTGAATTGAC 130  
 QY 121 GGTGAAGTTCAAGACATGTGTGCAAGAAGATGAGAGAGAGAGAGAGAGAGAGAG 180  
 Db 131 GGTGAAGTTCAAGACATGTGTGCAAGAAGATGAGAGAGAGAGAGAGAGAGAGAG 190  
 QY 181 CCGAGATCTCTGTATCATCAGCGGCTGTCTCATGCTCTGCGGGTACAGTCTT 240  
 Db 191 CCGAGATCTCTGTATCATCAGCGGCTGTCTCATGCTCTGCGGGTACAGTCTT 250  
 QY 241 CTGCTCCCGAGGAACTGAACCTGTTGATCAGTCTGCTGCAACCCCTTTGTAA 300  
 Db 251 CTGCTCCCGAGGAACTGAACCTGTTGATCAGTCTGCTGCAACCCCTTTGTAA 310  
 QY 301 CGGGCCAGGCCCCAAGAAAGGAGAA--GTTCTGCTCGGCGCTCAGAGGCGCTCCG 358  
 Db 311 CGGGCCAGGCCCCAAGAAAGGAGAAAGTTCTGCTGCTCGGCGCTCAGAGGCGCTCCG 370  
 QY 359 ACCACATCTCTGTCTCAATTAAGC 384  
 Db 371 ACCACATCTCTGTCTCAATTAAGC 396

# RESULT 14

US-09-867-701-1532  
 ; Sequence 1532, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1532  
 ; LENGTH: 390  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(390)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-867-701-1532

Query Match 21.9%; Score 354; DB 10; Length 390;

Best Local Similarity 98.7%; Pred. No. 6.4e-91;  
Matches 387; Conservative 0; Mismatches 2; Indels 3; Gaps 3;  
QY 1210 AAAACGCTCCGAGAGGAGAGATCATGTACGCCGGGAAGTGGACCTCGCCAG 1269  
DB 1 AAAACGCTCCGAGAGGAGAGATCATGTACGCCGGGAAGTGGACCTCGCCAG 60  
QY 1270 TCGTGGTGGGTTGGCCGAGCAGCATGATCTCCGATCTGGTTGGGCAATCCAGCATACG 1329  
DB 61 TCGTGGTGGGTTGGCCGAGCAGCATGATCTCCGATCTGGTTGGGCAATCCAGCATACG 119  
QY 1330 GCCAATGTACAAATCATCAGCCCTGGGCGACACAGCAGAGGAGAGAGAGAAAAG 1389  
DB 120 GCCAATGTACAAATCATCAGCCCTGGGCGACACAGCAGAGGAGAGAGAGAAAAG 178  
QY 1390 AAAACACAGCATGAGACACAGTAATGATAAACCATTAATTTAGCCCTCTGT 1449  
DB 179 AAAACACAGCATGAGACACAGTAATGATAAACCATTAATTTAGCCCTCTGT 238  
QY 1450 TCTGTCTTACTGGCCAGGAAATGTACCAATTTTCACTGTGGACTTGACAGCTTC-T 1508  
DB 239 TCTGTCTTACTGGCCAGGAAATGTACCAATTTTCACTGTGGACTTGACAGCTTC-T 298  
QY 1509 TTTGCCACAGCAAGAGAAATTTTACACTGTTTCAAAACCCGGGAGTGGCTGTGTTA 1568  
DB 299 TTTGCCACAGCAAGAGAAATTTTACACTGTTTCAAAACCCGGGAGTGGCTGTGTTA 358  
QY 1569 AAGAAAGACCATTAATGCTTTAGACAGTGA 1600  
DB 359 AAGAAAGACCATTAATGCTTTAGACAGTGA 390  
RESULT 15  
US-09-867-701-7826  
; Sequence 7826, Application us/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7826  
; LENGTH: 381  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-7826  
Query Match 20.4%; Score 330.8; DB 10; Length 381;  
Best Local Similarity 98.4%; Pred. No. 2.5e-84;  
Matches 376; Conservative 0; Mismatches 2; Indels 4; Gaps 4;  
QY 846 CAAACTTCATGCTCTGTAACCAATTCCTGACAGAGAAATGGTGGTTCGGCCTGAG 905  
DB 4 CAAACTTCATGCTCTGTAACCAATTCCTGACAGAGAAATGGTGGTTCGGCCTGAG 63  
QY 906 TTGGGCTCTAGTACTCGAGACTCAATGACTGGACTTAGACTGGGGCTCGGCTCGCTC 965  
DB 64 TTGGGCTCTAGTACTCGAGACTCAATGACTGGACTTAGACTGGGGCTCGGCTCGCTC 122  
QY 966 TGAAGAAGTCTTAAGAAATCTTCTCAGTTCCTCTTGCAGAGAGACTGGCCGGGACGCG 1025  
DB 123 TGAAGAAGTCTTAAGAAATCTTCTCAGTTCCTCTTGCAGAGAGACTGGCCGGGACGCG 182  
QY 1026 AAGAGCAAGGGGCGTGCACAAAGCGGGGCGTGTGGTGGTGGATGGCATGTACGGCG 1085  
DB 183 AAGAGCAAGGGGCGTGCACAAAGCGGGGCGTGTGGTGGTGGATGGCATGTACGGCG-C 241

QY 1086 AGCGCTTCTGTGGTGGCGTGTGTCAGACAGCGCGACACAGCACCCTTGCAGAA 1145  
DB 242 AGCGCTTCTGTGGTGGCGTGTGCTGCGACAGCGCGACACAGCACC-TGCAGAA 300  
QY 1146 CACCGCGGAAACTGTCTGCGAGACACCGGTGTACAGAGCGGGTTGATGACCGAGTGA 1205  
DB 301 CACCGCGGAAACTGTCTGCGAGACACCGGTGTACAGAGCGGGTTGATGACCGAGTGA 360  
QY 1206 GTAGAAAACGTCTCCGAGAG 1227  
DB 361 GTAG-AAAACGTCTCCGAGAG 381

Search completed: November 7, 2002, 18:00:15  
Job time : 80.3601 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:55:08 : Search time 3627.85 Seconds  
(without alignments)  
11220.326 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619

Sequence: 1 ggcacatttcgcatgtt.....aaaaaaaaaaaaaaaaaaaa 1619

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Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pna/US0958_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US0958_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US0958_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US0958_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US0958_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1619	100.0	1619	PCT-US01-45395-205	Sequence 205, App
2	1619	100.0	1619	PCT-US01-45395-211	Sequence 211, App
3	1619	100.0	1619	US-09-713-550-205	Sequence 205, App
4	1619	100.0	1619	US-09-825-294-205	Sequence 205, App
5	1619	100.0	1619	US-09-825-294-211	Sequence 211, App
6	1619	100.0	1619	US-09-970-966-205	Sequence 205, App
7	1619	100.0	1619	US-09-970-966-211	Sequence 211, App
8	1619	100.0	1619	US-10-212-677-205	Sequence 205, App
9	1619	100.0	1619	US-10-212-677-211	Sequence 211, App
10	1606.2	99.2	1897	PCT-US01-45395-214	Sequence 214, App
11	1606.2	99.2	1897	US-09-825-294-214	Sequence 214, App
12	1606.2	99.2	1897	US-09-970-966-214	Sequence 214, App
13	1606.2	99.2	1897	US-10-212-677-214	Sequence 214, App
14	1595.8	98.6	1967	PCT-US02-29864-16	Sequence 16, App
15	1592.2	98.3	1918	US-09-387-022-4454	Sequence 4454, App
16	1592.2	98.3	1918	US-09-808-383-4454	Sequence 4454, App
17	1586	98.0	1925	US-09-652-121-7293	Sequence 7293, App
18	1586	98.0	1925	US-09-652-128-9375	Sequence 9375, App
19	1586	98.0	1925	US-09-652-917-3346	Sequence 3346, App
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c 22 1586 98.0 1925 29 US-09-726-805-1608 Sequence 1608, App
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c 25 1574.2 97.2 1953 36 US-09-950-083-1914 Sequence 1914, Ap
c 26 1574.2 97.2 1953 40 US-10-105-299-2414 Sequence 2414, Ap
c 27 1574.2 97.2 1956 1 PCT-US00-14973-23 Sequence 23, App1
c 28 1574.2 97.2 1956 36 US-09-950-083-1915 Sequence 1915, Ap
c 29 1574.2 97.2 1956 40 US-10-105-299-2415 Sequence 2415, Ap
c 30 1573.8 97.2 1917 17 US-09-371-168-7188 Sequence 7188, Ap
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c 39 1548.8 95.7 1890 23 US-09-611-523-203 Sequence 203, App
c 40 1418.2 87.6 43729 70 US-60-261-974-9 Sequence 9, App1
c 41 1416.6 87.5 1866 42 US-10-208-408-26 Sequence 26, App1
c 42 1416.6 87.5 1866 74 US-60-295-262-26 Sequence 26, App1
c 43 1416.6 87.5 1866 74 US-60-308-868-26 Sequence 26, App1
c 44 1395 86.2 1608 1 PCT-US01-18569-111 Sequence 111, App
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## ALIGNMENTS

## RESULT 1

PCT-US01-45395-205

Sequence 205, Application PC/TUS0145395  
GENERAL INFORMATION:

APPLICANT: Corixa Corporation

APPLICANT: Xu, Jlangchun

APPLICANT: Stolk, John A.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Molesh, David Alan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.48401PC

CURRENT APPLICATION NUMBER: PCT/US01/45395

CURRENT FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 215

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 205

LENGTH: 1619

TYPE: DNA

ORGANISM: Homo sapiens

PCT-US01-45395-205

Query Match 100.0%; Score 1619; DB 1; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCGAATTTTGGGATTTGTTCTTCCAGGCTTTGGCGTGAATTCAGTCTACCA 60
QY 61 GTGGAAGAAATTCAGGCTGAACAAGAGCTGCTCCCGGAGTCAATTCAGTCTAC 120
DB 61 GTGGAAGAAATTCAGGCTGAACAAGAGCTGCTCCCGGAGTCAATTCAGTCTAC 120
QY 121 GGTGAAGCTTCAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
DB 121 GGTGAAGCTTCAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
QY 181 CCGGAATTCCTGTGATCATCAGCGGCTGTCTCATGCTTCCGCGGATACAGTCTT 240
DB 181 CCGGAATTCCTGTGATCATCAGCGGCTGTCTCATGCTTCCGCGGATACAGTCTT 240
QY 241 CTGCTCCCAAGGAAAGTGAAGTCAAGTTTGCATCAGCTGCTGCAACACCCCTTTGTAA 300
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DB 241 CTGCTCCCAAGGAAAGTGAAGTCAAGTTTGCATCAGCTGCTGCAACACCCCTTTGTAA 300
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DB 301 CGGGCAAGGCCCCAAGAAAGGGAAGTTCGCTCGGCCCTCAGGCGGAGGATCCGCAC 360
QY 361 CACCATCTCTGTCTCAATTAATAGCCCTCTTCTGCGCACACTGCTGAAGCTGAAGAGATG 420
DB 361 CACCATCTCTGTCTCAATTAATAGCCCTCTTCTGCGCACACTGCTGAAGCTGAAGAGATG 420
QY 421 CCACCCCTCTGATGTTCTTCCAGACCTCGGCCCAACCCCAACCCCTCGTGTGA 480
DB 421 CCACCCCTCTGATGTTCTTCCAGACCTCGGCCCAACCCCAACCCCTCGTGTGA 480
QY 481 GTTCTTCTGCGGTCTCTTATTTCTGAGGAGGAGGAGGAGTCCGTTCTTCTTGT 540
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QY 541 CTTGTCAATTAATGAAGAGCTCGGTAAGCATTTCTGAATTAATTCAGCTGATGAAT 600
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QY 661 CGGAGTCAAGGCGGAGGCTGAGATGATCTTTAAGATCACTGAGTGGGATCTGCC 720
DB 661 CGGAGTCAAGGCGGAGGCTGAGATGATCTTTAAGATCACTGAGTGGGATCTGCC 720
QY 721 TTTTGTAAAGCTTCAGATGTCATTCATCCCGATGGGGGCAATTTGAGACTGCA 780
DB 721 TTTTGTAAAGCTTCAGATGTCATTCATCCCGATGGGGGCAATTTGAGACTGCA 780
QY 781 GTGAGAGTCAAGTTCCTTAAGGCTGAGGCGGAGTCCCACTCAAGGCTCCGCTTG 840
DB 781 GTGAGAGTCAAGTTCCTTAAGGCTGAGGCGGAGTCCCACTCAAGGCTCCGCTTG 840
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DB 841 ACPPTCAATTTATCTCTCTGAACCAATTCCTCTCAGACAGAAATTTGCTGGCC 900
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DB 1021 ACGGGAAGGCAACGGGCGCTGACAAAGCGGCGCTGTCGGTGGTGGAGTCCGATGTA 1080
QY 1081 CGGCGAGGCGCTTCTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1140
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DB 1261 CTGCTCACTGCTGCTGGGTTGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
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DB 1321 CAGCATAGGCGCAATGTCAACAATCAAGCCCTGGGAGAGAGAGGAGAGAGAGAGAGAC 1380
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Db	1381	CAGCATACGGCCATGTCACACAAATCAGCCCTGGGCGACAGACGAGCAGGAGGAGAC	1380
Qy	1381	AGCAAAAGAAAAACACAGATATGAGAACACAGTAAATGAATAAACATATAAATTTTAg	1440
Db	1381	AGAAAAAGAAAAACACAGCATATGAAACACAGTAAATGAATAAACATATAAATTTTAg	1440
Qy	1441	CCCTCTGTTCTGTGCTTACTGAGGCCAGGAATGGTACCAATTTTCAGTGTGGACTGTA	1500
Db	1441	CCCCCTGTTCTGTGCTTACTGGCCAGGAATGGTATGCCAATTTTCAGTGTGGACTTGA	1500
Qy	1501	CAGCTTCTTTTGGCCACAGCAGAGAAATTTAACACTGTTTCAAAACCCGGGGGAGTTGG	1560
Db	1501	CAGCTTCTTTTGGCCACAGCAGAGAAATTTTAACCTGTTCAAACCCGGGGGAGTTGG	1560
Qy	1561	CTGCTGTTAAAGAAAGACCAATTAATGCTTTAGACACTGTAAAAAAAAAAAAAAAAAAAAAA	1619
Db	1561	CTGCTGTTAAAGAAAGACCAATTAATGCTTTAGCACTGTAAAAAAAAAAAAAAAAAAAAAAA	1619

RESULT 2  
PCT-US01

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: Sequence 211, Application PC/US0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Flinn, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF INHERITED AND ACQUIRED FORMS OF OVARIAN CANCER
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PC/US01/45395
: CURRENT FILING DATE: 2001-11-13
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 211
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
PC/US01-45395-211

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Query Match	100.0%;	Score 1619;	DB 1;	Length 1619;
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Matches 1619; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Db	1	GGCAACTTTTGGCGATTGTTCTTGCTTCCAG6GCTTTTGCGCTGCAAAITCCAGTGTACCA	60
Qy	61	GTTGTAAGATTTCCAGCTGAGCAACGACGTGCTCCGCCAGTTCATTTGTAATTGAC	120
Db	61	GTTGTAAGATTTCCAGCTGAGCAACGACGTGCTCCGCCAGTTCATTTGTAATTGAC	120
Qy	121	GGTGAACGTTCAAGACATGTGTCAAAAAGTAGTAGAGCAAAAGTCCGGGATCATGTA	180
Db	121	GGTGAACGTTCAAGACATGTGTCAAAAAGTAGTAGAGCAAAAGTCCGGGATCATGTA	180
Qy	181	CCGCAAGTCGTGTCATCATCAGCGGCGCTGTCTATGCTCTGCCGGTATCCAGTCTTT	240
Db	181	CCGCAAGTCGTGTCATCATCAGCGGCGCTGTCTATGCTCTGCCGGTATCCAGTCTTT	240
Qy	241	CTGCTCCCCAGGAAACTGAACTCAGTTTGATCAGCGTGTGCAACACCCCTCTTTGTAA	300
Db	241	CTGCTCCCCAGGAAACTGAACTCAGTTTGATCAGCTGTGTGCAACACCCCTCTTTGTAA	300
Qy	301	CGGECCAAGGCCCAAGAAAAGGGAAGTTGTGCTCGGCGCTCAGGCCAAGGCTCCGCAC	360
Db	301	CGGECCAAGGCCCAAGAAAAGGGAAGTTGTGCTCGGCGCTCAGGCCAAGGCTCCGCAC	360
Qy	361	CACCATCTGTGTTCCCAAAATTAGCCCTTCTCGGCAACCTGCTGAAGCTGAAGAATG	420
Db	361	CACCATCTGTGTTCCCAAAATTAGCCCTTCTCGGCAACCTGCTGAAGCTGAAGAATG	420

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Db	421	CCACCCCCCTCGATGATGTCTTCACAGCCCTGGCCCCAACCCCCACCTCCCTAGTGA	480
OY	481	GTTCCTCTGGGGTGCCTTTTATCTCGGGTAGGGACGGGAGTCCGTCTCTTTTGT	540
Db	481	GTTCCTCTGGGGTGCCTTTTATCTCGGGTAGGGAGCGGAGTCCGTCTCTTTTGT	540
OY	541	CCCTGCAATTAATGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAT	600
Db	541	CCCTGCAATTAATGAAAGAGCTCGGTAAAGCATTTCTGAATTAATTCAGCTGACTGAT	600
OY	601	TTTACATATGTACTTGAAGAGAGAGAGTGGAGTGAAGTTCAACCCCACTGCTGTGTAAAC	660
Db	601	TTTACATATGTACTTGAAGAGAGAGAGTGGAGTGAAGTTCACCCCACTGCTGTGTAAAC	660
OY	661	CGAGTCAGAGCCAGGCTGGCAGAGTCACTCTTAGAATCACTAGGTGGGACTGTGCC	720
Db	661	CGAGTCAGAGCCAGGCTGGCAGAGTCACTCTTAGAATCACTAGGTGGGACTGTGCC	720
OY	721	TTTTGTAAAGCTCCACATGTCACATTCACCTCGAATGGGGGGATAGTTGAGATCGACGA	780
Db	721	TTTTGTAAAGCTCCACATGTCACATTCACCTCGAATGGGGGGATAGTTGAGATCGACGA	780
OY	781	GTGAGAGTGAAGTTTTCTTTAGGGCTGGAGGGCCAGTTTCCACTCAAGGCTCCCTGCTTG	840
Db	781	GTGAGAGTGAAGTTTTCTTTAGGGCTGGAGGGCCAGTTTCCACTCAAGGCTCCCTGCTTG	840
OY	841	ACATTCAAACTTCATGCTCCTGTA AAAACATTCCTCTACAGACAAATTTGGTGGTTTCGCC	900
Db	841	ACATTCAAACTTCATGCTCCTGTA AAAACATTCCTCTACAGACAAATTTGGTGGTTTCGCC	900
OY	901	CTGAGTTGGGCTCAGAGTCACTCAGACATCAATGACTGAGACTTAACTGGGCTGGGCT	960
Db	901	CTGAGTTGGGCTCAGAGTCACTCAGACATCAATGACTGAGACTTAACTGGGCTGGGCT	960
OY	961	CGCTCTGAAAAGTGCCTTAAAGAAATCTTCTCAATTCTCTTGACAGAGCACTGGCCGGG	1020
Db	961	CGCTCTGAAAAGTGCCTTAAAGAAATCTTCTCAATTCTCTTGACAGAGCACTGGCCGGG	1020
OY	1021	ACGGGAAGAGCAACGGGCGGTGGACAAAGCGGGCGCTGTCGGTGGGAGAGTCCGATTA	1080
Db	1021	ACGGGAAGAGCAACGGGCGGTGGACAAAGCGGGCGCTGTCGGTGGGAGAGTCCGATTA	1080
OY	1081	CGCGCAGCGGCTTCTCTGTGTGGCGTGTGTGACACAGCGCGGACGACACACTTTCG	1140
Db	1081	CGCGCAGCGGCTTCTCTGTGTGGCGTGTGTGACACAGCGCGGACGACACACTTTCG	1140
OY	1141	ACGAACACCCGCCGAAACTCTGTGCGAGAGACACCGTGTACAGAGCGGGTGTATACCCAG	1200
Db	1141	ACGAACACCCGCCGAAACTCTGTGCGAGAGACACCGTGTACAGAGCGGGTGTATACCCAG	1200
OY	1201	CTGAGGTAGAAAACGTCCTCGAAGAGGGAGAGAGATCATGTACGCCCGGAAGTAGACAC	1260
Db	1201	CTGAGGTAGAAAACGTCCTCGAAGAGGGAGAGAGATCATGTACGCCCGGAAGTAGACAC	1260
OY	1261	CTGCTCAGTGTCTGTGGGTTTTGGCCGCGACCCATGATCCTCCGAATCTGTGTGGGCAATC	1320
Db	1261	CTGCTCAGTGTCTGTGGGTTTTGGCCGCGACCCATGATCCTCCGAATCTGTGTGGGCAATC	1320
OY	1321	CAGCATACGGGCATGTGCACAAACATTCAGCCCTGGGCGACACGAGCAGAGAGGAGAAC	1380
Db	1321	CAGCATACGGGCATGTGCACAAACATTCAGCCCTGGGCGACACGAGCAGAGAGGAGAAC	1380
OY	1381	AGAGAAAAGAAAAACACAGCATGAGAACACAGTAAATGAAATTAACATTAATTTATTTAG	1440
Db	1381	AGAGAAAAGAAAAACACAGCATGAGAACACAGTAAATGAAATTAACATTAATTTATTTAG	1440
OY	1441	CCCCCTGTGTCTGTGCTTACTGGCCAGAGAAATGTATACAAATTTTTCAGTGTGGACTTGA	1500
Db	1441	CCCCCTGTGTCTGTGCTTACTGGCCAGAGAAATGTATACAAATTTTTCAGTGTGGACTTGA	1500

1501 CAGCTTCTTTGGCCACAGACAGAGAAATTTAACACTGTTTCAACCCCGGGAGCTGG 1560  
1501 CAGCTTCTTTGGCCACAGACAGAGAAATTTAACACTGTTTCAACCCCGGGAGCTGG 1560  
1561 CTGTGTTAAAGAAAGACCATTAATCTTTAGACAGTGTAAAAA 1619  
1561 CTGTGTTAAAGAAAGACCATTAATCTTTAGACAGTGTAAAAA 1619

RESULT 3  
US-09-713-550-205  
; Sequence 205, Application US/09713550  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolk, John A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: 210121.484C4  
; CURRENT APPLICATION NUMBER: US/09/713,550  
; NUMBER OF SEQ ID NOS: 205  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 205  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-713-550-205

Query Match 100.0%; Score 1619; DB 28; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGGACATTTTGGGAGTGTCTTCTGCTCCAGGCTTGGCTGCAAAATCCAGGCTACCA 60  
1 GGGACATTTTGGGAGTGTCTTCTGCTCCAGGCTTGGCTGCAAAATCCAGGCTACCA 60  
61 GTGTGAAGATTCAGCTGAACAGAGCTGCTCCGCCGAGTTGTAATGTCAC 120  
61 GTGTGAAGATTCAGCTGAACAGAGCTGCTCCGCCGAGTTGTAATGTCAC 120  
121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGGAGCAAAAGTGGGATCATGTA 180  
121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGGAGCAAAAGTGGGATCATGTA 180  
181 CCGCAAGTCTGTGATCATCAAGGCTGTCTCATCGGCTGCGGGGTACAGTCTT 240  
181 CCGCAAGTCTGTGATCATCAAGGCTGTCTCATCGGCTGCGGGGTACAGTCTT 240  
181 CCGCAAGTCTGTGATCATCAAGGCTGTCTCATCGGCTGCGGGGTACAGTCTT 240  
241 CTGCTCCCGAGGGAACGTAGTGTGATCAGCTGCTGCAACACCCCTCTTTGTA 300  
241 CTGCTCCCGAGGGAACGTAGTGTGATCAGCTGCTGCAACACCCCTCTTTGTA 300  
301 CCGGCGCAAGGCCCAAGAAAGGGAAGTCTGCTGCGGCTCAGGCGGCTCCGCAC 360  
301 CCGGCGCAAGGCCCAAGAAAGGGAAGTCTGCTGCGGCTCAGGCGGCTCCGCAC 360  
361 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTGCGACACTGTAAGTGAAGAGATG 420  
361 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTGCGACACTGTAAGTGAAGAGATG 420  
361 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTGCGACACTGTAAGTGAAGAGATG 420  
421 CCAACCCCTCTGTCATGTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGAGTGA 480  
421 CCAACCCCTCTGTCATGTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGAGTGA 480  
481 GTTCTCTTGGGAGTCTTCTTATCTGAGGTAGGAGCGGAGTCCGTCTCTTTGTT 540  
481 GTTCTCTTGGGAGTCTTCTTATCTGAGGTAGGAGCGGAGTCCGTCTCTTTGTT 540  
541 CCTGTCAATATTAAGAAAGCTCGGTAAGCAATTTCAATTAATTCAGCTGACGAT 600  
541 CCTGTCAATATTAAGAAAGCTCGGTAAGCAATTTCAATTAATTCAGCTGACGAT 600  
601 TTTCAATATTAAGAAAGCTCGGTAAGCAATTTCAATTAATTCAGCTGACGAT 660  
601 TTTCAATATTAAGAAAGCTCGGTAAGCAATTTCAATTAATTCAGCTGACGAT 660

601 TTTCAATATTAAGAAAGCTCGGTAAGCAATTTCAATTAATTCAGCTGACGAT 660  
661 CGGAGTCAAGGCGAGGCTGCGAGAGTCACTTTAAGAGTCACTAGAGTGGCATCTGCC 720  
661 CGGAGTCAAGGCGAGGCTGCGAGAGTCACTTTAAGAGTCACTAGAGTGGCATCTGCC 720  
721 TTTGTAAAGCTCCAGTGTCCATCCCTGATGGGGCATAGTTTGAGACTGAGA 780  
721 TTTGTAAAGCTCCAGTGTCCATCCCTGATGGGGCATAGTTTGAGACTGAGA 780  
781 GTGAGAGTGAAGTCTTCTTAAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCC 840  
781 GTGAGAGTGAAGTCTTCTTAAAGGCTGAGGCGCAGTTCCCACTCAAGGCTCCCTGCC 840  
841 ACATTCAAACTTCACTGCTCTGAAACCATTTCTGCAAGCAATTTGGCTGTTGCCGC 900  
841 ACATTCAAACTTCACTGCTCTGAAACCATTTCTGCAAGCAATTTGGCTGTTGCCGC 900  
901 CTGAGTTGGGCTAGTGAAGTCAAGTCAATGATGAGTGGGCTGAGGCTGAGGCT 960  
901 CTGAGTTGGGCTAGTGAAGTCAAGTCAATGATGAGTGGGCTGAGGCTGAGGCT 960  
961 CGCTCTGAAAGTCTTAAAGAAATCTTCTCAAGTCTCTTCTGCAAGAGTGGCGCCGG 1020  
961 CGCTCTGAAAGTCTTAAAGAAATCTTCTCAAGTCTCTTCTGCAAGAGTGGCGCCGG 1020  
1021 ACGGAGAGCAAGAGGCGGCTGCAAGAAAGGCGGCTGCTGAGTGGTGGATGCCATGTA 1080  
1021 ACGGAGAGCAAGAGGCGGCTGCAAGAAAGGCGGCTGCTGAGTGGTGGATGCCATGTA 1080  
1081 CGCGAGGCGCTTCTGCTGAGTGGGCTGCTGAGTGGGCTGAGTGGGCTGAGTGG 1140  
1081 CGCGAGGCGCTTCTGCTGAGTGGGCTGCTGAGTGGGCTGAGTGGGCTGAGTGG 1140  
1141 ACGAAGACCCCGCAAACTGCTGCGAGACACCGTGTACAGAGAGCGGGTGTATGCCAG 1200  
1141 ACGAAGACCCCGCAAACTGCTGCGAGACACCGTGTACAGAGAGCGGGTGTATGCCAG 1200  
1201 CTGAGTGAAGAAACGCTCTCGAAGAGGAGGAGATCATGTAAGCCCGGAATAGGAC 1260  
1201 CTGAGTGAAGAAACGCTCTCGAAGAGGAGGAGATCATGTAAGCCCGGAATAGGAC 1260  
1261 CTGCTCAAGTGTGCTGAGTGGGCTGCGAGCAATGATCTCCGAATCTGTTGGGATC 1320  
1261 CTGCTCAAGTGTGCTGAGTGGGCTGCGAGCAATGATCTCCGAATCTGTTGGGATC 1320  
1321 CAGCATACGGCCAAATGTCACAAATCAGCCCTGGGAGACACGAGAGGAGAGAC 1380  
1321 CAGCATACGGCCAAATGTCACAAATCAGCCCTGGGAGACACGAGAGGAGAGAC 1380  
1381 AGAGAAAGAAAGAAACACAGCATGAGAAACAGTAAATTAATTAATTAATTTAG 1440  
1381 AGAGAAAGAAAGAAACACAGCATGAGAAACAGTAAATTAATTAATTAATTTAG 1440  
1441 CCGCTCTGCTGCTGCTTACTAGGCGAGAAATGATACCAATTTTCTGAGTGGACTGA 1500  
1441 CCGCTCTGCTGCTGCTTACTAGGCGAGAAATGATACCAATTTTCTGAGTGGACTGA 1500  
1501 CAGCTTCTTTGGCCACAGACAGAGAAATTTAACACTGTTTCAACCCCGGGAGTGG 1560  
1501 CAGCTTCTTTGGCCACAGACAGAGAAATTTAACACTGTTTCAACCCCGGGAGTGG 1560  
1561 CTGTGTTAAAGAAAGACCATTAATCTTTAGACAGTGTAAAAA 1619  
1561 CTGTGTTAAAGAAAGACCATTAATCTTTAGACAGTGTAAAAA 1619

RESULT 4  
US-09-825-294-205  
; Sequence 205, Application US/09825294  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun

```

; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.4845
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-825-294-205

Query Match      100.0%; Score 1619; DB 31; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGCGGATTTCTTCTGCTCCAGGCTTGGCGTGCAGAAATCCAGTGTACCA 60
DB 1 GGCACATTTTGGCGGATTTCTTCTGCTCCAGGCTTGGCGTGCAGAAATCCAGTGTACCA 60
QY 61 GTGTGAAGATTCACAGTCAACAGACAGTCTCTCCCGAGTTTCATTTGTAATGAC 120
DB 61 GTGTGAAGATTCACAGTCAACAGACAGTCTCTCCCGAGTTTCATTTGTAATGAC 120
QY 121 GGTGAAGATTCACAGTCAACAGACAGTCTCTCCCGAGTTTCATTTGTAATGAC 180
DB 121 GGTGAAGATTCACAGTCAACAGACAGTCTCTCCCGAGTTTCATTTGTAATGAC 180
QY 181 CCGCAAGCTCTGTGATCATACAGGCGCTGTCTCATGCTCTGCGGGGTACAGTCCT 240
DB 181 CCGCAAGCTCTGTGATCATACAGGCGCTGTCTCATGCTCTGCGGGGTACAGTCCT 240
QY 241 CTCTCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 300
DB 241 CTCTCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 300
QY 301 CCGGCGCAAGGCGCAAGGAAAGGAAAGTTCGCTCGGCGCTGAGGCGAGGGCTCCG 360
DB 301 CCGGCGCAAGGCGCAAGGAAAGGAAAGTTCGCTCGGCGCTGAGGCGAGGGCTCCG 360
QY 361 CACCATCTCTCTCTCAATTAAGCCCTCTCTGCGACACTGCTGAAGCGTAAGATG 420
DB 361 CACCATCTCTCTCTCAATTAAGCCCTCTCTGCGACACTGCTGAAGCGTAAGATG 420
QY 421 CCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
DB 421 CCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 481 GTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 481 GTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 541 CCTGTCAAAATTAAGAGAGCTCGTAAGAGCATTTGTAATTAATTCAGCTGACTGAAT 600
DB 541 CCTGTCAAAATTAAGAGAGCTCGTAAGAGCATTTGTAATTAATTCAGCTGACTGAAT 600
QY 601 TTTTCAGTATCTTGAAGAGAGAGTGTGAAGAGTTCACCCCATGCTGTGTGAAC 660
DB 601 TTTTCAGTATCTTGAAGAGAGAGTGTGAAGAGTTCACCCCATGCTGTGTGAAC 660
QY 661 CCGAGTCAAGGCGCAGGCTGGAGAGTCACTTGAAGAGTCACTGAGAGTGGCATTCGCC 720
DB 661 CCGAGTCAAGGCGCAGGCTGGAGAGTCACTTGAAGAGTCACTGAGAGTGGCATTCGCC 720
QY 721 TTTTGTAAAGCTCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGACTGAGA 780
DB 721 TTTTGTAAAGCTCAGTGTCCATTCATCCCTGATGGGGCATAGTTTGAAGACTGAGA 780
QY 781 GTGAGAGTACGCTTTCTTGAAGGCTGGAGGCGCATTCGCCACTCAAGGCTCCCTGCTG 840

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DB 781 GTGAGAGTACGCTTTCTTGAAGGCTGGAGGCGCATTCGCCACTCAAGGCTCCCTGCTG 840
QY 841 ACATTTCAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
DB 841 ACATTTCAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
QY 901 CTGAGTGGGCTCTAGTACTGAGACTCAATGACTGAGACTGAGACTGAGACTGAGACTGAG 960
DB 901 CTGAGTGGGCTCTAGTACTGAGACTCAATGACTGAGACTGAGACTGAGACTGAGACTGAG 960
QY 961 CGCTCTGAAAAGTCTTGAAGAAATCTTCTCAGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
DB 961 CGCTCTGAAAAGTCTTGAAGAAATCTTCTCAGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1021 ACAGGAGAGCAAGGCGCTGCAACAAAGCGGCGCTGTGGTGTGGAGTGGGAGTGGAGTGA 1080
DB 1021 ACAGGAGAGCAAGGCGCTGCAACAAAGCGGCGCTGTGGTGTGGAGTGGGAGTGGAGTGA 1080
QY 1081 CCGCAGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
DB 1081 CCGCAGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
QY 1141 ACGAACACCCCGGAACTGCTGAGAGACACCGTGTACAGAGCGGGTGTATACCGAG 1200
DB 1141 ACGAACACCCCGGAACTGCTGAGAGACACCGTGTACAGAGCGGGTGTATACCGAG 1200
QY 1201 CTGAGTGAAGAAACGCTCCGAGAGAGGAGAGAGATCATGTCGCGCGGAGTAGAGAC 1260
DB 1201 CTGAGTGAAGAAACGCTCCGAGAGAGGAGAGAGATCATGTCGCGCGGAGTAGAGAC 1260
QY 1261 CTCTCTCAGTCTGTCTGTGGTGGTGGCGCAGCAGTATCTCTCGAATCTGTTGGGATC 1320
DB 1261 CTCTCTCAGTCTGTCTGTGGTGGTGGCGCAGCAGTATCTCTCGAATCTGTTGGGATC 1320
QY 1321 CAGCATACGCGCAATGTACAAATCAGCCCTGGGAGACAGCGAGGAGGAGAGAC 1380
DB 1321 CAGCATACGCGCAATGTACAAATCAGCCCTGGGAGACAGCGAGGAGGAGAGAC 1380
QY 1381 AGAGAAAGAAAGAAACAGAGATGAGAGACAGTAATTAATTAATTAATTAATTAATTAAT 1440
DB 1381 AGAGAAAGAAAGAAACAGAGATGAGAGACAGTAATTAATTAATTAATTAATTAATTAAT 1440
QY 1441 CCGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1500
DB 1441 CCGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1500
QY 1501 CAGCTCTCTTCTGCAACAGAGAGAGATTAACAGTGTTCACAAACCGGGGGAGTTGG 1560
DB 1501 CAGCTCTCTTCTGCAACAGAGAGAGATTAACAGTGTTCACAAACCGGGGGAGTTGG 1560
QY 1561 CTGTGTTAAAGAACATTAATGCTTTAGACAGTGTAAAGAGAGAGAGAGAGAGAGAGAG 1619
DB 1561 CTGTGTTAAAGAACATTAATGCTTTAGACAGTGTAAAGAGAGAGAGAGAGAGAGAGAG 1619

RESULT 5
US-09-825-294-211
; Sequence 211, Application us/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.4845
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 211
; LENGTH: 1619

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QY 61 GTGTGAAGAAATTCAGCTGTAACCAAGACTGCTCTCCCGAGTTTCATTTGAAATTCAC 120
    |||
Db 61 GTGTGAAGAAATTCAGCTGTAACCAAGACTGCTCTCCCGAGTTTCATTTGAAATTCAC 120
QY 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAAAGTGTGAGCAAGATGCCGGGATCATGTA 180
    |||
Db 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAAAGTGTGAGCAAGATGCCGGGATCATGTA 180
QY 181 CCGCAAGTCTCTGATCATCAGCGGCTGTCTCATCGCTCTGCGGGGTACAGATCTT 240
    |||
Db 181 CCGCAAGTCTCTGATCATCAGCGGCTGTCTCATCGCTCTGCGGGGTACAGATCTT 240
QY 241 CTGCTCCCGAGGAAATGAACTCAAGTTGCAATCAGCTGTCGCAACACCCCTTTTGTAA 300
    |||
Db 241 CTGCTCCCGAGGAAATGAACTCAAGTTGCAATCAGCTGTCGCAACACCCCTTTTGTAA 300
QY 301 CCGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCCAGGGCTCCGCAC 360
    |||
Db 301 CCGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCCAGGGCTCCGCAC 360
QY 361 CAGCATCTCTGTCCTCAATTAATAGCCCTCTCTCGGCAACACTGTAAGTGAAGAGATG 420
    |||
Db 361 CAGCATCTCTGTCCTCAATTAATAGCCCTCTCTCGGCAACACTGTAAGTGAAGAGATG 420
QY 421 CCACCCCTCTCTGATTTCTTCCAGCCCTCGCCCAACCCCTCCCTCCCTGAGTGA 480
    |||
Db 421 CCACCCCTCTCTGATTTCTTCCAGCCCTCGCCCAACCCCTCCCTCCCTGAGTGA 480
QY 481 GTTTCTTCTGGGTGTCTTTTATTTCTGGGTAGGAGCGGGAATCCGTGTCTCTTTTGT 540
    |||
Db 481 GTTTCTTCTGGGTGTCTTTTATTTCTGGGTAGGAGCGGGAATCCGTGTCTCTTTTGT 540
QY 541 CCTGTGCAATATATGAAAGAGCTCGTAAAGATTCGTAATTAATTCAGCTGATGAT 600
    |||
Db 541 CCTGTGCAATATATGAAAGAGCTCGTAAAGATTCGTAATTAATTCAGCTGATGAT 600
QY 601 TTTTCAATATGATTAAGGAAGAGGTGAGTGAAGTTCAACCCCTGCTGTGTAAAC 660
    |||
Db 601 TTTTCAATATGATTAAGGAAGAGGTGAGTGAAGTTCAACCCCTGCTGTGTAAAC 660
QY 661 CCGAGTCAAGGGCAGGCTGGCAGAGTCACTCTTGAAGTCACTAGGAGGCTGCTGCC 720
    |||
Db 661 CCGAGTCAAGGGCAGGCTGGCAGAGTCACTCTTGAAGTCACTAGGAGGCTGCTGCC 720
QY 721 TTTTGAAGCTCTCAGTCTCCATTCATCCCTGATGGGGATGATTTGAGATGACAGA 780
    |||
Db 721 TTTTGAAGCTCTCAGTCTCCATTCATCCCTGATGGGGATGATTTGAGATGACAGA 780
QY 781 GTGAGAGTACGTTTTCTTAGGGCTGAGGGCCAGTTCCCACTCAAGGCTCCCTGCTTG 840
    |||
Db 781 GTGAGAGTACGTTTTCTTAGGGCTGAGGGCCAGTTCCCACTCAAGGCTCCCTGCTTG 840
QY 841 ACATTTCAACTTCATGCTCTCTGAAAACCATTTCTGACACAAATTTGGCTGTTCGCGC 900
    |||
Db 841 ACATTTCAACTTCATGCTCTCTGAAAACCATTTCTGACACAAATTTGGCTGTTCGCGC 900
QY 901 CTGAGTTGGGCTCTAGTCACTGAGACTCAATGACTGGGACTTAAGCTGGGGCTGGGCT 960
    |||
Db 901 CTGAGTTGGGCTCTAGTCACTGAGACTCAATGACTGGGACTTAAGCTGGGGCTGGGCT 960
QY 961 CGCTGTGAAAAGTGTAAAGAAAATCTTCTCAGTTCTCTTCCAGAGAGCATGGCGCGGG 1020
    |||
Db 961 CGCTGTGAAAAGTGTAAAGAAAATCTTCTCAGTTCTCTTCCAGAGAGCATGGCGCGGG 1020
QY 1021 AGCGGAAGCAACGGGCGCTGACAAAGCGGGCGCTGTGCGGTGTGTGAGTGCATGTA 1080
    |||
Db 1021 AGCGGAAGCAACGGGCGCTGACAAAGCGGGCGCTGTGCGGTGTGTGAGTGCATGTA 1080
QY 1081 CCGGCAAGGCTCTCTGCTGTGTGCTGTGCTGACAGACAGGCGGCGACAGACACTTTC 1140
    |||
Db 1081 CCGGCAAGGCTCTCTGCTGTGTGCTGTGCTGACAGACAGGCGGCGACAGACACTTTC 1140
QY 1141 ACGAACACCCCGGAAAGTGTGCGAGGACACCGTGTACAGAGCGGCTTGTGATGACCGAG 1200

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Db 1141 ACGAACACCCCGGAAAGTGTGCGAGGACACCGTGTACAGGAGCGGCTGTGATGACCGAG 1200
QY 1201 CTGAGTAGAAGAAAGCTCTCCGAGAAAGGAGAGAGTCAATGACCGCGGAGTAGAGAC 1260
    |||
Db 1201 CTGAGTAGAAGAAAGCTCTCCGAGAAAGGAGAGAGTCAATGACCGCGGAGTAGAGAC 1260
QY 1261 CTGCTCCAGTCTGCTGGGTTTGGCCGACAGCATATCTCCGAATCTGTGGGCTATC 1320
    |||
Db 1261 CTGCTCCAGTCTGCTGGGTTTGGCCGACAGCATATCTCCGAATCTGTGGGCTATC 1320
QY 1321 CAGCATACGGCAATGTACACAAATACAGCTGCTGGCAGACAGAGCAGAGAGAGAGAC 1380
    |||
Db 1321 CAGCATACGGCAATGTACACAAATACAGCTGCTGGCAGACAGAGCAGAGAGAGAGAC 1380
QY 1381 AGAGAAAAGAAAACACAGCATGGAACAGTAAATGATTAACCATTAATPATTTAG 1440
    |||
Db 1381 AGAGAAAAGAAAACACAGCATGGAACAGTAAATGATTAACCATTAATPATTTAG 1440
QY 1441 CCCCTGTCTGTGTCTTACTGAGCCAGGAAATGTACCAATTTTTCAGTGTGACTTGA 1500
    |||
Db 1441 CCCCTGTCTGTGTCTTACTGAGCCAGGAAATGTACCAATTTTTCAGTGTGACTTGA 1500
QY 1501 CAGCTTCTTTTGCACAGCAGAGAGAAATTAACACTGTTTCAACCCCGGGAGTTGG 1560
    |||
Db 1501 CAGCTTCTTTTGCACAGCAGAGAGAAATTAACACTGTTTCAACCCCGGGAGTTGG 1560
QY 1561 CTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGTAAAAAATTTTAAAAA 1619
    |||
Db 1561 CTGTGTTAAAGAAACCATTAATGCTTTAGACAGTGTAAAAAATTTTAAAAA 1619

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RESULT 7
US-09-970-966-211
; Sequence 211, Application us/09970966
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Filling, Steven P.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970.966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-211

```

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Query Match 100.0%; Score 1619; DB 36; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 GGCACCTTTTGGCGATGTCTCTGCTCCAGGCTTTGGCGTGAATTCAGTCTACCA 60
    |||
Db 1 GGCACCTTTTGGCGATGTCTCTGCTCCAGGCTTTGGCGTGAATTCAGTCTACCA 60
QY 61 GTGTGAAGAAATTCAGCTGTAACCAAGACTGCTCTCCCGAGTTTCATTTGAAATTCAC 120
    |||
Db 61 GTGTGAAGAAATTCAGCTGTAACCAAGACTGCTCTCCCGAGTTTCATTTGAAATTCAC 120
QY 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAAAGTGTGAGCAAGATGCCGGGATCATGTA 180
    |||
Db 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAAAGTGTGAGCAAGATGCCGGGATCATGTA 180
QY 181 CCGCAAGTCTCTGATCATCAGCGGCTGTCTCATCGCTCTGCGGGGTACAGATCTT 240
    |||
Db 181 CCGCAAGTCTCTGATCATCAGCGGCTGTCTCATCGCTCTGCGGGGTACAGATCTT 240

```

QY	241	CTGCTCCAGGAAACGAACTCAGTTTGATAGCTGCTGCAACACCCCTCTTGTA	300
Db	241	CTGCTCCAGGAAACTGAACCTGTTGCATGCTGTGCAACACCCCTCTTGTA	300
QY	301	CGGGCCAAAGCCCAAGAAAAGGGGAAGTTCTGCTCGGCCCTCAGGCCAAGGCTCCGCAC	360
Db	301	CGGGCCAAAGGCCCAAGAAAAGGGGAAGTTGCTCGGCCCTCAGGCCAAGGCTCCGCAC	360
QY	361	CACCAATCCTGTTCCCTCAAAATTAAGCCCTCTTCTCGGCACTGCTGAAGCTGAAGAGATG	420
Db	361	CACCAATCCTGTTCCCTCAAAATTAAGCCCTCTTCTCGGCACTGCTGAAGCTGAAGAGATG	420
QY	421	CCACCCCTCCTGCATGTTGTTCTTCACGCCCTCGGCCCAACCCCCACCTCCCTGAGTA	480
Db	421	CCACCCCTCCTGCATGTTGTTCTTCACGCCCTCGGCCCAACCCCCACCTCCCTGAGTA	480
QY	481	GTTTCTCTGGGTGTCCTTTTATTTCTGGGTAGGAGCGCGGAGTCCGTCTCTTTGTT	540
Db	481	GTTTCTCTGGGTGTCCTTTTATTTCTGGGTAGGAGCGCGGAGTCCGTCTCTTTGTT	540
QY	541	CCTGTGCAAAATATGAAGAAGCCTCGGTAAAGCATTTGATTAATTAATTCAGCTCAGT	600
Db	541	CCTGTGCAAAATATGAAGAAGCCTCGGTAAAGCATTTGATTAATTAATTCAGCTCAGT	600
QY	601	TTTCACTATGTACTTGAAGAAGAGGTGAGTGAAGATTACACCCCATGTCGTGTAAAC	660
Db	601	TTTCACTATGTACTTGAAGAAGAGGTGAGTGAAGATTACACCCCATGTCGTGTAAAC	660
QY	661	CGGAGTCAAGGCGAAGGCTGGCAGAGTAGTACCTTGAAGTCACTGAGAGTGGCATATGCG	720
Db	661	CGGAGTCAAGGCGAAGGCTGGCAGAGTAGTACCTTGAAGTCACTGAGAGTGGCATATGCG	720
QY	721	TTTTGTAAAGCCTCAGTGTCCATTCGCATCCCTGATGGGGGCATAGTTTGAGACTGCA	780
Db	721	TTTTGTAAAGCCTCAGTGTCCATTCGCATCCCTGATGGGGGCATAGTTTGAGACTGCA	780
QY	781	GTAGAGTAGAGTTCCTTCTTGAAGGCTGGAAGGGCCAGTTCCACACTAAGGCTCCCTGCTTG	840
Db	781	GTAGAGTAGAGTTCCTTCTTGAAGGCTGGAAGGGCCAGTTCCACACTAAGGCTCCCTGCTTG	840
QY	841	ACATTCAAACTTCATGCTCCTCGAANAACATTTCTCGACAGATAATGGCTGTTTCGCG	900
Db	841	ACATTCAAACTTCATGCTCCTCGAANAACATTTCTCGACAGATAATGGCTGTTTCGCG	900
QY	901	CTGAGTTGGGCTCTAGTAGTACTCGAGACTCAATAGACTGGGACTTGAAGCTGGGCTCG	960
Db	901	CTGAGTTGGGCTCTAGTAGTACTCGAGACTCAATAGACTGGGACTTGAAGCTGGGCTCG	960
QY	961	CGCTCTGAAGAAGTCTTAAAGAAATCTTTCACGTCCTCGTAGAGAGACTGGGCGCGGG	1020
Db	961	CGCTCTGAAGAAGTCTTAAAGAAATCTTTCACGTTCTCTTGACAGAGACTGGGCGCGGG	1020
QY	1021	ACGCGAAGAGCAACGGGCGCTGCAAAAGCGGGCGCTGTGCGGTGTGAGTCCGATGTA	1080
Db	1021	ACGCGAAGAGCAACGGGCGCTGCAAAAGCGGGCGCTGTGCGGTGTGAGTCCGATGTA	1080
QY	1081	CGCGAGGCGCTTCTGCTGGTGGGCGTGTGACAGCAACGCGGACACAGCACTACTTGC	1140
Db	1081	CGCGAGGCGCTTCTGCTGGTGGGCGTGTGACAGCAACGCGGACACAGCACTACTTGC	1140
QY	1141	ACGAACAACCCGCGAATCTGCTCGAGAGCACCGTGTACAGAGAGCGGATTGATGACAG	1200
Db	1141	ACGAACAACCCGCGAATCTGCTCGAGAGCACCGTGTACAGAGAGCGGATTGATGACAG	1200
QY	1201	CTGAGGTGAAGAAAACGTCCTCCGAGAAAGGAGAGATCATGTACGCCCGGAAGTAGAGAC	1260
Db	1201	CTGAGGTGAAGAAAACGTCCTCCGAGAAAGGAGAGATCATGTACGCCCGGAAGTAGAGAC	1260
QY	1261	CTCCTCAAGTGTACTTGGGTTTGGCGGACCATATCTCCGAAATCTGTTGGGCAATC	1320
Db	1261	CTCCTCAAGTGTACTTGGGTTTGGCGGACCATATCTCTCCGAATCTGTTGGGCAATC	1320
QY	1321	CAGCATACGGGCATGTCTACACAATATGACCTTGGGCGAGACAGAGCAGAGGAGAGAC	1380

Db	1321	CAGCATTACGGCCAAATGTACACACATATAGCCCTGGGCGACACGACACGAGAGGAGAGC	1380
Qy	1381	AGAGAAAAAGAAAAACACAGCATGAGAAACACAGTAAATGATAAAACCATTAATAATTATTTAG	1440
Db	1381	AGAGAAAAAGAAAAACACAGCATGAGAAACACAGTAAATGATAAAACCATTAATAATTATTTAG	1440
Qy	1441	CCCCCTGTTCTGTGCTTTACTGCGCGACAGAAATGTAACCAATTTTTCAGTGTGACATCTGA	1500
Db	1441	CCCCCTGTTCTGTGCTTTACTGCGCGACAGAAATGTAACCAATTTTTCAGTGTGACATCTGA	1500
Qy	1501	CAGCTCTTTTGGCCACAGCAAGCAAGAGAAATTAAACCTTTTCAAAACCCGGGGGAGTTGG	1560
Db	1501	CAGCTCTTTTGGCCACAGCAAGCAAGAGAAATTAAACCTTTTCAAAACCCGGGGGAGTTGG	1560
Qy	1561	CTGTGTTAAAGAAAGACCATTAATGTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAAAAA	1619
Db	1561	CTGTGTTAAAGAAAGACCATTAATGTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAAAAA	1619

```

RESULT 8
US-10-212-677-205
; Sequence 205, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ. ID NOS: 288
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-205

Query Match          100.0%; Score 1619; DB 42; Length 1619;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGGATGTTCTTGCTTCCAGGCTTTGCGCTGCAAAATTCAGTGTCTACCA 60
DB 1 GGCACACTTTTGGCGGATGTTCTTGCTTCCAGGCTTTGCGCTGCAAAATTCAGTGTCTACCA 60

QY 61 GTGGAAGATTCCACCTGACAGACGACGCTCCGCCGAGTTTCATTTGAAATTTGCAC 120
DB 61 GTGTGAAGATTCCACCTGACAGACGACGCTCCGCCGAGTTTCATTTGAAATTTGCAC 120

QY 121 GGTGAACGTTCAAGACATGTGTACAGAAAGAGTGTAGAGCAAGATCCCGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTGTACAGAAAGAGTGTAGAGCAAGATCCCGGATCATGTA 180

QY 181 CCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCGCTTCGCGGATACCAATGCTTT 240
DB 181 CCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCGCTTCGCGGATACCAATGCTTT 240

QY 241 CTGCTCCCAAGGGAACCTGAACCTAGTTTGGATCAGTGTGTGCAACGCCCTTTTGTAA 300
DB 241 CTGCTCCCAAGGGAACCTGAACCTAGTTTGGATCAGTGTGTGCAACGCCCTTTTGTAA 300

QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTTCTGCTCGGACCTTCAGGCGCAGGCGTCCGCAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTTCTGCTCGGACCTTCAGGCGCAGGCGTCCGCAC 360

QY 361 CACCATCTGTTCTCTCAAAATTAGCCCTTCTTGCGGACACTGCTGAAGCTGAAGGAGATG 420
DB 361 CACCATCTGTTCTCTCAAAATTAGCCCTTCTTGCGGACACTGCTGAAGCTGAAGGAGATG 420

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Dp	541	CTGTGCAAAATTAATGAAGAGCTCGTGAAGACATTCGTAATTAATTACAGCTGACTGAAAT	600
Qy	601	TTTTCAGTATGTACTTTGAAGAGAGAGGTGGAGTGAAGATTCAACCCCATGTCTGTGTAAAC	660
Dp	601	TTTTAGATGTACTTTGAAGAGAGAGAGGTGGAGTGAAGATTCAACCCCATGTCTGTGTAAAC	660
Qy	661	CGGAGTCAAGGCCACAGGCTGGCAGAGTGAAGTCACTTAGAAGTCACTGAGAGTGGCATGTGGC	720
Dp	661	CGGAGTCAAGGCCACAGGCTGGCAGAGTGAAGTCACTTAGAAGTCACTGAGAGTGGCATGTGGC	720
Qy	721	TTTTGTAAAGCTTCCAGTGTCCATGTCATCCCTGATGTGGGGCATTAAGTTTGACACTCAAA	780
Dp	721	TTTTGTAAAGCTTCCAGTGTCCATGTCATCCCTGATGTGGGGCATTAAGTTTGACACTCAAA	780
Qy	781	GTGAGAGTGAAGCTTTCTTGAAGGCTGAGAGGCCAGTTCCACATCAAGAGCTCCCTGCTTG	840
Dp	781	GTGAGAGTGAAGCTTTCTTGAAGGCTGAGAGGCCAGTTCCACATCAAGAGCTCCCTGCTTG	840
Qy	841	ACATTCAAACTTCAATGCTCTGAAAAACCAATCTCTGCAAGCAGAAATTGGCTGTTTGCGGC	900
Dp	841	ACATTCAAACTTCAATGCTCTGAAAAACCAATCTCTGCAAGCAGAAATTGGCTGTTTGCGGC	900
Qy	901	CTGAGTTGGGCTCTAATGTACTCCAGACTCAATGATGTGGACTTAAGACTGGGGCTCGGGCT	960
Dp	901	CTGAGTTGGGCTCTAATGTACTCCAGACTCAATGATGTGGACTTAAGACTGGGGCTCGGGCT	960
Qy	961	CGCTCTGAAAAGTGCTTAAGAAAATCTTCTCAGTTCTCTTGTGAGAGAGATGTGGCGCGGG	102
Dp	961	CGCTCTGAAAAGTGCTTAAGAAAATCTTCTCAGTTCTCTTGTGAGAGAGATGTGGCGCGGG	102
Qy	1021	ACGCGAAGACGACACGGGCGCTGACCAAAAGGGGCGCTGTGGGTGTGTGAATGGCGCATGTA	108
Dp	1021	ACGCGAAGACGACACGGGCGCTGACCAAAAGGGGCGCTGTGGGTGTGTGAATGGCGCATGTA	108
Qy	1081	CGCGCAGCGCTTCTCGTGGTGTGGCGTGTGACGACGACAGCGGACACAGCACTTGGC	114
Dp	1081	CGCGCAGCGCTTCTCGTGGTGTGGCGTGTGACGACGACAGCGGACACAGCACTTGGC	114
Qy	1141	ACGAACACCCCGCAAACTGCTCGAGAGACACCGTGTACAGAGACGGGGTTGATGCCGAG	120
Dp	1141	ACGAACACCCCGCAAACTGCTCGAGAGACACCGTGTACAGAGACGGGGTTGATGCCGAG	120
Qy	1201	CTGAGGTGAAGAAAACGTCTCCGAGAAGGGGAGAGATCATGTACGCGCGGAAGTGAAGAC	126
Dp	1201	CTGAGGTGAAGAAAACGTCTCCGAGAAGGGGAGAGATCATGTACGCGCGGAAGTGAAGAC	126
Qy	1261	CTCGTCAAGTGTGTGGGTTTGGCCGCAACATGATCTCCGAAATCTGTGGTGGCATC	132
Dp	1261	CTCGTCAAGTGTGTGGGTTTGGCCGCAACATGATCTCCGAAATCTGTGGTGGCATC	132
Qy	1321	CAGCATACGGGCATGTGCACAACAATCAGCCCTGGGAGACAGAGCAGAGAGGGAAGGAC	138
Dp	1321	CAGCATACGGGCATGTGCACAACAATCAGCCCTGGGAGACAGAGCAGAGAGGGAAGGAC	138
Qy	1381	AGAGAAAAGAAAACACAGCATGAGAACACAGTAAATGAATTAAAACCATAAATATTTAG	144
Dp	1381	AGAGAAAAGAAAACACAGCATGAGAACACAGTAAATGAATTAAAACCATAAATATTTAG	144
Qy	1441	CCCCTCTGTCTGTGTCTTACTGGCCAGGAAATGTTACCAATTTTTCAGTGTGGACTTGA	150
Dp	1441	CCCCTCTGTCTGTGTCTTACTGGCCAGGAAATGTTACCAATTTTTCAGTGTGGACTTGA	150
Qy	1501	CAGCTTCTTTTGCACAAGCAAGAGAGAAATTAACTGTTTCAAAACCGGGGGAGTTGG	156
Dp	1501	CAGCTTCTTTTGCACAAGCAAGAGAGAAATTAACTGTTTCAAAACCGGGGGAGTTGG	156
Qy	1561	CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTTTTTTTT	1619
Dp	1561	CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTTTTTTTT	1619



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Oy 721 TTTTGTAAAGCCTCAGTGTCCATTCATCCCTGATGGGGGAGTGTGAGTGCAGA 780
    |||||
Db 1000 TTTTGTAAAGCCTCAGTGTCCATTCATCCCTGATGGGGGAGTGTGAGTGCAGA 1059
Oy 781 GTGAGAGTGCAGTGTCTTCTAGGGCTGGAGGGCCAGTTCCTCACTAAGGCTCCCTGCTTG 840
    |||||
Db 1060 GTGAGAGTGCAGTGTCTTCTAGGGCTGGAGGGCCAGTTCCTCACTAAGGCTCCCTGCTTG 1119
Oy 841 ACATTCAAACCTCATGCTCCGTAACCAATCTCTGACGAGAAATGGCTGTTTGGCG 900
    |||||
Db 1120 ACATTCAAACCTCATGCTCCGTAACCAATCTCTGACGAGAAATGGCTGTTTGGCG 1179
Oy 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGGCT 960
    |||||
Db 1180 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGGCT 1239
Oy 961 CGCTGTGAAAGTGTCTTAAAGAAATCTTCTCAATCTCTCTTGCAGAGAGTGGCGCGG 1020
    |||||
Db 1240 CGCTGTGAAAGTGTCTTAAAGAAATCTTCTCAATCTCTCTTGCAGAGAGTGGCGCGG 1299
Oy 1021 ACGGGAAGAGCAAGGGGGGCTGCACAAAGGGGGGCTGCTGGTGGTGGAGTGGCGATGA 1080
    |||||
Db 1300 ACGGGAAGAGCAAGGGGGGCTGCACAAAGGGGGGCTGCTGGTGGTGGAGTGGCGATGA 1359
Oy 1081 CGCGCAGGCGCTTCTCTGTGTGGCTGTGCAGCAGCAGGCGGCGACACAGCAGCCTTGC 1140
    |||||
Db 1360 CGCGCAGGCGCTTCTCTGTGTGGCTGTGCAGCAGCAGGCGGCGACACAGCAGCCTTGC 1418
Oy 1141 ACGAAGACCCCGGAACTGCTGCGAGAGACACCGTGTACAGAGGCGGTTGATGACCGAG 1200
    |||||
Db 1419 ACGAAGACCCCGGAACTGCTGCGAGAGACACCGTGTGTACAGAGGCGGTTGATGACCGAG 1478
Oy 1201 CTGAGTGAAGAAAGCTCTCCGAGAAAGGGAGAGATCATGTACGCCGGAAGTAGAGAC 1260
    |||||
Db 1479 CTGAGTGAAGAAAGCTCTCCGAGAAAGGGAGAGATCATGTACGCCGGAAGTAGAGAC 1538
Oy 1261 CTGCTGCAGTCTGCTGGTGGTGGCTGCGCAGCAGCATGATCTCTCCGAATCTGTTGGGCTATC 1320
    |||||
Db 1539 CTGCTGCAGTCTGCTGGTGGTGGCTGCGCAGCAGCATGATCTCTCCGAATCTGTTGGGCTATC 1598
Oy 1321 CAGCATACGGCCCAATGTCAACATCATCAGCCCTGGGCGAGACACGAGAGGAGGAGAAC 1380
    |||||
Db 1599 CAGCATACGGCCCAATGTCAACATCATCAGCCCTGGGCGAGACACGAGAGGAGGAGAAC 1658
Oy 1381 AAGAGAAAGAAAGAAAGACAGCATGAGAAACAGATTAATGAATTAATTAATTAATTAAT 1440
    |||||
Db 1659 AAGAGAAAGAAAGAAAGACAGCATGAGAAACAGATTAATGAATTAATTAATTAATTAAT 1718
Oy 1441 CCCCTCTGTTCTGTCTACTGCGCAGAGAAATGTAACCAATTTTTCAGTGTGAGCTTGA 1500
    |||||
Db 1719 CCCCTCTGTTCTGTCTACTGCGCAGAGAAATGTAACCAATTTTTCAGTGTGAGCTTGA 1778
Oy 1501 CAGCTCTCTTGGCCCAAGCAGAGAGAAATTAACACCTTTCANACCCGGGGGAGTGG 1560
    |||||
Db 1779 CAGCTCTCTTGGCCCAAGCAGAGAGAAATTAACACCTTTCANACCCGGGGGAGTGG 1838
Oy 1561 CTGTGTAAAGAAAGACATTAATGCTTGTAGACAGTGTAAAGAAAGAAAGAAAGAAAG 1619
    |||||
Db 1839 CTGTGTAAAGAAAGACATTAATGCTTGTAGACAGTGTAAAGAAAGAAAGAAAGAAAG 1897

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RESULT 11
US-09-825-294-214
: Sequence 214, Application us/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825.294

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: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1897)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

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Query Match          99.2%; Score 1606.2; DB 31; Length 1897;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Oy 1 GGCACATTTTGGCGGATGTCTTCTTCCAGGCTTTGGCTCAAAATCCAGTGTACCA 60
    |||||
Db 280 GGCACATTTTGGCGGATGTCTTCTTCCAGGCTTTGGCTCAAAATCCAGTGTACCA 339
Oy 61 GTGTGAAGATTCAGCTGAACAAAGCACTCTCCCGGAGTTCATGTGAATGGAC 120
    |||||
Db 340 GTGTGAAGATTCAGCTGAACAAAGCACTCTCCCGGAGTTCATGTGAATGGAC 399
Oy 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
    |||||
Db 400 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 459
Oy 181 CCGCAAGTCTGTGCATCATACAGCGGCTGTCTCATCTGCTCGCGGGTACCAATGCTT 240
    |||||
Db 460 CCGCAAGTCTGTGCATCATACAGCGGCTGTCTCATCTGCTCGCGGGTACCAATGCTT 519
Oy 241 CTGCTCCCGAGGGAAGCACTGATTCATACAGTGTGATGATGATGATGATGATGATGAT 300
    |||||
Db 520 CTGCTCCCGAGGGAAGCACTGATTCATACAGTGTGATGATGATGATGATGATGATGAT 579
Oy 301 CGGGCAAGGCGCCAAAGAAAGGGGAAGTTCGCTCGGCCCTCAGGCGAGGCTCCGAC 360
    |||||
Db 580 CGGGCAAGGCGCCAAAGAAAGGGGAAGTTCGCTCGGCCCTCAGGCGAGGCTCCGAC 639
Oy 361 CACCATCTGTCTCTCAAAATTAAGCCCTTCTGCGCACACTGCTGAAGCTGAAGAGATG 420
    |||||
Db 640 CACCATCTGTCTCTCAAAATTAAGCCCTTCTGCGCACACTGCTGAAGCTGAAGAGATG 699
Oy 421 CCACCCCTCTGATGTTCTTCCAGCCCTCGGCCCAACCCGCCACCTCCCTGAGTGA 480
    |||||
Db 700 CCACCCCTCTGATGTTCTTCCAGCCCTCGGCCCAACCCGCCACCTCCCTGAGTGA 759
Oy 481 GTTCTCTTGGGCTGCTTCTTATCTGGGTAAGGAGCGGAGTCCGTTCTCTTGTGT 540
    |||||
Db 760 GTTCTCTTGGGCTGCTTCTTATCTGGGTAAGGAGCGGAGTCCGTTCTCTTGTGT 819
Oy 541 CCTGTGCAATTAATGAAGAGCTCGGTAAGACATTCATTAATTAATTAAGCTGACTAAT 600
    |||||
Db 820 CCTGTGCAATTAATGAAGAGCTCGGTAAGACATTCATTAATTAATTAAGCTGACTAAT 879
Oy 601 TTTGAGTATGACTTGAAGAGAGGAGGAGTGAAGATTCACCCCATGCTGTGTAAAC 660
    |||||
Db 880 TTTGAGTATGACTTGAAGAGAGGAGGAGTGAAGATTCACCCCATGCTGTGTAAAC 939
Oy 661 CGGAGTCAAGGCGAGGCTGCGAGAGTCACTCTTGAAGTCACTGAGTGGGCAATTCGCC 720
    |||||
Db 940 CGGAGTCAAGGCGAGGCTGCGAGAGTCACTCTTGAAGTCACTGAGTGGGCAATTCGCC 999
Oy 721 TTTTGTAAAGCCTCAGTGTCCATTCATCCCTGATGGGGGAGTGTGAGTGCAGA 780
    |||||
Db 1000 TTTTGTAAAGCCTCAGTGTCCATTCATCCCTGATGGGGGAGTGTGAGTGCAGA 1059
Oy 781 GTGAGAGTGCAGTGTCTTCTAGGGCTGGAGGGCCAGTTCCTCACTAAGGCTCCCTGCTTG 840
    |||||
Db 1060 GTGAGAGTGCAGTGTCTTCTAGGGCTGGAGGGCCAGTTCCTCACTAAGGCTCCCTGCTTG 1119

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QY 841 ACATTCAACTTCATCTCTCTGAAAAACATTCCTGACAGCAATTCGCTGCTTCGCGC 900
    |||||||
Db 1120 ACATTCAACTTCATCTCTCTGAAAAACATTCCTGACAGCAATTCGCTGCTTCGCGC 1179
QY 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGAGCTTGAAGTGGGCTCGGCT 960
    |||||||
Db 1180 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGAGCTTGAAGTGGGCTCGGCT 1239
QY 961 CGCTGAAAAAGTCTTAGAAAAATCTCTCAATCTCTCTGACAGCAATTCGCTGCTTCG 1020
    |||||||
Db 1240 CGCTGAAAAAGTCTTAGAAAAATCTCTCAATCTCTCTGACAGCAATTCGCTGCTTCG 1299
QY 1021 ACAGCAAGAGCAACGGGCGCTGCACAAAGCGGCGCTGTGCTGGTGGAGTGCATGTA 1080
    |||||||
Db 1300 ACAGCAAGAGCAACGGGCGCTGCACAAAGCGGCGCTGTGCTGGTGGAGTGCATGTA 1359
QY 1081 CGGCGAGGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
    |||||||
Db 1360 CGGCGAGGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
QY 1141 ACAGCAACCCCGCGCAAACTGCTGCGAGACACGCTGTACAGAGGCGGCTTGAACCGAG 1200
    |||||||
Db 1419 ACAGCAACCCCGCGCAAACTGCTGCGAGACACGCTGTGTACAGAGGCGGCTTGAACCGAG 1478
QY 1201 CTGAGCTAGAAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCGGAAGTAGAGAC 1260
    |||||||
Db 1479 CTGAGCTAGAAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCGGAAGTAGAGAC 1538
QY 1261 CTGCTGCAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
    |||||||
Db 1539 CTGCTGCAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1598
QY 1321 CAGCATATCGGCGCAATGTCAACAACATCAACCCCTGGGCGAGACAGCAGAGAGAGAGAC 1380
    |||||||
Db 1599 CAGCATATCGGCGCAATGTCAACAACATCAACCCCTGGGCGAGACAGCAGAGAGAGAGAC 1658
QY 1381 AAGAAAAAAGAAAAACACAGCATGAGAACAGTAATGATTAATCAATTAATATTTAG 1440
    |||||||
Db 1659 AAGAAAAAAGAAAAACACAGCATGAGAACAGTAATGATTAATCAATTAATATTTAG 1718
QY 1441 CCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
    |||||||
Db 1719 CCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1778
QY 1501 CAGCTCTCTTTCGCAACAAGAGAGAGATTTAACACTGTTTCAAAACCCGGGGAGTTGG 1560
    |||||||
Db 1779 CAGCTCTCTTTCGCAACAAGAGAGAGATTTAACACTGTTTCAAAACCCGGGGAGTTGG 1838
QY 1561 CTGCTTTAAAGAAACCATTTAATGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAAA 1619
    |||||||
Db 1839 CTGCTTTAAAGAAACCATTTAATGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAAA 1897

```

## RESULT 12

```

US-09-970-966-214
: Sequence 214, Application US/09/970966
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesth, David Alan
: APPLICANT: Filing, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.4846
: CURRENT APPLICATION NUMBER: US/09/970,966
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-970-966-214

```

Query Match 99.28; Score 1606.2; DB 36; Length 1897;  
 Best Local Similarity 99.88; Pred. No. 0;  
 Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```

QY 1 GGCACATTTTGGGATTTGTTCTTGTCTCCAGGCTTTGGCGGTGCAATTCAGTGTCCCA 60
    |||||||
Db 280 GGCACATTTTGGGATTTGTTCTTGTCTCCAGGCTTTGGCGGTGCAATTCAGTGTCCCA 339
QY 61 GTGTGAAGAAATTCACGCTGAAACAAGACTGCTCTCCCGGAGTTCAATTTGAATTCAC 120
    |||||||
Db 340 GTGTGAAGAAATTCACGCTGAAACAAGACTGCTCTCCCGGAGTTCAATTTGAATTCAC 399
QY 121 GGTGAGCTTTCAGACATGTGTGCAAAAAGATGATGAGCAAAAGTCCCGGATCATGTA 180
    |||||||
Db 400 GGTGAGCTTTCAGACATGTGTGCAAAAAGATGATGAGCAAAAGTCCCGGATCATGTA 459
QY 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATGCTCTGCGGATACAGTCTT 240
    |||||||
Db 460 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATGCTCTGCGGATACAGTCTT 519
QY 241 CTGCTCCCGAGGAACTGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 300
    |||||||
Db 520 CTGCTCCCGAGGAACTGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 579
QY 301 CGGGCCAAAGGCGCAAGAAAGGGAAGTTGCTGCTGCGGCTGACAGGCAAGGCTCCGAC 360
    |||||||
Db 580 CGGGCCAAAGGCGCAAGAAAGGGAAGTTGCTGCTGCGGCTGACAGGCAAGGCTCCGAC 639
QY 361 CACCATCTGCTCTCAATTAATGACCTCTTCTGCGCACACTGCTGTAAGTGAAGAGATG 420
    |||||||
Db 640 CACCATCTGCTCTCAATTAATGACCTCTTCTGCGCACACTGCTGTAAGTGAAGAGATG 699
QY 421 CCACCCCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
    |||||||
Db 700 CCACCCCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 759
QY 481 GTTCTCTGCGGCTGCTCTTATCTGCTGAGGAGGAGGAGTCCGCTCTTCTTGTGTT 540
    |||||||
Db 760 GTTCTCTGCGGCTGCTCTTATCTGCTGAGGAGGAGGAGTCCGCTCTTCTTGTGTT 819
QY 541 CTGTGCAAAATATGAAGAGCTGCTGTAAGACATTCGTAATTAATTCAGCTGATGAT 600
    |||||||
Db 820 CTGTGCAAAATATGAAGAGCTGCTGTAAGACATTCGTAATTAATTCAGCTGATGAT 879
QY 601 TTTCAGTATGACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATGTCTGTATAC 660
    |||||||
Db 880 TTTCAGTATGACTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATGTCTGTATAC 939
QY 661 CGGAGTCAAGGCGAGGCTGCGACAGTCACTCTTAAGAGTCACTGAAGTGGGATCTGCC 720
    |||||||
Db 940 CGGAGTCAAGGCGAGGCTGCGACAGTCACTCTTAAGAGTCACTGAAGTGGGATCTGCC 999
QY 721 TTTTGTAAAGCTTCACAGTCTTCATTCATCCGTGATGGGGCATTTTGAAGTCTGACA 780
    |||||||
Db 1000 TTTTGTAAAGCTTCACAGTCTTCATTCATCCGTGATGGGGCATTTTGAAGTCTGACA 1059
QY 781 GTGAGAGTACGTTTCTTGAAGGCTGAGGCGAGTTCACATCAAGGCTCCCTGCTGG 840
    |||||||
Db 1060 GTGAGAGTACGTTTCTTGAAGGCTGAGGCGAGTTCACATCAAGGCTCCCTGCTGG 1119
QY 841 ACATTCAACTTCATGCTCTGAAAAACATTCCTGACAGAGAAATGCGTGTTCGCGC 900
    |||||||
Db 1120 ACATTCAACTTCATGCTCTGAAAAACATTCCTGACAGAGAAATGCGTGTTCGCGC 1179
QY 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGAGCTTGAAGTGGGCTCGGCT 960
    |||||||
Db 1180 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGAGCTTGAAGTGGGCTCGGCT 1239
QY 961 CGCTGAAAAAGTCTTAGAAAAATCTCTCAATCTCTCTGACAGCAATTCGCTGCTTCG 1020
    |||||||
Db 1240 CGCTGAAAAAGTCTTAGAAAAATCTCTCAATCTCTCTGACAGCAATTCGCTGCTTCG 1299

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Oy	1021	ACGCCAAGAGCAACGGGGCGTCACAAAAGCGGGCGCTGTCGGGTGGAGATCCGATGTA	1080
Oy	1300	ACGCCAAGAGCAACGGGGCGCTGTCACAAAAGCGGGCGCTGTCGGGTGGAGATCCGATGTA	1359
Oy	1081	CGCGCAGGCGCTCTTCGTGTTGGCGTGCAGCGACAGGCGGCAGCAGCACACTTGC	1140
Db	1360	CGCGCAGGCGCTCTTCGTGTTGGCGTGCAGCGACAGGCGGCAGCAGCACACTTGC	1418
Oy	1141	ACGAACACCCCGCGGAAATGCTGTCGAGAGACACCCTGTATACAGAGCGGGTGTATGACCGAG	1200
Db	1419	ACGAACACCCCGCGGAAATGCTGTCGAGAGACACCCTGTATACAGAGCGGGTGTATGACCGAG	1478
Oy	1201	CTGAGGTAGAAAACGTCCTCCGAGAAAGGAGAGAGATCATGTATACGCCCGAAGTAAAGAC	1260
Db	1479	CTGAGGTAGAAAACGTCCTCCGAGAAAGGAGAGAGATCATGTATACGCCCGAAGTAAAGAC	1538
Oy	1261	CTCTGTCAGTCGTCGTTGGGTTTGGCCGACGCATGATCTTCGAAATCTGTTGGGCATC	1320
Db	1539	CTCTGTCAGTCGTCGTTGGGTTTGGCCGACGCATGATCTTCGAAATCTGTTGGGCATC	1598
Oy	1321	CAGCATACGGCCAAATGTCAACACATTCAGCCCTGGGGCAGACACGAGAGAGAGAGAC	1380
Db	1599	CAGCATACGGCCAAATGTCAACACATTCAGCCCTGGGGCAGACACGAGAGAGAGAGAC	1658
Oy	1381	AGAGAAAAGAAAACACACAGCATGAGAACACAGTAATGAATAAACCAATAAATATTAG	1440
Db	1659	AGAGAAAAGAAAACACACAGCATGAGAACACAGTAATGAATAAACCAATAAATATTAG	1718
Oy	1441	CCCCTCTGTTCTGTGCTTACTGCGCCAGGAATGTATACCAATTTTTCAGTGTGACTTGA	1500
Db	1719	CCCCTCTGTTCTGTGCTTACTGCGCCAGGAATGTATACCAATTTTTCAGTGTGACTTGA	1778
Oy	1501	CAGCTTCTTTTCCCAACAGCAGAGAGAAATTAACACTGTTCCAAACCGGGGAGCTGG	1560
Db	1779	CAGCTTCTTTTCCCAACAGCAGAGAGAAATTAACACTGTTCCAAACCGGGGAGCTGG	1838
Oy	1561	CTGTGTTAAAGAAAGCATTAAATGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAAA	1619
Db	1839	CTGTGTTAAAGAAAGCATTAAATGCTTTAGACAGTGTAAAAAAGAAAAAAGAAAAA	1897
RESULT 13			
US-10-212-677-214			
: Sequence 214, Application US/10212677			
: GENERAL INFORMATION:			
: APPLICANT: Chenuault, Ruth A.			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Harlocker, Susan L.			
: APPLICANT: McNeill, Patricia D.			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
: FILE REFERENCE: 210121.484C7			
: CURRENT APPLICATION NUMBER: US/10/212.677			
: CURRENT FILING DATE: 2002-08-02			
: NUMBER OF SEQ ID NOS: 288			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 214			
: LENGTH: 1897			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
US-10-212-677-214			





Qy	901	CTGAGTTGGGCTCTAGACTCCGAGCTCAATATACAGTGGACTTACAGCTGGGCTCGGGCT	960
Db	1136	CTGAGTTGGGCTCTAGACTCCGAGCTCAATATACAGTGGACTTACAGCTGGGCTCGGGCT	12555
Qy	961	CGCTCTGAAAAGTGCCTTAAAGAAAATCTTCTCAGTTCTCCTTGACAGAGACTGGCCCGGG	1020
Db	1256	CGCTCTGAAAAGTGCCTTAAAGAAAATCTTCTCAGTTCTCCTTGACAGAGACTGGCCCGGG	1315
Qy	1021	ACGGGAAGAGCAACGGGCGGTGCACAAAGGGGCGGTGTCGGTGGGAGTCCGATGTA	1080
Db	1316	ACGGGAAGAGCAACGGGCGGTGCACAAAGGGGCGGTGTCGGTGGGAGTCCGATGTA	1375
Qy	1081	CGCGCAGGCGCTTCTCGTGGTTGGCGTGTGCAGCACAGGGGCGAGCACAGACCTTGC	1140
Db	1376	CGCGCAGGCGCTTCTCGTGGTTGGCGTGTGCAGCACAGGGGCGAGCACAGACCTTGC	1434
Qy	1141	ACGAAACACCCGCGCAACCTCTCCGAGAGACACCTGTACAGAGAGGGGTTGATACCGAG	1200
Db	1435	ACGAAACACCCGCGCAACCTCTCCGAGAGACACCTGTACAGAGAGGGGTTGATACCGAG	1494
Qy	1201	CTGAGGTAGAAAAACGTCTCCGAGAGGGGAGAGATCATGTACGCCCGGAATGAGAGAC	1260
Db	1495	CTGAGGTAGAAAAACGTCTCCGAGAGGGGAGAGATCATGTACGCCCGGAATGAGAGAC	1554
Qy	1261	CTGCTCCAGTCTGCTTGGGTTTGGCCGACACCATATCTCCGAATCTGTTGGGCATC	1320
Db	1555	CTGCTCCAGTCTGCTTGGGTTTGGCCGACACCATATCTCCGAATCTGTTGGGCATC	1614
Qy	1331	CAGCATACGGCATAATGTACAAACAATCAGGCCCTGGGCAACAGAGCAGAGGAGGAGAAC	1380
Db	1615	CAGCATACGGCATAATGTACAAACAATCAGGCCCTGGGCAACAGAGCAGAGGAGGAGAAC	1674
Qy	1381	AGAGAAAAGAAAAACACAGCATGAGAACACAGTAAATGAAATAAACCATAAATATTTAG	1440
Db	1675	AGAGAAAAGAAAAACACAGCATGAGAACACAGTAAATGAAATAAACCATAAATATTTAG	1734
Qy	1441	CCGCTCGTTCTGTGCTTACTGTGCGCAGGAAATGGTACCAATTTTCAGTGTGGACTGA	1500
Db	1735	CCGCTCGTTCTGTGCTTACTGTGCGCAGGAAATGGTACCAATTTTCAGTGTGGACTGA	1794
Qy	1501	CAGCTTCTTTGGCACAAGCAGAGAGAAATTTAACACTTTTCAAAACCGGGGAGTTGG	1560
Db	1795	CAGCTTCTTTGGCACAAGCAGAGAGAAATTTAACACTTTTCAAAACCGGGGAGTTGG	1854
Qy	1561	CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATAAAAAA	1609
Db	1855	CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATAAAAAA	1903

Search completed: November 7, 2002, 17:54:32  
Job time : 3636.85 secs

383

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 10:10:48 ; Search time 45.2315 Seconds  
(without alignments)  
3937.596 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619

Sequence: 1 ggcacatttgcgattgt.....aaaaaaaaaaaaaaaaaaaaa 1619

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 193892 seqs, 55004114 residues

Total number of hits satisfying chosen parameters: 387784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/pna/US00\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1373	84.8	1524	6	US-10-230-437-15
2	40.6	2.5	2196	6	US-10-270-333-38
3	40.6	2.5	6472	6	US-10-270-333-37
4	38.8	2.4	667	7	US-60-416-172-67
5	34.8	2.1	990	6	US-10-270-333-116
6	34.8	2.1	5927	6	US-10-270-333-115
7	34.6	2.1	15825	6	US-10-240-485-111
8	34.6	2.1	135259	6	US-10-240-485-1585
9	34.4	2.1	1024	6	US-10-270-377-1
10	34.4	2.1	1201	6	US-10-240-425-334
11	34	2.1	18331	6	US-10-267-255-96
12	33.2	2.1	4902	6	US-10-267-255-76
13	33.2	2.1	23683	6	US-10-270-333-193
14	33.2	2.1	2158	6	US-10-240-485-176
15	33	2.0	2158	6	US-10-264-237-1277
16	33	2.0	2706	1	PCT-US02-33408-3
17	33	2.0	2845	6	US-10-131-813A-207
18	33	2.0	2845	6	US-10-131-819A-207
19	33	2.0	2845	6	US-10-131-823A-207
20	33	2.0	2845	6	US-10-131-824A-207
21	33	2.0	2845	6	US-10-131-826A-207
22	33	2.0	2845	6	US-10-131-829A-207
23	33	2.0	2845	6	US-10-125-926A-207
24	33	2.0	2845	6	US-10-127-829A-207
25	33	2.0	2845	6	US-10-127-831A-207
26	33	2.0	2845	6	US-10-127-835A-207

27	33	2.0	2845	6	US-10-127-837A-207	Sequence 207, App
28	33	2.0	2845	6	US-10-127-842A-207	Sequence 207, App
29	33	2.0	2845	6	US-10-127-850A-207	Sequence 207, App
30	33	2.0	2845	6	US-10-127-901A-207	Sequence 207, App
31	33	2.0	2845	6	US-10-128-689A-207	Sequence 207, App
32	33	2.0	2845	6	US-10-131-830A-207	Sequence 207, App
33	33	2.0	2845	6	US-10-131-833A-207	Sequence 207, App
34	33	2.0	2845	6	US-10-131-837A-207	Sequence 207, App
35	33	2.0	2845	6	US-10-125-930A-207	Sequence 207, App
36	33	2.0	2845	6	US-10-127-825A-207	Sequence 207, App
37	33	2.0	2845	6	US-10-127-838B-207	Sequence 207, App
38	33	2.0	2845	6	US-10-127-843A-207	Sequence 207, App
39	33	2.0	2845	6	US-10-127-849A-207	Sequence 207, App
40	33	2.0	2845	6	US-10-128-684A-207	Sequence 207, App
41	33	2.0	2845	6	US-10-128-685A-207	Sequence 207, App
42	33	2.0	2845	6	US-10-128-686A-207	Sequence 207, App
43	33	2.0	2845	6	US-10-128-690A-207	Sequence 207, App
44	33	2.0	2845	6	US-10-128-693A-207	Sequence 207, App
45	33	2.0	2845	6	US-10-131-821A-207	Sequence 207, App

## ALIGNMENTS

RESULT 1  
US-10-230-437-15  
Sequence 15, Application US/10230437  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P350P1C94  
CURRENT FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-230-437-15  
Query Match 84.8%; Score 1373; DB 6; Length 1524;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 GGCACATTTTTCGCGATTTCTTCCAGGCTTGGCGTCAAAATCCAGTCTACCA 60
Db 141 GGCACATTTTTCGCGATTTCTTCCAGGCTTGGCGTCAAAATCCAGTCTACCA 200
QY 61 GTGTGAAGAAATTCACAGTCTGCTCTCCCGGATTCATTGTGAATTTGAC 120
Db 201 GTGTGAAGAAATTCACAGTCTGCTCTCCCGGATTCATTGTGAATTTGAC 260
QY 121 GGTGAAGCTTCAAGACATGTCTCAGAAAGATGTGAGCAAAATGGCGGATCATGTA 180
Db 261 GGTGAAGCTTCAAGACATGTCTCAGAAAGATGTGAGCAAAATGGCGGATCATGTA 320
QY 181 CGCAGATCTCTGCATCATCAGCGGCTGTCTCATCGCTCTGCGGGTACCACTCTT 240
Db 321 CGCAGATCTCTGCATCATCAGCGGCTGTCTCATCGCTCTGCGGGTACCACTCTT 380
QY 241 CTGCTCCCGAGGAAATCACTCACTGATTTGCATCAGCTGCTCAACACCCCTTTGTGA 300
Db 381 CTGCTCCCGAGGAAATCACTCACTGATTTGCATCAGCTGCTCAACACCCCTTTGTGA 440
QY 301 CGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGCTCCGAC 360
Db 441 CGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGCTCCGAC 500
QY 361 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTTCGCGACACTGTGAAGTGAAGATG 420
Db 501 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTTCGCGACACTGTGAAGTGAAGATG 560
QY 421 CCACCCCTCTGCTGATTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGATGGA 480
Db 561 CCACCCCTCTGCTGATTTCTTCCAGCCCTGCGCCCAACCCCACTCCCTGATGGA 620
QY 481 GTTTCCTTGGGCTCTCTTTTATTTGCGGTAGGAGCGGAGTCCGTTCTCTTTGTT 540
Db 621 GTTTCCTTGGGCTCTCTTTTATTTGCGGTAGGAGCGGAGTCCGTTCTCTTTGTT 680
QY 541 CCTGTCCAAATAATGAAGAAGCTCGGTAAAGCAATTTCTGAATTAATTCAGCTGACTGAAT 600
Db 681 CCTGTCCAAATAATGAAGAAGCTCGGTAAAGCAATTTCTGAATTAATTCAGCTGACTGAAT 740
QY 601 TTTCACTATGTAAGTGAAGAAGAGTGAAGTGAAGTCAACCCCATGCTGTGTATAC 660
Db 741 TTTCACTATGTAAGTGAAGAAGAGTGAAGTGAAGTCAACCCCATGCTGTGTATAC 800
QY 661 CGGAGTCAAGGCGGCTGCGAGAGTCACTCTTGAAGTCACTGAGTGGGCATCTGCC 720
Db 801 CGGAGTCAAGGCGGCTGCGAGAGTCACTCTTGAAGTCACTGAGTGGGCATCTGCC 860
QY 721 TTTTGTAAAGCTCCAGTGTCCATTTCCATTCCTGATGGGGGCAATGTTGAAGTGCAGA 780
Db 861 TTTTGTAAAGCTCCAGTGTCCATTTCCATTCCTGATGGGGGCAATGTTGAAGTGCAGA 920
QY 781 GTGAGAGTACGTTTCTTAAAGGCTGGAGGCGAGTTCACACTCAAGAGTCCCTGCTG 840
Db 921 GTGAGAGTACGTTTCTTAAAGGCTGGAGGCGAGTTCACACTCAAGAGTCCCTGCTG 980
QY 841 ACATTCAAACTTCATCTCTGAAAAACATTTCTGACAGACAGAAATTTGGCTTTCGCGC 900
Db 981 ACATTCAAACTTCATCTCTGAAAAACATTTCTGACAGACAGAAATTTGGCTTTCGCGC 1040
QY 901 CTGAGTTGGGCTCTAGTGCATGAGACTCAATGACTGGGACTTAACTGAGGCTGCGCT 960
Db 1041 CTGAGTTGGGCTCTAGTGCATGAGACTCAATGACTGGGACTTAACTGAGGCTGCGCT 1100
QY 961 CGCTTGAAAAGTGTAAAGAAATCTCTCACTTCTCTTCAAGAGGAGCTGGCGCGG 1020
Db 1101 CGCTTGAAAAGTGTAAAGAAATCTCTCACTTCTCTTCAAGAGGAGCTGGCGCGG 1160
QY 1021 ACAGCAAGAGCAAGGCGGCTGCACAAAGCGGCGCTGCGGTGAGTGCAGATGTA 1080

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Db 1161 ACAGCAAGAGCAAGGCGGCTGCACAAAGCGGCGGCTGCGGTGAGTGCAGATGTA 1220
QY 1081 CGCGCAGCGCTTCTGTTGTTGGCTGTCTGACGACGACGAGCGGACACAGACCTTGC 1140
Db 1221 CGCGCAGCGCTTCTGTTGTTGGCTGTCTGACGACGACGAGCGGACACAGACCTTGC 1279
QY 1141 ACAGCAAGCGGCGGAACTGTCGAGAGACACGCTGACAGAGAGCGGCTGATGACGAG 1200
Db 1280 ACAGCAAGCGGCGGAACTGTCGAGAGACACGCTGACAGAGAGCGGCTGATGACGAG 1339
QY 1201 CTGAGTAGAAGAAACGTCCTCGAGAGAGGAGAGAGATCATGTACGCCGGAAGTAGAC 1260
Db 1340 CTGAGTAGAAGAAACGTCCTCGAGAGAGGAGAGAGATCATGTACGCCGGAAGTAGAC 1399
QY 1261 CTGCTCCAGTCTCTTGGGTTTGGCGGACGACATGATCTCTCGAATCTGTTGGGATC 1320
Db 1400 CTGCTCCAGTCTCTTGGGTTTGGCGGACGACATGATCTCTCGAATCTGTTGGGATC 1459
QY 1321 CAGCATACGGCCCAATGTACACAAATCAGCCCTGGGAGAGACAGAGAGAGAGAGAC 1380
Db 1460 CAGCATACGGCCCAATGTACACAAATCAGCCCTGGGAGAGACAGAGAGAGAGAGAC 1519
QY 1381 AGAGA 1385
Db 1520 AGAGA 1524

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RESULT 2
US-10-270-333-38/c
: Sequence 38, Application US/10270333
: GENERAL INFORMATION:
: APPLICANT: Craychik, Anbal
: TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
: FILE REFERENCE: CLO00733CON
: CURRENT APPLICATION NUMBER: US/10/270,333
: PRIOR FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/168,677
: PRIOR FILING DATE: 1999-12-03
: PRIOR APPLICATION NUMBER: 60/175,691
: PRIOR FILING DATE: 2000-01-12
: PRIOR APPLICATION NUMBER: 60/191,638
: PRIOR FILING DATE: 2000-03-23
: NUMBER OF SEQ ID NOS: 198
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 38
: LENGTH: 2196
: TYPE: DNA
: ORGANISM: Drosophila
US-10-270-333-38

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Query Match 2.5%; Score 40.6; DB 6; Length 2196;  
Best Local Similarity 49.8%; Pred. No. 0.069;  
Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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QY 1139 GCAGAAACACCCGCGCAAGCTGCGAGGACACGCTGACAGAGCGGTTGATGACG 1198
Db 799 GCTTGAACCCCTTGAAGTGTGCTGACATCAGCTTGTAAAGAAATGGAATTCATGCGCG 740
QY 1199 AGCTGAGTAGAAGAAACGCTCTCCGAGAGGAGAGAGATCATGTACGCCGGAAGTAGG 1258
Db 739 AGTTGAGGTACACATATGATCTCTACAGAAAGTACACAAAGCTGTAGTACGACCAATCCCA 680
QY 1259 ACTCTGCACTGCTGCTTGGGTTTGGCGGACGACATGATCTCTCGAATCTGTTGGGCA 1318
Db 679 GATCTGCACTGCTTGGGTTTGGCGGCTGAGATGATCCACAGGTTGAGAGACCGGAGGGA 620
QY 1319 TCACAGATACGCGCAATGTACACAA 1345
Db 619 GCAGCAGACGAGAGAGACGACAA 593

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? CURRENT FILING DATE: 2002-10-15
? PRIOR APPLICATION NUMBER: 60/168, 677
? PRIOR FILING DATE: 1999-12-03
? PRIOR APPLICATION NUMBER: 60/175, 691
? PRIOR FILING DATE: 2000-01-12
? PRIOR APPLICATION NUMBER: 60/191, 638
? PRIOR FILING DATE: 2000-03-23
? NUMBER OF SEQ ID NOS: 198
? SOFTWARE: FastSeq for Windows Version 4.0.
? SEQ ID NO 115
? LENGTH: 5927
? TYPE: DNA
? ORGANISM: Drosophila
US-10-270-333-115
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Query Match	2.18;	Score 34.8;	DB 6;	Length 5927;
Best Local Similarity	55.98;	Pred. No. 5.5;		
Matches 66;	Conservative 0;	Mismatches 52;	Indels 0;	Gaps 0;

Accession	Sequence	Position
OY 1143	GAAACACCCGGCGAATCGTCTGCAGAGACACCGGTGTACAGACGGGGTTGATATGACGACT	1202
OY 1380	GAAAGCCTTCGGAAATCTTCGGAGAGGAAAGGGGTAGACACGGATTGATACAGACT	1439
OY 1203	GAGTACGAAAAAGCTCTCCGAGAAAGGGAGAGAGATCATGTACGCCCGGAACTAGAC	1260
DB 1440	GCTGTACCCAGATCTGGGGCGGTGACTGGATGATCTACTTGGTAGAGGTGTTCGTC	1497

```

RESULT 7
US-10-240-485-111/C
; Sequence 111, Application US/10240485
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240.485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058. 8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173. 8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529. 7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 111
; LENGTH: 15625
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-111

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Query Match	2.1%	Score 34.6	DB 6	length 15825
Best Local Similarity	46.5%	Pred. No. 11		
Matches 112	Conservative 0	Mismatches 129	Indels 0	Gaps 0
Qy 1379	ACAGAGAAAAGAAAACACAGCATGAGAACACAGTAATGAATAAACCATTAATATTT	1438		
Db 1338	AAAAAAAAAATAAATACTAAACAATTTAAAAAATAAAAAACCATAAATATTA	1279		
Qy 1439	AGCCCTCTGTCTGTGCTTACGGCCAGGAATGGTACCAATTTTTCAGTGTGACCT	1498		
Db 1278	ACCTAAGCTTCACATTTCTTCTATACATTAATACTCAACAAATCTTTAACA	1219		
Qy 1499	GACAGCTTTTGGCCACAGACAGAGCAATTTTAACACTGTTTCAACCCGGGGAGTT	1558		

Db	1218	AA	CTCTCCCTAACTCAAAAAAACTTTCATTAATACCGAAATCAACACACTACACTCC	1159
Qy	1559	GGCTGTGTTTAAAGAAAGACATTAATATGCTTAGACAGTGTAAAAA	1618	AAAAAAAAAAAAAAAAAAAA
Db	1158	AACTAATTTACAAACGAATTCCTCATCTCAAAAAACAAAAA	1099	AAAAAAAAAAAAAAAAAAAA
Qy	1619	A	1619	
Db	1098	A	1098	

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RESULT 8
US-10-240-425-1585/c
; Sequence 1585, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scheerl, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240.425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1585
; LENGTH: 135259
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. Z83838
US-10-240-425-1585

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Query Match	Similarity	2.1%	Score 34.6	DB 6	Length 135259
Best Local	Similarity	55.4%	Pred No. 40		
Matches	67	Conservative	0	Mismatches 54	Indels 0
					Gaps 0
QY 1499	GACAGCTTCCTTTGCCACAAGAGAGAAATTAACTGTTTCAACCCGGGGAGTT				1558
Db 86356	GACAGCTGATGTGTGCTCCAGGGGAAATGTGTAATGCTGAGACACACCACTGGAATT				86297
QY 1559	GGCTGTGTTAAAGAAAGACCATTAAATGCTTTGACAGTGTAAACAAAAAAAAAAAAA				1618
Db 86296	ACTGATGTGACTATGGAACAAAGAAAGATCCTATAGGATCCAGGCCAAAAAAAAAAAAA				86237
QY 1619	A 1619				
Db 86236	A 86236				

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,
, RESULT 9
US-10-270-377-1
, Sequence 1, Application US/10270377
, GENERAL INFORMATION:
, APPLICANT: Hudson, et al.
, TITLE OF INVENTION: Prostatic Growth Factor
, FILE REFERENCE: P1149D2
, CURRENT APPLICATION NUMBER: US/10/270,377
, CURRENT FILING DATE: 2002-10-15
, PRIOR APPLICATION NUMBER: 09/361,741
, PRIOR FILING DATE: 1999-07-28
, PRIOR APPLICATION NUMBER: 09/461,418
, PRIOR FILING DATE: 1999-11-18
, PRIOR APPLICATION NUMBER: 08/411,607
, PRIOR FILING DATE: 1995-04-11
, PRIOR APPLICATION NUMBER: US94/14578
,
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PRIOR FILING DATE: 1994-12-15  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1024  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (64)..(948)  
OTHER INFORMATION:  
US-10-270-377-1

Query Match 2.1%; Score 34.4; DB 6; Length 1024;  
Best Local Similarity 48.5%; Pred. No. 2.5;  
Matches 128; Conservative 0; Mismatches 131; Indels 5; Gaps 1;

QY 1031 CAACGGGGCGCTGACAAAGCGGGCGCTGCTGCTGATGAGTGGCGCATGTACGCGGACGCG 1090  
DB 591 CAGGGGGCGCGCCGACAGCGCGCTGCGCGCAACGGGGACGACTGCTGCGGGCGCGCG 650  
QY 1091 CTTCTCGGTGGTGGCGTGTGCGAGCGACAGCGCGGACGACACCTTGACGACACCC 1150  
DB 651 TTGCTGCGGTGTGCGACAGCGTCCGCGGCTGTGGAAGACCTGGGCGGCGGCGGCGT 710  
QY 1151 GCGGAACCTGCTG-----CGAGGACACCGGTGTACAGAGCGGGTTGATGACCGAGCTGAG 1205  
DB 711 GCTGTGCGCACGCGAGGTGCAAGTGCATGTGCGCGCGTCCGCGAGCGACATGTCG 770  
QY 1206 GTAGAAAAAGCTCCGAGAGGGAGGAGTCAATGTATACCGCGCGGAGTGTAGACCTGCT 1265  
DB 771 GCGCGCAACATGACAGCGCGCAATCAAGACGAGCCTGCAACCGCTGAAGCCGACGCGT 830  
QY 1266 CCAGTCTGCTGCTGGTGGTGGCGCG 1289  
DB 831 GCCAGCGCGCTGCTGCTGCGCGCG 854

## RESULT 10

US-10-240-425-334  
Sequence 334, Application US/10240425  
GENERAL INFORMATION:  
APPLICANT: Williams, Amanda  
APPLICANT: Boland, Joseph F.  
APPLICANT: Lord, Reginald V.  
APPLICANT: Alvarez, Chris  
APPLICANT: Metzger, Jon C.  
APPLICANT: Scherf, Uwe  
APPLICANT: Vockley, Joseph G.  
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
FILE REFERENCE: 44921-5026  
CURRENT APPLICATION NUMBER: US/10/240.425  
PCT FILING DATE: 2002-09-30  
PCT/US01/09847  
PRIORITY FILING DATE: 2001-03-28  
PRIORITY APPLICATION NUMBER: US 60/193,446  
PRIORITY FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 1588  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 334  
LENGTH: 1201  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. AB000584  
US-10-240-425-334

Query Match 2.1%; Score 34.4; DB 6; Length 1201;  
Best Local Similarity 48.5%; Pred. No. 2.7;  
Matches 128; Conservative 0; Mismatches 131; Indels 5; Gaps 1;  
QY 1031 CAACGGGGCGCTGACAAAGCGGGCGCTGCTGCTGATGAGTGGCGCATGTACGCGGACGCG 1090  
DB 591 CAGGGGGCGCGCCGACAGCGCGCTGCGCGCAACGGGGACGACTGCTGCGGGCGCGCG 650  
QY 1091 CTTCTCGGTGGTGGCGTGTGCGAGCGACAGCGCGGACGACACCTTGACGACACCC 1150  
DB 651 TTGCTGCGGTGTGCGACAGCGTCCGCGGCTGTGGAAGACCTGGGCGGCGGCGGCGT 710  
QY 1151 GCGGAACCTGCTG-----CGAGGACACCGGTGTACAGAGCGGGTTGATGACCGAGCTGAG 1205  
DB 711 GCTGTGCGCACGCGAGGTGCAAGTGCATGTGCGCGCGTCCGCGAGCGACATGTCG 770  
QY 1206 GTAGAAAAAGCTCCGAGAGGGAGGAGTCAATGTATACCGCGCGGAGTGTAGACCTGCT 1265  
DB 771 GCGCGCAACATGACAGCGCGCAATCAAGACGAGCCTGCAACCGCTGAAGCCGACGCGT 830  
QY 1266 CCAGTCTGCTGCTGGTGGTGGCGCG 1289  
DB 831 GCCAGCGCGCTGCTGCTGCGCGCG 854

DB 599 CAGGGGGCGCGCCGACAGCGCGTGGCGCGCAACGGGGACGACTGCTGCGGGCGCGCG 658  
QY 1091 CTTCTCGGTGGTGGCGTGTGCGAGCGACAGCGCGGACGACACCTTGACGACACCC 1150  
DB 659 TTGCTGCGGTGTGCGACAGCGTCCGCGGCTGTGGAAGACCTGGGCGGCGGCGGCGT 718  
QY 1151 GCGGAACCTGCTG-----CGAGGACACCGGTGTACAGAGCGGGTTGATGACCGAGCTGAG 1205  
DB 719 GCTGTGCGCACGCGAGGTGCAAGTGCATGTGCGGCGGCGGCGGCGGCGGCGGCGG 778  
QY 1206 GTAGAAAAAGCTCCGAGAGGGAGGAGATGATGTACCGCGGAGTGAAGACCTGCT 1265  
DB 779 GCGCGCAACATGACAGCGCGCAATCAAGACGAGCCTGCAACCGCTGAAGCCGACGCGT 838  
QY 1266 CCAGTCTGCTGCTGGTGGTGGCGCG 1289  
DB 839 GCCAGCGCGCTGCTGCTGCGCGCG 862

## RESULT 11

US-10-267-255-96/c  
Sequence 96, Application US/10267255  
GENERAL INFORMATION:  
APPLICANT: Sherman, D  
APPLICANT: Mao, Y  
APPLICANT: Varoglu, M  
APPLICANT: He, M  
APPLICANT: Sheldon, P  
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
FILE REFERENCE: 600.456051  
CURRENT APPLICATION NUMBER: US/10/267.255  
PCT FILING DATE: 2002-10-09  
PCT/US01/11279  
PRIORITY FILING DATE: 1999-03-12  
PRIORITY APPLICATION NUMBER: US 08/624,447  
PRIORITY FILING DATE: 1996-08-19  
PRIORITY APPLICATION NUMBER: PCT/US94/11279  
PRIORITY FILING DATE: 1994-10-06  
PRIORITY APPLICATION NUMBER: US 08/133,963  
PRIORITY FILING DATE: 1993-10-07  
NUMBER OF SEQ ID NOS: 145  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 96  
LENGTH: 18331  
TYPE: DNA  
ORGANISM: Streptomyces lavendulae  
US-10-267-255-96

Query Match 2.1%; Score 34; DB 6; Length 18331;  
Best Local Similarity 50.6%; Pred. No. 18;  
Matches 82; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 309 GCGCCAGAAAGGAGGAGTGTGCTGCGGCGCTGAGGCGGAGGCGTCCGACCACTCC 368  
DB 16079 GGTCTACGCAAGAGGTGCTGCGGCGCGCGCGCTCCACACACAGAGTCCGATCACC 16020  
QY 369 TGTCTCTCAATTAAGCCCTTCTGCGACACATGCTGAAGCTGAAGAGATGCCACCCC 428  
DB 16019 GGTCTACGCAAGAGGTGCTGCGGCGCGCGCGCTCCACACACAGAGTCCGATCACC 15960  
QY 429 TGTCTCTCAATTAAGCCCTTCTGCGACACATGCTGAAGCTGAAGAGATGCCACCCC 470  
DB 15959 CCAAGCGCTGATGCTGCAACTGCGGCGCGCGCGCTCCACGCACT 15918

## RESULT 12

US-10-267-255-96/c  
Sequence 76, Application US/10267255  
GENERAL INFORMATION:  
APPLICANT: Sherman, D  
APPLICANT: Mao, Y  
APPLICANT: Varoglu, M  
APPLICANT: He, M

```

; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456U51
; CURRENT APPLICATION NUMBER: US/10/267,255
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/624,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 76
; LENGTH: 53500
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-10-267-255-76

```

```

Query Match
Best Local Similarity 2.1%; Score 34; DB 6; Length 53500;
Best Local Similarity 50.6%; Pred. No. 34;
Matches 82; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

```

```

Qy 309 GGGCCAGAAAGGGAGTTCTGCTGGCCCTCAGGCGCAGGCGCTCCACCATCC 368
Db 3930 GGTCCAGCAGACAGGTGCTGCTGGCCCTCCAGCAGCATGATGAGCGCCC 3871
Qy 369 TGTTCCTCAATTAAGCCTCTTCTCGGACACACTGCTGAAGTGAAGATGCCACCCC 428
Db 3870 GGTGCGGAGCGCTCCGCGCCCTCGAGATCCAGCGGAGGATGATCCACCTCT 3811
Qy 429 TCTTCGATTTCTTCTTCAGCCCTCGCCCGCAACCCCACT 470
Db 3810 CCACCGCTGATGCTCGCACTGGCGCCCTCCACGCAACT 3769

```

## RESULT 13

```

US-10-270-333-193
; Sequence 193, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; FILE REFERENCE: C1000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 193
; LENGTH: 4902
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-193

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Query Match
Best Local Similarity 2.1%; Score 33.2; DB 6; Length 4902;
Best Local Similarity 49.6%; Pred. No. 14;
Matches 114; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

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```

Qy 1144 AACACCCCGCGAAGCTGTCGAGACACCGTGTACAGAGCGGGTGTACCGAGCTG 1203
Db 2139 AAGGCTCAGAACTGTGCTGCTATGATGTGTAGACAGCGGGTGTATGCAATTGAG 2198
Qy 1204 AGGTGAAAGAAAGCTCTCCGAGAGAGGAGAGGATGATGTACCGCCGGAAGTAGACCTC 1263

```

```

Db 2199 AGGAAGTAGAAGAACCCGAGCATATAGTCGAGGATGCTGAACAGCTGTGAACCACTGG 2258
Qy 1264 GTC---CAGTCGTGCTGGGTTGGCCGACGCATATCTCCGATTCGTGGGCATC 1320
Db 2259 GATCAATGCGCCGAGGATGATCATAGACCGCATATGACCGCTGGCGGTGAAGGGGGCC 2318
Qy 1321 CAGCATAGCGCCCAATGTACACAAATCAGCCCTGGCGACAGCAGCAGG 1370
Db 2319 CAGCATATGAAGAGGCGCAGCGCCACCGCATCTGGGAAGTGGATAGG 2368

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## RESULT 14

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US-10-240-485-176/c
; Sequence 176, Application US/10240485
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO: 176
; LENGTH: 23683
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-176

```

```

Query Match
Best Local Similarity 2.1%; Score 33.2; DB 6; Length 23683;
Best Local Similarity 48.8%; Pred. No. 36;
Matches 121; Conservative 0; Mismatches 123; Indels 4; Gaps 1;

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```

Qy 1375 AGAAGACAGAGAAAGAAACACAGCATGAGAACAGTAAATGAATTAACATTAAT 1434
Db 15435 ATATTAACATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15376
Qy 1435 ATTAAAGCCCTGTGTTGCTTACTGCGCAGGAATGTACCAATTTTTCAGTGTGG 1494
Db 15375 AATTAAACCTTATCTTACTGCTCTCTCTCGAAAAAATTAATCTTATTAATTAATTC 15316
Qy 1495 A-----CTTGACAGCTTCTTTTGCACAGCAAGAGAGAAATTAACACTGTTCAACCCG 1550
Db 15315 AATATTTTAACTTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15256
Qy 1551 GGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGTTTAGACAGTGAATTAATTAAT 1610
Db 15255 AAAATATATTAATCTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15196
Qy 1611 AAAAAAAAA 1618
Db 15195 AACACAAA 15188

```

## RESULT 15

```

US-10-264-237-1277
; Sequence 1277, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```

FILE REFERENCE: PA131P1  
 CURRENT APPLICATION NUMBER: US/10/264,237  
 CURRENT FILING DATE: 2002-10-04  
 PRIOR APPLICATION NUMBER: PCT/US01/16450  
 PRIOR FILING DATE: 2001-05-18  
 PRIOR APPLICATION NUMBER: US 60/205,515  
 PRIOR FILING DATE: 2000-05-19  
 NUMBER OF SEQ ID NOS: 2876  
 SOFTWARE: PatentIn Ver. 3.1  
 SEQ ID NO: 1277  
 LENGTH: 2158  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-264-237-1277

Query Match 2.0%; Score 33; DB 6; Length 2158;  
 Best Local Similarity 73.7%; Pred. No. 9.7;  
 Matches 42; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 Oy 1563 GTGTTAAGAAAGACCATTAATGCTTTAGACAGTGTAAAAA 1619  
 Db 2085 GTTGTAAAGCCAGCTAATAAATGCTTGTGAGCATAAAAA 2141

Search completed: November 7, 2002, 18:01:51  
 Job time : 331.231 secs

482

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:56:48 ; Search time 4825.36 Seconds  
(without alignments)  
11441.218 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897  
Sequence: 1 gccacaccgcgagcctcgcg.....aaaaaaaaaaaaaaaaaa 1897

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10

Total number of hits satisfying chosen parameters: 2188596

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
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7: gb\_ph:\*  
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41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526	80.4	1832	AK094501	AK094501 Homo sapi
2	1422	75.0	1524	AX358762	AX358762 Sequence
3	1422	75.0	1524	AX362255	AX362255 Sequence
4	1344	70.8	1890	AX136281	AX136281 Sequence
5	1328	70.0	129676	AC079773	AC079773 Homo sapi
6	1218	65.2	2528	AX319944	AX319944 Sequence
7	858	44.2	946	BC017318	BC017318 Homo sapi
8	661	34.8	826	BC011449	BC011449 Homo sapi
9	511	26.9	591	AX136556	AX136556 Sequence
10	506	26.7	1362	AX319942	AX319942 Sequence
11	506	26.7	1362	AF034633	AF034633 Homo sapi
12	366	19.3	587	AX136698	AX136698 Sequence
13	364	19.2	444	AX150120	AX150120 Sequence
14	316	16.7	396	AX093191	AX093191 Sequence
15	315	16.6	369	AX093381	AX093381 Sequence
16	294	15.5	147131	AC010974	AC010974 Homo sapi
17	47	2.5	209885	AC124493	AC124493 Homo sapi
18	38	2.0	1797	AB041649	AB041649 Mus muscu
19	30	1.6	125703	AC123338	AC123338 Rattus no
20	27	1.4	487	AF150733	AF150733 Homo sapi
21	27	1.4	1086	AF082874	AF082874 Medicago
22	27	1.4	1114	AY118558	AY118558 Drosophila
23	27	1.4	1368	AX285020	AX285020 Sequence
24	27	1.4	1614	AK026521	AK026521 Homo sapi
25	27	1.4	2625	BC028978	BC028978 Homo sapi
26	26	1.4	3155	AY094780	AY094780 Drosophila
27	27	1.4	48206	AL645986	AL645986 Mouse dna
28	27	1.4	92874	AC112072	AC112072 Rattus no
29	27	1.4	127524	AL807806	AL807806 Mus muscu
30	27	1.4	138851	AL645938	AL645938 Mouse DNA
31	27	1.4	151602	AC126321	AC126321 Polypteru
32	27	1.4	170255	AC027118	AC027118 Homo sapi
33	27	1.4	179364	AC074245	AC074245 Homo sapi
34	27	1.4	195782	AC074389	AC074389 Homo sapi
35	27	1.4	209572	AC099615	AC099615 Mus muscu
36	27	1.4	212690	AC110232	AC110232 Mus muscu
37	27	1.4	214411	AC069297	AC069297 Mus muscu
38	27	1.4	217929	AL133395	AL133395 Human DNA
39	26	1.4	1275	AF297044	AF297044 zea may
40	26	1.4	1409	AF176571	AF176571 Alternari
41	26	1.4	2481	AX056894	AX056894 Sequence
42	26	1.4	2745	AF314845	AF314845 Rana caca
43	26	1.4	3889	BC034500	BC034500 Homo sapi
44	26	1.4	7940	AF044209	AF044209 Homo sapi
45	26	1.4	94336	AC005250	AC005250 Homo sapi

## ALIGNMENTS

RESULT 1	AK094501	1832 bp	mRNA	linear	PRI 15-JUL-2002
LOCUS	AK094501		Homo sapiens CDNA FLJ37182 fls, clone BRAL22001350, weakly similar to Homo sapiens Gz-selective GTPase-activating protein (RG520)		
DEFINITION	AK094501		mRNA.		
ACCESSION	AK094501		AK094501.1 GI:21753575		
VERSION	AK094501.1		GI:21753575		
KEYWORDS	oligo capping, fls (full insert sequence).				
SOURCE	Homo sapiens		Homo sapiens a1zhelmer cortex CDNA to mRNA, clone_jlb:BRAL22		
ORGANISM	clone:BRAL22001350.				
REFERENCE	Homo sapiens				
REFERENCE	1		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		

**AUTHORS**  
 Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,  
 Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,  
 Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,  
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,  
 Magetsuna, M., Murekawa, K., Kanemori, K., Takahashi-Fujii, A.,  
 Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K.,  
 and Isogai, T.  
**TITLE**  
 NEDO human cDNA sequencing project  
**JOURNAL**  
 Unpublished  
**REFERENCE**  
 2 (bases 1 to 1832)  
**AUTHORS**  
 Isogai, T. and Yamamoto, J.  
**TITLE**  
 Direct Submission  
**JOURNAL**  
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7  
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan: cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction: Helix Research Institute (HRI) (supported by Japan  
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
 HRI, and Biotechnology Center, National Institute of Technology and  
 Evaluation; Clone selection for full insert sequencing: HRI and  
 RAB; annotation: HRI and RAB.

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**CDS**  
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 /note="cloning vector: pME18SFJ3"

**BASE COUNT**  
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**ORIGIN**

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 Matches 1676; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

619 CCTCAGGCCAGGCGCTCCGACACCATCTCTTCTCAATTTAGCCCTTTCTGGCACA 678  
 574 CCTCAGGCCAGGCGCTCCGACACCATCTCTTCTCAATTTAGCCCTTTCTGGCACA 633  
 679 CTGCGAAGCTGAAGAGATGCCACCCCTCTCATTTGTTCTTCAGCCCTGGCCCCCA 728  
 634 CTGCGAAGCTGAAGAGATGCCACCCCTCTCATTTGTTCTTCAGCCCTGGCCCCCA 693  
 739 ACCCCCACTCCCTGAGTGAATTTCTTGGGTCTTCTTATTTCTGGTAGGAGCGG 798  
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 799 GAGTCCGTTCTCTTTTGTTCCTGTCGCAATATTAAGAGAGCTGGTAAAGCATTTGA 858  
 754 GAGTCCGTTCTCTTTTGTTCCTGTCGCAATATTAAGAGAGCTGGTAAAGCATTTGA 813  
 859 ATAAATTCAGCTGACTGAATTTTCACTATGTACTTGAAGAGAGAGTGAAGT 918  
 814 ATAAATTCAGCTGACTGAATTTTCACTATGTACTTGAAGAGAGTGAAGT 873  
 919 TCACCCCATCTCTGTTGTAACCGAGTCAAGGCCAGCTGGCAGAGTCTTGAAG 978  
 874 TCACCCCATCTCTGTTGTAACCGAGTCAAGGCCAGCTGGCAGAGTCTTGAAG 933  
 979 TCACCTGAGTGGGATCTGCTTTTGAAGCCCTCCAGTCCATTCCTGATGGG 1038  
 934 TCACCTGAGTGGGATCTGCTTTTGAAGCCCTCCAGTCCATTCCTGATGGG 993  
 1039 GGCATTAATTTGAGACTCAGAGTGAAGTGAAGTCTTCTTGAAGGCTGAAGGCGCAATTCC 1098  
 994 GGCATTAATTTGAGACTCAGAGTGAAGTGAAGTCTTCTTGAAGGCTGAAGGCGCAATTCC 1053  
 1099 CACATCAGGCTCCCTGCTGCTGATTAATTAATTTCTTGAAGGCTGAAGGCGCAATTCC 1158  
 1054 CACATCAGGCTCCCTGCTGCTGATTAATTAATTTCTTGAAGGCTGAAGGCGCAATTCC 1113  
 1159 CAGAAATGGCTGTTTGGCCCTGAGTGGGCTCTAGTGAAGTCAATGATGGG 1218  
 1114 CAGAAATGGCTGTTTGGCCCTGAGTGGGCTCTAGTGAAGTCAATGATGGG 1173  
 1219 ACTTAGACTGGGCTGCTGCTGATTAATTAATTTCTTGAAGGCTGAAGGCGCAATTCC 1278  
 1174 ACTTAGACTGGGCTGCTGCTGATTAATTAATTTCTTGAAGGCTGAAGGCGCAATTCC 1233  
 1279 TTGAGAGGACTGGGCTGCTGCTGATTAATTAATTTCTTGAAGGCTGAAGGCGCAATTCC 1338  
 1234 TTGAGAGGACTGGGCTGCTGCTGATTAATTAATTTCTTGAAGGCTGAAGGCGCAATTCC 1293  
 1339 CGGTGTGAGTGGGCTGCTGCTGATTAATTAATTTCTTGAAGGCTGAAGGCGCAATTCC 1398  
 1294 CGGTGTGAGTGGGCTGCTGCTGATTAATTAATTTCTTGAAGGCTGAAGGCGCAATTCC 1353  
 1399 GGGGGAGGACACACACTCTGACAGAACACCCGCGGAATCTGTCGAGACACCTGTACA 1458  
 1354 GGGGGAGGACACACACTCTGACAGAACACCCGCGGAATCTGTCGAGACACCTGTACA 1413  
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 AC079773.8 GI:15145561  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 AUTHORS Sulston, J.E. and Waterston, R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 MEDLINE 99063792  
 PUBMED 9847074

REFERENCE  
 AUTHORS Shah, N., Meyer, R., Boyer, E. and Dignan, G.  
 TITLE The sequence of Homo sapiens BAC clone RP11-258B17  
 JOURNAL Unpublished (2001)  
 REFERENCE 3 (bases 1 to 129676)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 4 (bases 1 to 129676)  
 Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 5 (bases 1 to 129676)  
 Waterston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Aug 9, 2001 this sequence version replaced gi:14468388.

COMMENT  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@wustl.wustl.edu](mailto:sapiens@wustl.wustl.edu)  
 ----- Summary Statistics  
 -----  
 Center project name: H\_NH0258B17  
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
 The RPc1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Caranese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6  
 NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RP11-1L22; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 6003 of RP11-159N20.

RP11-258B17 contains a single plasmid region from 1230 to 1239.

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 DB 120741 GGGATCATGTACCGAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCCTGCGCGG 120682

QY 509 TACGAGTCTTCTGCTCCCGAGGAACTGAACATGATTGTCATGACTGCTGCAACACC 568

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QY 809 TCTCTTTGTCTCTGTCGAATTAATGAAGACCTGGTAAACATTTGGAATTAATTCAG 868
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ACCESSION AX319944.1 GI:17901491  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Galvin, K.A. and Rudolph-Owen, L.A.  
TITLE Methods and compositions for the diagnosis and treatment of  
cardiovascular and tumorigenic disease using 4941  
JOURNAL Patent: WO 0181634-A 3 01-NOV-2001;  
Millennium Pharmaceuticals, Inc. (US)  
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VERSION   BC017318.1  GI:16878239
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SOURCE    Homo sapiens.
ORGANISM  Homo sapiens
REFERENCE Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS   Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
TITLE      1 (bases 1 to 946)
JOURNAL   Direct Submission
          Submitted (05-NOV-2001) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: National Institutes of Health Intramural
          Sequencing Center (NISC),
          Gaithersburg, Maryland:
          Web site: http://www.nisc.nih.gov/
          Contact: nisc_mgc@ngf1.nih.gov
          Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
          Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
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          Tongson, E.E., Touchman, J.W., Tsurgeno, C., Vogt, V.L., Walker, M.A.,
          Zhang, L., H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 39 Row: D Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
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Best Local Similarity 99.9%; Pred. No. 0;
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19 GGTGCTCGGCGCGGAGCGCGGAGGAGACACAGACCCGACCGGAGCGCGAGCG 78
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Db	20	66TGTCTCGCCCGGAGGCGGAGCGGAGGAGACAGAGACCCGCGAGCCGGAGCCGAGACGG	79
QY	79	CGGGGATGACAGAGCTCCCGGAGCGGCACTCGGCTCCTCTAAGTACGACCGTGTCTC	138
Db	80	CGGGGATGACAGAGCTCCCGGAGCGGCACTCGGCTCCTCTAAGTACGACCGTGTCTC	139
QY	139	CGCGGACAGAGCGGCGGCGCCAGACAGCCTCGGACAGCCAGCGGCTGACGCGGGGAGC	198
Db	140	CGCGGACAGAGCGGCGGCGCCAGACAGCCTCGGACAGCCAGCGGCTGACGCGGGGAGC	199
QY	199	CTCCGCTCTGTCTGCGCTCTGTATGCGCTTGCCCTCTCCGCGGCCGGGACCTCCGGAG	258
Db	200	CTCCGCTCTGTCTGCGCTCTGTATGCGCTTGCCCTCTCCGCGGCCGGGACCTCCGGAG	259
QY	259	AATGTGGGTCTTACGACATCGCGGCACTTTTGGCGATTGTCTTCTTCCAGCTTTGC	318
Db	260	AATGTGGGTCTTACGACATCGCGGCACTTTTGGCGATTGTCTTCTTCCAGCTTTTGC	319
QY	319	GCTGCAATTCAGTCTCTACAGTGCAGGAATTCAGGTGAACAGACGATGCTCTCCG	378
Db	320	GCTGCAATTCAGTCTCTACAGTGCAGGAATTCAGGTGAACAGACGATGCTCTCCG	379
QY	379	CGAGTTCAATTGTGAATTCACAGGTGTAACGATGATGTCGAGAAAGAGATGATGA	438
Db	380	CGAGTTCAATTGTGAATTCACAGGTGTAACGATGATGTCGAGAAAGAGATGATGA	439
QY	439	GCAAGTGGCGGGATCATGTATCCGCAAGTCTGTGCATCATATCAGCGGCTGTCTATGC	498
Db	440	GCAAGTGGCGGGATCATGTATCCGCAAGTCTGTGCATCATATCAGCGGCTGTCTATGC	499
QY	499	CTCTCCCGGGTACAGTCTCTGTCTCCCGAGGAACTGAATCTAGTTTGATCAGCTG	558
Db	500	CTCTCCCGGGTACAGTCTCTGTCTCCCGAGGAACTGAATCTAGTTTGATCAGCTG	559
QY	559	CTGCAACACCCCTCTTTGTAAAGGCGCAAGGCGCAAGAAAGGGGAAGTTCTGCTCGC	618
Db	560	CTGCAACACCCCTCTTTGTAAAGGCGCAAGGCGCAAGAAAGGGGAAGTTCTGCTCGC	619
QY	619	CCTCAGGCCAGGGCTCCGCAACCACTCTGTTCTCTCAAAATTAGCCCTCTCTCGGACA	678
Db	620	CCTCAGGCCAGGGCTCCGCAACCACTCTGTTCTCTCAAAATTAGCCCTCTCTCGGACA	679
QY	679	CTGCTGAAGCTTAAGAGATGCGCACCCCTCTCGATGTCTTCTCAGCCCTCGGCCCA	738
Db	680	CTGCTGAAGCTTAAGAGATGCGCACCCCTCTCGATGTCTTCTCAGCCCTCGGCCCA	739
QY	739	ACCCGCCACCTCCGTGAGTGAAGTTCTTCTGCGGTCTCTTATCTGCGGTGAGGAGCG	798
Db	740	ACCCGCCACCTCCGTGAGTGAAGTTCTTCTGCGGTCTCTTATCTGCGGTGAGGAGCG	799
QY	799	GAGTCCGTGCTCTTTGTTCTCTGTGCAAAATATGAAAGAGCTCGTAAACATTTCTGA	858
Db	800	GAGTCCGTGCTCTTTGTTCTCTGTGCAAAATATGAAAGAGCTCGTAAACATTTCTGA	859
QY	859	ATAAATTACGCTTGACTGAATTTTCAATGTACTTTGAAGAGAGGTGAGGTAAAGT	918
Db	860	ATAAATTACGCTTGACTGAATTTTCAATGTACTTTGAAGAGAGGTGAGGTAAAGT	919
QY	919	TCACCCCGCA 927	
Db	920	TCACCCCGCA 928	
RESULT 8			
BC011449			
LOCUS	BC011449	826 bp	mRNA
DEFINITION	Homo sapiens, clone IMAGE:4028092,		linear
ACCESSION	BC011449		
VERSION	BC011449.1	GI:15277472	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		



REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Mammalia: Eutheria: Primates: Catarrhini; Hominoidea: Homo.  
1 (bases 1 to 826)  
Strausberg R.  
Direct Submission  
Submitted (25-JUL-2001) National Institutes of Health, Mammalian

REMARK	COMMENT
NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a>	Contact: MGC help desk

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAL Protein; 25 Row: n Column: 18  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES	Location/Qualifiers
source	1. .826

BASE COUNT ORIGIN	237 a	197 c	228 g	164 t
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79	100	100	100	100

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Query Match      34.88; Score 661; DB 9; Length 826;
Best Local Similarity 99.98; Pred. No. 0;
Matches 711; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY	1186	TGGGCTCTAGAGATCTCAGACTCAATAGACGGGACTTAACATCGGGGCTGGGCTGGGCT	1245
Db	105	TGGGCTCTAGGACTCGAGCTCAATGACTCGGACTTTAACTGGGGCTGGGCTGGGCTGCT	164
QY	1246	GAAGAATGCTTAAAGAAATATCTTCAGTTCTCCCTTGACAGAGACTGGCGCCGGAGCGGA	1305
Db	165	GAAGAATGCTTAAAGAAATATCTTCAGTTCTCTTCACAGAGACTGGCGCCGGAGCGGA	224
QY	1306	AGACACAAGGGGCGCTGCACAACAACGGGGCCTGTCGGTGGGAGTGGCGATATACGGCA	1365
Db	225	AGACACAAGGGGCGCTGCACAACAACGGGGCCTGTCGGTGGGAGTGGCGATATACGGCA	284
QY	1366	GGCGCTTCTCGTGGTTGGCCCTGCTGCAGGACAGGGGGGACACAGCACTGCACGACA	1425
Db	285	GGCGCTTCTCGTGGTTGGCCCTGCTGCAGGACAGGGGGGACACAGCACTGCACGACA	344
QY	1426	CCCCGCCAAACTGCTCGAGGACACCGTGTACAGAGCGGGTGTATGATCCGACGTGAGGT	1485
Db	345	CCCCGCCAAACTGCTCGAGGACACCGTGTACAGAGCGGGTGTATGATCCGACGTGAGGT	404
QY	1486	AGAAAAAGCTCTCCGAGAAAGGGGAGGAGATCATGTAGCCCGGGAAGTAAAGACCTCGTCC	1545
Db	405	AGAAAAAGCTCTCCGAGAAAGGGGAGGAGATCATGTAGCCCGGGAAGTAAAGACCTCGTCC	464
QY	1546	AGTCGTCTTGGGTTTGGCCGACGCCATGATCCTCGAATTCGTTGGGATATCCAGATA	1605
Db	465	AGTCGTCTTGGGTTTGGCCGACGCCATGATCCTCGAATTCGTTGGGATATCCAGATA	524
QY	1606	CGGCGAATGTACAAACAAATACGCCCTTGGGCAACACAGACAGAGAGAGACAGACAAA	1665
Db	525	CGGCGAATGTACAAACAAATACGCCCTTGGGCAACACAGACAGAGAGAGAGACAGACAAA	584

Oy	1666	AGAAAAACACGCACTGTGAGACACAGTAAATGATTAATAAACCTAAAAATTTTGGCCCCCT	1725
Oy	1666	AGAAAAACACGCACTGTGAGACACAGTAAATGATTAATAAACCTAAAAATTTTGGCCCCCT	1725
Db	565	AGAAAAACACGCACTGTGAGACACAGTAAATTAATAAACCTAAAAATTTTGGCCCCCT	644
Oy	1726	GTCTGTGCTTACGTACGGCCAGAGAAATGGTACCAATTTTTCAGTGTGGACTTGACAGCTTC	1785
Db	645	GTCTGTGCTTACGTACGGCCAGAGAAATGGTACCAATTTTTCAGTGTGGACTTGACAGCTTC	704
Oy	1786	TTTTGCGCACAAGCAGAGAGAAATTTAAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGT	1845
Db	705	TTTTGCGCACAAGCAGAGAGAAATTTAAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGT	764
Oy	1846	AAAGAAAGACCATTAATGCTTTAGACAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTT	1897
Db	765	AAAGAAAGACCATTAATGCTTTTAGCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTT	816

RESULT 9			
AX136556	AX136556	591 bp	DNA
LOCUS	AX136556		
DEFINITION	Sequence 478 from Patent		linear.
ACCESSION	AX136556		PAT 30-MAY-2001
VERSION	AX136556.1	GI:14272960	
KEYWORDS			
SOURCE	human.		

BASE COUNT	108	a	198	c	173	g	109	t	3	others
ORIGIN										

Query Match	26.9%;	Score 511;	DB 6;	Length 591;
Best Local Similarity	100.0%;	Pred. No. 2.8e-294;		
Matches 511; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY	19	GGTGTCTGGCCCGGGAGCGCAGCGGGAGAGCAGAGACCGACCGGAGCCCGGACG	78
Db	33	GGTGTCTGGCCCGGGAGCGCAGCGGGAGAGCAGAGACCGACCGGAGCCCGGACG	92
QY	79	CGGGCGATCGACGGTCGCCGAGCGGGACGTCGGCGTCCTTAAGCTACGACCGTCGTCTC	138
Db	93	CGGGCGATCGACGGTCGCCGAGCGGGACCTGCGGCTCTCTTAAGCTACGACCGTCGTCTC	152
QY	139	CGCGGCGAGCAGCGCGGGGCCCGCAGCAGCCTCGGCGACAGCGCGCTGCAGCGCGGGGAGC	198
Db	153	CGGGCGAGCAGCGCGGGGCCCGCAGCAGCGCTCGGCGACAGCGCGCTGCAGCGGGGAGC	212
QY	199	CTCCGCTGCTGTCCCTCTCTGATGGCGTTGCCCTTCCGGGCCCGGAGCTCCGGAG	258
Db	213	CTCCGCTGCTGTCCCTCTCTGATGGCGTTGCCCTTCCGGGCCCGGAGCTCCGGAG	272
QY	259	AATGTGGGTCTCAAGCATCGCGGCACTTTTTCGGGATTTGTTCTTGTCATTCAAGGCTTTGC	318
Db	273	AATGTGGGTCTCAAGCATCGCGGCACTTTTTCGGGATTTGTTCTTGCTTCCAAGGCTTTGC	332
QY	319	GCTGCAAAATCCAGTCTACACAGTGTGAAGAAATTCAGACTGAACAACGACTCTCTCCCC	378
Db	333	GCTGCAAAATCCAGTCTACACAGTGTGAAGAAATTCAGACTGAACAACGACTCTCTCCCC	392
QY	379	CGAGTTCATTGTGAATTTGCACGCGTGAACGTTTCAAGACATGTCTCAAGAAAGATGATGGA	438
Db	393	CGAGTTCATTGTGAATTTGCACGCGTGAACGTTTCAAGACATGTCTCAAGAAAGATGATGGA	452



QY 439 GCAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCG 498  
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 DB 453 GCAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCG 512  
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 QY 499 CTTCTCCGGGTACCAATCTTCTGCTCCCA 529  
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 DB 513 CTTCTCCGGGTACCAATCTTCTGCTCCCA 543  
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RESULT 10  
 LOCUS AX319942 1362 bp DNA linear PAT 14-DEC-2001  
 DEFINITION Sequence 1 from Patent WO0181634.  
 ACCESSION AX319942  
 VERSION AX319942.1 GI:17901489  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 Galvin, K.A. and Rudolph-Owen, L.A.  
 TITLE Methods and compositions for the diagnosis and treatment of  
 JOURNAL Cardiovascular and tumorigenic disease using 4941  
 Patent: WO 0181634-A 1 01-NOV-2001;  
 Millennium Pharmaceuticals, Inc. (US)  
 FEATURES  
 source location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 HEV"

BASE COUNT 263 a 435 c 362 g 302 t  
 ORIGIN

Query Match 26.7%; Score 506; DB 6; Length 1362;  
 Best Local Similarity 100.0%; Pred. No. 3e-291;  
 Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 TCACAACTTCATGCTCTGCTGAAAAACATTCCTGACAGAGAAATGGCTGGTTGGCGCTTA 1183  
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 DB 1362 TCACAACTTCATGCTCTGCTGAAAAACATTCCTGACAGAGAAATGGCTGGTTGGCGCTTA 1303  
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 QY 1184 GTTGGGCTAGTACTGAGACTCAATGACTGAGACTTACTGAGGCTCGGCTCGCT 1243  
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 DB 1302 GTTGGGCTAGTACTGAGACTCAATGACTGAGACTTACTGAGGCTCGGCTCGCT 1243  
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 QY 1244 CTGAAAAAGTCTTAAAGAAATCTTCTCAGTTCTCTTGGAGAGACTGGCGCGGAGCGC 1303  
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 DB 1242 CTGAAAAAGTCTTAAAGAAATCTTCTCAGTTCTCTTGGAGAGACTGGCGCGGAGCGC 1183  
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 QY 1304 GAGAGACACAGGCGCTGACAAAGGCGCTGTGGTGGTGGAGTGGCGCATGTACGGG 1363  
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 QY 1364 CAGGCGCTTCTGCTGTGGCTGTGACGACGACGCGGACGACGACGACGACGAA 1423  
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 DB 1122 CAGGCGCTTCTGCTGTGGCTGTGACGACGACGCGGACGACGACGACGACGAA 1063  
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 QY 1424 CACCGCGCAAACTGCTGCGAGGACACCGGTGTACAGAGCGGGTGTATGACCGAGCTGAG 1483

DB 1062 CACCGCGCAAACTGCTGCGAGGACACCGTGTACAGAGGCGGGTGTATGACCGAGCTGAG 1003  
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 QY 1544 CCAATGCTGCTTGGTGGTGGCGGACGACCATGATCTCCGATCTGTGTGGCATCCAGCA 1603  
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 DB 942 CCAATGCTGCTTGGTGGTGGCGGACGACCATGATCTCCGATCTGTGTGGCATCCAGCA 883  
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 QY 1604 TACGCGCAATGTCAACAAATCAGCC 1629  
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 DB 882 TACGCGCAATGTCAACAAATCAGCC 857  
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RESULT 11  
 AF034633/c 1362 bp mRNA linear PRI 13-JUL-1998  
 LOCUS AF034633  
 DEFINITION Homo sapiens orphan G protein-coupled receptor (GPR39) mRNA,  
 complete cds.  
 ACCESSION AF034633  
 VERSION AF034633.1 GI:2654160  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 (bases 1 to 1362)  
 AUTHORS McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D.,  
 TITLE Hreniuk, D.L., Smith, R.G., Howard, A.D. and Van der Ploeg, L.H.  
 JOURNAL Cloning and characterization of two human G protein-coupled  
 MEDLINE receptor genes (GPR38 and GPR39) related to the growth hormone  
 98110578  
 PUBMED 9411746

REFERENCE  
 2 (bases 1 to 1362)  
 AUTHORS McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D.,  
 TITLE Hreniuk, D.L., Smith, R.G., Van Der Ploeg, L.H.T. and Howard, A.D.  
 JOURNAL Direct Submission  
 Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.,  
 Inc., PO Box 2000, Rahway, NJ 07065, USA  
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 VTSALVALPLFLANGTEYPLVNNPSHRLGLCNSSRTHHNPPTSNNSTCTNLSST  
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 HEV"

BASE COUNT 263 a 435 c 362 g 302 t  
 ORIGIN

Query Match 26.7%; Score 506; DB 9; Length 1362;  
 Best Local Similarity 100.0%; Pred. No. 3e-291;  
 Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 TCAACTTCATGCTCCTGAAACCATTTCTGACAGCAATTTGGCTTGGCGGCTGA 1183  
 DB 1362 TCAAACTTCATGCTCCTGAAACCATTTCTGACAGCAATTTGGCTTGGCGGCTGA 1303  
 QY 1184 GTTGGGCTAGTACTGAGCACTCAATGACTGAGCAATTTGGGCTTGGCGGCTT 1243  
 DB 1302 GTTGGGCTAGTACTGAGCACTCAATGACTGAGCAATTTGGGCTTGGCGGCTT 1243  
 QY 1244 CTGAAAGTCTTAAAGAAATCTTCTCACTTCTCTTGGACAGAGCACTGGCGGAGCC 1303  
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 DB 1182 GAAGAGCAACGGGCGCTGCAAAAGCGGCGCTGTGGTGGTGGAGTGGCATGTACGGC 1123  
 QY 1364 CAGGCGCTTCTGCTGGTGGCGCTGCTGACAGCGACAGCGGCGAGCAAGCTGCGACGA 1423  
 DB 1122 CAGGCGCTTCTGCTGGTGGCGCTGCTGACAGCGACAGCGGCGAGCAAGCTGCGACGA 1063  
 QY 1424 CACCCGCGCAAACTGCTGCGAGAGCACGCTGTACAGAGCGGGTGTGATGACCGAGCTGAG 1483  
 DB 1062 CACCCGCGCAAACTGCTGCGAGAGCACGCTGTACAGAGCGGGTGTGATGACCGAGCTGAG 1003  
 QY 1484 GTGAAAAACGCTGCTCGAGAAAGGAGAGATCATGTACGCCCGCAATAGAGACTGCT 1543  
 DB 1002 GTGAAAAACGCTGCTCGAGAAAGGAGAGATCATGTACGCCCGCAATAGAGACTGCT 943  
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 DB 942 CCAAGTGTGCTGGTGGTGGCGCCAGCAAGTATCTCCGAATCTGGTGGGATCCAGCA 883  
 QY 1604 TACGCCCAATGTACAAACATCAGCC 1629  
 DB 882 TACGCCCAATGTACAAACATCAGCC 857

RESULT 12  
 AX136698/c 587 bp DNA linear PAT 30-MAY-2001  
 LOCUS AX136698  
 DEFINITION Sequence 620 from Patent EP1067182.  
 ACCESSION AX136698  
 VERSION AX136698.1 GI:14273102  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 587)  
 Ote.T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and  
 Hayashi,K.  
 Secretory protein or membrane protein  
 Patent: EP 1067182-A 620 10-JAN-2001;  
 Helix Research Institute (JP)  
 FEATURES  
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BASE COUNT 117 a 162 c 140 g 162 t 6 others  
 ORIGIN

Query Match 19.3%; Score 366; DB 6; Length 587;  
 Best Local Similarity 99.8%; Pred. No. 3e-207;  
 Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1461 ACCGGGTTATGACGAGCTGAGTAGAAGAAACGCTCCGGAAGGAGAGAGATCATG 1520  
 DB 417 ACCGGGTTATGACGAGCTGAGTAGAAGAAACGCTCCGGAAGGAGAGAGATCATG 358

QY 1521 TACGCCCGAAGTAGACCTGCTCCAGTGTGCTTGGGCTTGGCGGAGCCATGCTC 1580  
 DB 357 TACGCCCGAAGTAGACCTGCTCCAGTGTGCTTGGGCTTGGCGGAGCCATGCTC 298  
 QY 1581 CGAATCTGTTGGGATCCAGCATATGCGCAATGTACACAAATCAGCCCTGGGAGACA 1640  
 DB 297 CGAATCTGTTGGGATCCAGCATATGCGCAATGTACACAAATCAGCCCTGGGAGACA 238  
 QY 1641 CGAGCAGAGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1700  
 DB 237 CGAGCAGAGGAG 178  
 QY 1701 AAACATATAATATTATAGCCCTCTGTTCTGCTGCTTACTGGCCAGAGAAATGATCAATT 1760  
 DB 177 AAACATATAATATTATAGCCCTCTGTTCTGCTGCTTACTGGCCAGAGAAATGATCAATT 118  
 QY 1761 TTTCACTTGGACTTGAACAGCTTCTTTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAG 1820  
 DB 117 TTTCACTTGGACTTGAACAGCTTCTTTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAG 58  
 QY 1821 CAACCCCGGGGAGTGGCTGTGTTAAAGAAACATTAATCTTTAGACAGTGT 1877  
 DB 57 CAACCCCGGGGAGTGGCTGTGTTAAAGAAACATTAATCTTTAGACAGTGT 1

RESULT 13  
 AX150120/c 444 bp DNA linear PAT 08-JUN-2001  
 LOCUS AX150120  
 DEFINITION Sequence 95 from Patent WO0136685.  
 ACCESSION AX150120  
 VERSION AX150120.1 GI:14348148  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 444)  
 Kroes,R.A., Moskal,J.R. and Yamamoto,H.  
 Differential gene expression in cancer  
 Patent: WO 0136685-A 95 25-MAY-2001;  
 Nixis Neurotherapies, Inc. (US)  
 FEATURES  
 source 1..444  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

BASE COUNT 95 a 113 c 94 g 142 t  
 ORIGIN

Query Match 19.2%; Score 364; DB 6; Length 444;  
 Best Local Similarity 99.8%; Pred. No. 4.6e-206;  
 Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1474 CCGAGCTGAGGTAGAAAAAGCTCTCCGAGAGGGGAGAGATCATGACCCCGAAGT 1533  
 DB 431 CCGAGCTGAGGTAGAAAAAGCTCTCCGAGAGGGGAGAGATCATGACCCCGAAGT 372  
 QY 1534 AGGACCTGCTCACTGCTGCTGGTGGTGGCCGAGGAGATCATGACCCCGAAGT 1593  
 DB 371 AGGACCTGCTCACTGCTGCTGGTGGTGGCCGAGGAGATCATGACCCCGAAGT 312  
 QY 1594 GCATCCAGCATACGCGCAATGTCAACAATCAGCCCTGGGAGACAGAGAGAGGGA 1653  
 DB 311 GCATCCAGCATACGCGCAATGTCAACAATCAGCCCTGGGAGACAGAGAGAGGGA 252  
 QY 1654 GAGACAG 1713  
 DB 251 GAGACAG 192  
 QY 1714 TTTAGCCCTCTGCTGCTGCTTACTGAGCAGAGAAATGATCAATTTTCACTGTTGA 1773  
 DB 191 TTTAGCCCTCTGCTGCTGCTTACTGAGCAGAGAAATGATCAATTTTCACTGTTGA 132  
 QY 1774 CTTGACAGCTTTCTTTTGCACAAGAGAGAAATTAACATGTTTCAAAACCGGGGGA 1833

|||||  
Db 131 CTGACAGCTCTTTTCCCAAGAGAGATTTTCAACTGTTTCAACCCGGGGA 72  
QY 1834 GTTGGCTGTGTTAAAGAACCATTAATGCTTTAGACAGTGTAAAAAAA 1888  
|||||  
Db 71 GTTGGCTGTGTTAAAGAACCATTAATGCTTTAGACAGTGTAAAAAAA 17  
|||||  
RESULT 14  
AX093191 396 bp DNA linear PAT 30-MAR-2001  
LOCUS  
DEFINITION Sequence 9 from Patent WO0118046.  
ACCESSION AX093191  
VERSION AX093191.1 GI:13509640  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 (bases 1 to 396)  
AUTHORS Xu, J. and Stolk, J. A.  
TITLE Ovarian tumor sequences and methods of use therefor  
JOURNAL Patent: WO 0118046-A 9 15-MAR-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source  
1. .396  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
misc\_feature 1. .396  
/note="n = A,T,C or G"  
BASE COUNT 90 a 117 c 95 g 92 t 2 others  
ORIGIN  
Query Match 16.7%; Score 316; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.9e-177; Indels 0; Gaps 0;  
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 274 CATCGGGGCACTTTTGGGATGTTCTTGTTCAGGCTTTGGCTGCAATCCAGTG 333  
|||||  
Db 5 CATCGGGGCACTTTTGGGATGTTCTTGTTCAGGCTTTGGCTGCAATCCAGTG 64  
|||||  
QY 334 CTAACGAGTGTGAAGATTCCAGCTGAACAGACGCTCTCTCCCGAGTTATTGTGA 393  
|||||  
Db 65 CTAACGAGTGTGAAGATTCCAGCTGAACAGACGCTCTCTCCCGAGTTATTGTGA 124  
|||||  
QY 394 TTGCACGGGTGAACGTTTCAGACATGTGTGAGAAAGATGATGAGCAAGTCCGGGAT 453  
|||||  
Db 125 TTGCACGGGTGAACGTTTCAGACATGTGTGAGAAAGATGATGAGCAAGTCCGGGAT 184  
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QY 454 CATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTGCCTGCGGGTACCA 513  
|||||  
Db 185 CATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTGCCTGCGGGTACCA 244  
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QY 514 GTTCCTTCTGCTCCCGGAGAACTGAACATGTTTGCATCAGCTGCTGCAACACCCCTCT 573  
|||||  
Db 245 GTTCCTTCTGCTCCCGGAGAACTGAACATGTTTGCATCAGCTGCTGCAACACCCCTCT 304  
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QY 574 TTGTACGGGCAAGG 589  
|||||  
Db 305 TTGTACGGGCAAGG 320  
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RESULT 15  
AX093381 369 bp DNA linear PAT 30-MAR-2001  
LOCUS  
DEFINITION Sequence 199 from Patent WO0118046.  
ACCESSION AX093381  
VERSION AX093381.1 GI:13509829  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 369)  
AUTHORS Xu, J. and Stolk, J. A.  
TITLE Ovarian tumor sequences and methods of use therefor  
JOURNAL Patent: WO 0118046-A 199 15-MAR-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source  
1. .369  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
misc\_feature 1. .369  
/note="n = A,T,C or G"  
BASE COUNT 82 a 109 c 90 g 86 t 2 others  
ORIGIN  
Query Match 16.6%; Score 315; DB 6; Length 369;  
Best Local Similarity 100.0%; Pred. No. 1.2e-176; Indels 0; Gaps 0;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 309 CAGGCTTGGCGCTGCAATCCAGTGTACAGTGTGAAGATTCCAGCTGACACAGCT 368  
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Db 30 CAGGCTTGGCGCTGCAATCCAGTGTACAGTGTGAAGATTCCAGCTGACACAGCT 89  
|||||  
QY 369 GCTCCTCCCCGAGTTCAATTGTGAATTGCACGGTGAACGTTCAAGACATGTGCAGAA 428  
|||||  
Db 90 GCTCCTCCCCGAGTTCAATTGTGAATTGCACGGTGAACGTTCAAGACATGTGCAGAA 149  
|||||  
QY 429 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCAATCCAGGCT 488  
|||||  
Db 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCAATCCAGGCT 209  
|||||  
QY 489 GTCTCATGCGCTTGGCGGATGACAGTCTTCTGCTCCCGAGGAACTGACATTT 548  
|||||  
Db 210 GTCTCATGCGCTTGGCGGATGACAGTCTTCTGCTCCCGAGGAACTGACATTT 269  
|||||  
QY 549 GCATCAGCTGCTGCAACACCCCTTTGTGAACGGGCCAAGGCCCAAGAAAGGGAATT 608  
|||||  
Db 270 GCATCAGCTGCTGCAACACCCCTTTGTGAACGGGCCAAGGCCCAAGAAAGGGAATT 329  
|||||  
QY 609 CTGCCTCGGCGCTCA 623  
|||||  
Db 330 CTGCCTCGGCGCTCA 344  
|||||  
RESULT 16  
AC010974/c 147131 bp DNA linear PRI 01-MAR-2002  
LOCUS  
DEFINITION Homo sapiens BAC clone RP11-159N20 from 2, complete sequence.  
ACCESSION AC010974  
VERSION AC010974.9 GI:19033964  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 147131)  
AUTHORS Sulston, J.E. and Waterston, R.  
TITLE Toward a complete human genome sequence  
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
MEDLINE 99063792  
PUBMED 9847074  
REFERENCE 2 (bases 1 to 147131)  
AUTHORS VanBrunt, A. and Strommatt, C.  
TITLE The sequence of Homo sapiens BAC clone RP11-159N20  
JOURNAL unpublished (2001)  
REFERENCE 3 (bases 1 to 147131)  
AUTHORS Waterston, R. H.  
TITLE Direct Submission  
JOURNAL Submitted (28-SEP-1999) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE 4 (bases 1 to 147131)  
AUTHORS Waterston, R. H.  
TITLE Direct Submission

## JOURNAL

Submitted (23-MAR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

5 (bases 1 to 147131)

## REFERENCE

Waterston, R.

## AUTHORS

Direct Submission

## JOURNAL

Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Mar 1, 2002 this sequence version replaced gi:13435273.

## COMMENT

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: [saplense@wustl.edu](mailto:saplense@wustl.edu)

----- Summary Statistics

Center project name: H\_NH0159N20

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

## SOURCE INFORMATION:

The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J. J. and de Jong, P. J. (1996) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBAC3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-458A7, 200 bp overlap; the clone sequenced to the right is RP11-258B17. Actual start of this clone is at base position 1 of RP11-159N20; actual end is at base position 147131 of RP11-159N20.

## FEATURES

## source

There are polymorphic base differences in the overlap between the clone RP11-159N20 and RP11-258B17.  
Location/Qualifiers

1. 147131

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="2"

/map="2"

/clone\_1lb="RPCT-11"

21. 67

/clone\_1lb="RP11-159N20"

/rpt\_family="MIR"

repeat\_region

118. 1013

/rpt\_family="L1"

984. 1176

/note="match to EST BG200048 (NID:g13721735)"

991. 1176

/note="match to EST BG184021 (NID:g13705708)"

991. 1176

/note="match to EST BG187166 (NID:g13708853)"

repeat\_region

1035. 1200

/rpt\_family="Alu"

repeat\_region

1525. 1552

/rpt\_family="(TTTA)n"

repeat\_region

1526. 1814

/rpt\_family="Alu"

repeat\_region

2299. 2596

/rpt\_family="Alu"

repeat\_region

4860. 5129

/rpt\_family="MALR"

repeat\_region

5738. 5757

/rpt\_family="(TG)n"

repeat\_region

6131. 6178

/rpt\_family="GA-rich"

misc\_feature

7310. 7364

/note="match to EST A1239596 (NID:g3834993) qh37b10.x1"

repeat\_region

7811. 7881

/rpt\_family="MIR"

repeat\_region

8227. 8260

/rpt\_family="(CATC)n"

repeat\_region

8373. 8683

/rpt\_family="L1"

misc\_feature

8640. 9120

/note="match to EST BF112212 (NID:g10941902)"

repeat\_region

8776. 8838

/rpt\_family="MIR"

misc\_feature

8810. 9257

/note="match to EST AA434316 (NID:g2139230) zw24e08.r1"

repeat\_region

9348. 9395

/rpt\_family="GA-rich"

misc\_feature

9731. 9895

/note="match to EST BF347279 (NID:g11294874)"

misc\_feature

9743. 9895

/note="match to EST BG184021 (NID:g13705708)"

misc\_feature

9743. 9895

/note="match to EST BG187166 (NID:g13708853)"

repeat\_region

10053. 10359

/rpt\_family="Alu"

repeat\_region

12424. 12509

/rpt\_family="MIR"

repeat\_region

12503. 12671

/rpt\_family="MER1-type"

misc\_feature

13456. 13776

/note="match to EST A1239596 (NID:g3834993) qh37b10.x1"

misc\_feature

13854. 13855

/note="match to EST A1239596 (NID:g3834993) qh37b10.x1"

misc\_feature

15183. 15321

/note="match to EST BE386060 (NID:g9331425)"

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15183. 15321

/note="match to EST BG704350 (NID:g13977603)"

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15183. 15321

/note="match to EST BG753617 (NID:g14064270)"

misc\_feature

15183. 15321

/note="match to EST H05756 (NID:g870288) y183b07.r1"

misc\_feature

15184. 15321

/note="match to EST BF347279 (NID:g11294874)"

misc\_feature

15184. 15320

/note="match to EST BG184021 (NID:g13705708)"

misc\_feature

15184. 15320

/note="match to EST BG187166 (NID:g13708853)"

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15767. 15789

/note="match to EST BG200048 (NID:g13721735)"

misc\_feature

15864. 18081

/rpt\_family="AT-rich"

repeat\_region

16665. 17055

/note="CpG island (%G-C=68.0, o/e=0.80, #CpGs=194)"

misc\_feature

16665. 17055

/note="match to EST BG704350 (NID:g13977603)"

misc\_feature

16665. 16984

/note="match to EST BF347279 (NID:g11294874)"

misc\_feature

16665. 16728

/note="match to EST BG753617 (NID:g14064270)"

misc\_feature

16665. 16686

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Best Local Similarity 100.0%; Pred. No. 6.8e-164;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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RESULT	17	AC124493/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
			AC124493	209885 bp	DNA	linear	HTG_05-JUL-2002		
				Mus musculus chromosome UKK clone RP23-462P13, WORKING DRAFT SEQUENCE, 5 unordered pieces.					
			AC124493						
			AC124493.2	GI:21699722					
				HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.					
				house mouse.					
				Mus musculus					

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bass 1 to 209885)  
McPherson, J.D. and Webster, R.H.  
The sequence of *Mus musculus* clone  
unpublished  
2 (bass 1 to 209885)  
McPherson, J.D. and Webster, R.H.  
Direct Submission  
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
----- Project Information -----  
Center project name: W\_BA0462P3

Parameter	Value
Sequencing vector	M13, 0%
Sequencing vector	plasmid, 100%
Chemistry	Dye-Primer ET, % of reads
Chemistry	Dye-terminator Big Dye, 100% of reads
Assembly program	Phrap, version 0.990319
Consensus quality	208484 bases at least Q40
Consensus quality	208931 bases at least Q30
Consensus quality	209285 bases at least Q20
Insert size	206000, agarose-fp
Insert size	212112, sum-of-contigs
Quality coverage	0.00 in Q20 bases, agarose-fp
Quality coverage	11.62 in Q20 bases, sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

Accession	Length	Gap	Unknown Length	Length
1	11331	config of 11331 bp in	length	
*	11332	gap of unknown length	length	
*	11431	gap of unknown length	length	
*	28617	config of 17286 bp in	length	
*	28618	gap of unknown length	length	
*	28718	gap of 2037 bp in	length	
*	49454	config of unknown length	length	
*	49554	gap of unknown length	length	
*	107354	config of 57830 bp in	length	
*	49555	gap of unknown length	length	
*	107385	gap of unknown length	length	
*	209884	config of 102401 bp in	length	
*	107485	gap of unknown length	length	

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/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-462P13"
1..11331
/misc_feature
/note="assembly_name:Contig8"
11432..28617
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/note="assembly_name:Contig9"
28718..49454
/misc_feature
/note="assembly_name:Contig10"
49555..107384
/misc_feature
/note="assembly_name:Contig11"
107485..209885
/misc_feature
/note="assembly_name:Contig12"
59789 a 44784 c 46164 g 58745 t 403 others
BASE COUNT
ORIGIN

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Query Match Similarity	2.5%;	Score 47;	DB 2;	Length 209885;
Best Local Similarity	100.0%;	Pred. No. 1,2e+15;		
Matches 47;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	401	GTTAAGCTTCAAGACATGTCGTAGAAAGATGATGAGCAAAATGC	447	
Db 103249	GTTAAGCTTCAAGACATGTCGTAGAAAGATGATGAGCAAAATGC	103203		



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----- Project Information
Center project name: GUSG
Center clone name: CH230-71J19
Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 82161 bases at least Q40
Consensus quality: 88014 bases at least Q30
Consensus quality: 92229 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.ngsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 52 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1165: contig of 1165 bp in length
1166: gap of unknown length
1266: contig of 1381 bp in length
2647: gap of unknown length
2747: contig of 1359 bp in length
4306: gap of unknown length
4406: contig of 1442 bp in length
5848: gap of unknown length
5948: contig of 1648 bp in length
7595: gap of unknown length
7695: contig of 1151 bp in length
8846: gap of unknown length
8947: contig of 1117 bp in length
10064: gap of unknown length
10163: contig of 1318 bp in length
11581: gap of unknown length
11582: contig of 1071 bp in length
12653: gap of unknown length
12752: contig of 1004 bp in length
13755: gap of unknown length
13856: contig of 1043 bp in length
13857: gap of unknown length
14900: contig of 1179 bp in length
15000: gap of unknown length
16179: contig of 1436 bp in length
16278: gap of unknown length
17714: contig of 1071 bp in length
17814: gap of unknown length
17815: contig of 1691 bp in length
19505: gap of unknown length
19506: contig of 2279 bp in length
21884: gap of unknown length
21885: contig of 1585 bp in length
21985: gap of unknown length
23569: contig of 1760 bp in length
23570: gap of unknown length
25429: contig of 1294 bp in length
25430: gap of unknown length
25529: contig of 1578 bp in length
26823: gap of unknown length
26824: contig of 1030 bp in length
28501: gap of unknown length
28502: contig of 1030 bp in length
28602: gap of unknown length
28631: contig of 1082 bp in length
29732: gap of unknown length
30813: contig of 1716 bp in length
30914: gap of unknown length
32629: contig of 1173 bp in length
32729: gap of unknown length
32730: contig of 1173 bp in length
33903: gap of unknown length
34003: contig of 1364 bp in length
35366: gap of unknown length
35466: contig of 1651 bp in length
37117: gap of unknown length
37218: contig of 1608 bp in length
38825: gap of unknown length
38925: gap of unknown length

```

```

38926 41573: contig of 2648 bp in length
41574 41574: gap of unknown length
41674 43020: contig of 1347 bp in length
43021 43120: gap of unknown length
43121 44790: contig of 1670 bp in length
44791 44890: gap of unknown length
44891 46626: contig of 1736 bp in length
46627 46726: gap of unknown length
46727 47819: contig of 1093 bp in length
47820 47919: gap of unknown length
47920 49621: contig of 1702 bp in length
49622 49721: gap of unknown length
49722 51446: contig of 1725 bp in length
51447 51546: gap of unknown length
51547 53382: contig of 1836 bp in length
53383 53482: gap of unknown length
53483 55863: contig of 2381 bp in length
55864 55963: gap of unknown length
55964 58398: contig of 2435 bp in length
58399 58498: gap of unknown length
58499 61923: contig of 3425 bp in length
61924 62023: gap of unknown length
62024 65252: contig of 3229 bp in length
65253 65352: gap of unknown length
65353 67262: contig of 1910 bp in length
67263 67362: gap of unknown length
67363 69711: contig of 2348 bp in length
69711 69810: gap of unknown length
73439: contig of 3629 bp in length
73440 73539: gap of unknown length
76475: contig of 2936 bp in length
76476 76575: gap of unknown length
76576 80568: contig of 3993 bp in length
80569 80668: gap of unknown length
80669 84177: contig of 3509 bp in length
84178 84277: gap of unknown length
84278 89159: contig of 4882 bp in length
89160 89259: gap of unknown length
89260 92924: contig of 3665 bp in length
92925 93025: gap of unknown length
93025 96972: contig of 3948 bp in length
96973 97072: gap of unknown length
97073 100972: contig of 3900 bp in length
100973 101072: gap of unknown length
101073 107076: contig of 6004 bp in length
107077 107176: gap of unknown length
107177 113525: contig of 6349 bp in length
113526 113625: gap of unknown length
113626 119430: contig of 5805 bp in length
119431 119530: gap of unknown length
119531 125703: contig of 6173 bp in length.

FEATURES
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1..125703
/organism="Rattus norvegicus"
/db_xref="taxon:10116"

Query Match
Best Local Similarity 100.0%; Score 30; DB 2: Length 125703;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1868 TAGCAGCTGTAAAAA 1897
Db 37842 TAGCAGCTGTAAAAA 37813

RESULT 20
AF150733
LOCUS Homo sapiens AD-014 protein mRNA, complete cds.
DEFINITION AF150733
ACCESSION AF150733.1 GI:7688664
VERSION
KEYWORDS
SOURCE Homo sapiens.

```

```

ORGANISM      Homo sapiens
REFERENCE      Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
AUTHORS       Fu, S., Gu, Y., Li, Y., Peng, Y., Gu, J., Zhang, L., Jiang, C., Yu, Y.,
              Fu, G., Wang, Y., Chen, Z., and Han, Z.
TITLE         A novel gene expressed in human adrenal gland
JOURNAL       Unpublished
REFERENCE      2 (bases 1 to 487)
AUTHORS       Fu, S., Gu, Y., Li, Y., Peng, Y., Gu, J., Zhang, L., Jiang, C., Yu, Y.,
              Fu, G., Wang, Y., Chen, Z., and Han, Z.
TITLE         Direct Submission
JOURNAL       Submitted (12-MAY-1999) Chinese National Human Genome Center at
              Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
              Shanghai 201203, P. R. China
FEATURES      source
              1..487
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               /db_xref="taxon:9606"
               /tissue_type="adrenal gland"
               /note="protein x 0007"
               /codon_start=1
               /product="AD-014 protein"
               /protein_id="AAF67473.1"
               /db_xref="GI:768865"
               /translation="MWKLSKAKKQRLQQLFKGSQFAIRMGFIPVIVYLGFKRGADPGM
               PEPVYSLIMG"
BASE COUNT    135 a      101 c      128 g      122 t      1 others
ORIGIN
Query Match   1.4%: Score 27; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAACAAAAA 1897
Db 452 ACAGTGTAACAAAAA 478

RESULT 21
AF082874      1086 bp      mRNA      linear      PLN 20-AUG-1998
LOCUS        Medicago sativa glycolate oxidase mRNA, partial cds.
DEFINITION   AF082874
ACCESSION    AF082874
VERSION      AF082874.1 GI:3435305
KEYWORDS     Medicago sativa.
SOURCE       Medicago sativa.
ORGANISM     Medicago sativa.
REFERENCE    1 (bases 1 to 1086)
AUTHORS      Stout, J.M. and McKersie, B.D.
TITLE        Gene expression in alfalfa
JOURNAL       Unpublished
REFERENCE    2 (bases 1 to 1086)
AUTHORS      Stout, J.M. and McKersie, B.D.
TITLE        Direct Submission
JOURNAL       Submitted (07-AUG-1998) Plant Biotechnology Division, Dept of Plant
              Agriculture, University of Guelph, Crop Science Building, Guelph,
              Ont N1G 2W1, Canada
FEATURES      source
              1..1086
               /organism="Medicago sativa"
               /db_xref="taxon:3879"
               /clone="N4-4-2"
               /tissue_type="shoot apical meristem"
               /note="Longest ORF"
               /protein_id="AAC32392.1"

```

```

/db_xref="GI:3435306"
/translation="EYATARAASAACTIMTISMAATSSVEEVAATSPGIRFOLYVYK
DRANVADLVNRAKAGKATALVTDPRIGRRADRNKFNVPRLPTLKEGKLNIGK
MDQANDSGLASVAGQMNRTLSWVKDQNTSLPLTKVGLTADDTLAVQSCAG
IIGPNHGAQLDIDVPPNNNGFKEVYAAAGRVVFLDGVGPRGTNFKALAGASIE
IGRPVYSILPAEEGAGRVKQLQMLRDEFELTMSLSCRSKETSIDSHIVADWDPKVN
PRAIPRL"
BASE COUNT    332 a      199 c      249 g      306 t
ORIGIN
Query Match   1.4%: Score 27; DB 8; Length 1086;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAACAAAAA 1897
Db 1053 ACAGTGTAACAAAAA 1079

RESULT 22
AY118558      1114 bp      mRNA      linear      INV 15-JUN-2002
LOCUS        Drosophila melanogaster full insert cDNA.
DEFINITION   AY118558
ACCESSION    AY118558
VERSION      AY118558.1 GI:21428533
KEYWORDS     F11.CDNA.
SOURCE       fruit fly
ORGANISM     Drosophila melanogaster
REFERENCE    1 (bases 1 to 1114)
AUTHORS      Stappleton, M., Brocks, P., Hong, L., Agbayani, A., Carlson, J.,
              George, R., Gonzalez, M., Guarin, H., Kromm, J., Paragas, V., Park, S.,
              Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
              and Ceiniker, S.
TITLE        Direct Submission
JOURNAL       Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
              Lawrence Berkeley National Laboratory, One Cyclotron Road,
              Berkeley, CA 94720, USA
COMMENT      Berkeley Drosophila Genome Project
              Lawrence Berkeley National Laboratory
              Berkeley, CA 94720
              This clone was sequenced as part of a high-throughput process to
              sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
              Science 2000). The sequence has been subjected to integrity checks
              for sequence accuracy, presence of a polyA tail and contiguity
              within 100 kb in the genome. Thus we believe the sequence to
              reflect accurately this particular cDNA clone. However, there are
              artifacts associated with the generation of cDNA clones that may
              have not been detected in our initial analyses such as internal
              priming, priming from contaminating genomic DNA, retained introns
              due to reverse transcription of unspliced precursor RNAs, and
              reverse transcriptase errors that result in single base changes.
              For further information about this sequence, including its location
              and relationship to other sequences, please visit our web site
              (http://fruitfly.berkeley.edu) or send email to
              cna@fruitfly.berkeley.edu.
FEATURES      source
              1..1114
               /organism="Drosophila melanogaster"
               /strain="y; cn bw sp"
               /db_xref="taxon:7227"
               /gene="CG13601"
               /db_xref="FlyBase:FBgn0039126"
               /gene="CG13601"
               /note="Longest ORF"
               /codon_start=1

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BASE COUNT 334 a 259 c 278 g 243 t

ORIGIN

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/product="LD37258bp"
/protein_id="AAM49927.1"
/db_xref="GI: 21428534"
/db_xref="FLYBASE:FBN0039126"
/translation="TWIGFPRALGILAIQVSKPIANVYKSNKSSPFRRYICMP
PAQRYNVEYVTKKMAALMGGRVNPPLNEMALIELGANLIGEFIIFSIGGLIFEE
SRQITKEKKNELQASEREMELJNNLTENFPLEBQDQAIIRMTFVLADLDSGRNFI
KEAIOEYVFPDPDTPDOSASARNPKKFDSDLPDQGAGAFRALHFLDIOIFVDGGRNRA
KFAIQLHDEVAVOLQEOSGEAATYAAVVASLPTKAADL"

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	Query Match	Score 27:	DB 3:	length 1114;
	Best Local Similarity	100.0%;	Pred. No.	0.00087;
Matches	27:	Conservative	0;	Mismatches 0;
				Indels 0; Gaps 0
Oy	1871	ACAGTGTA	AAAAAAAAAAAAA	1897
Db	1066	ACAGTGT	AAAAAAAAAAAAA	1092

RESULT	23			
AX285020				
LOCUS	AX285020	1368 bp	DNA	
DEFINITION	Sequence 825 from Patent WO0179556.		linear	PAT 20-NOV-2001
ACCESSION	AX285020			
VERSION	AX285020.1	GI:17045708		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1	Millie, J., Brown, J. L., Bolt, A., and van Hufel, C.	Novel genes, compositions and methods for the identification, assessment, prevention, and therapy of human cancers	Patent: WO 0179556-A 825 25-OCT-2001;	Millennium Predictive Medicine, Inc. (US)	Location/Qualifiers I. .1368
	Mammalia; Eutheria; Primates; Carnathi; Homnidae; Homo.				

BASE COUNT	517	a	312	c	321	g	213	t	5	others
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606"									
Query Match	1.4%;	Score 27;	DB 6;	Length 1368;						
Best Local Similarity	100.0%;	Pred. No. 0.00088;								
Matches 27;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;						

QY	1871	ACAGTGTAAAAA	1897
Db	459	ACAGTGTAAAAA	485

RESULT 24					
AK026521					
LOCUS	AK026521	1614 bp	mRNA	linear	PRI 29-SEP-2000
DEFINITION	Homo sapiens cDNA: FLJ22868 fis, clone KAT02340, highly similar to				
ACCESSION	HUMFSL1C Homo sapiens transcription factor SL1 mRNA.				
	AK026521				

ORGANISM Homo sapiens  
 SOURCE Homo sapiens signet-ring cell carcinoma cell\_line:KATO III CDNA tc  
 KEYWORDS oligo capping; fis (full insert sequence).  
 VERSION AK026521.1 GI:10439398  
 DESCRIPTION AK026521.1 GI:10439398

REFERENCE	AUTHORS	TITLE	JOURNAL
Eukaryota; Chordates; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (sites)	Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H., Ota,T., Suzuki,Y., Obayashi,M., Nishii,T., Shibahara,T., Tanaka,T., Nakamura,Y., Iisagoi,T. and Sugano,S.	NEDO human cDNA sequencing project	Unpublished

REFERENCE 2 (pages 1 to 1614)  
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,  
TITLE Shibahara,T., Tanaka,T. and Nakamura,Y.  
JOURNAL Direct Submission  
Submitted (29-AUG-2000) Sumto Sugano, Institute of Medical Science

COMMENT

University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@ems.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Affairs

COMMENT 1  
MBCO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' & 3'-end one pass sequencing: Department of Virology and Human genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency);

FEATURES	Location/Qualifiers
source	1. .1614

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT02340"
/cell_line="KATO III"
/cell_type="signet-ring cell carcinoma"
/clone_lib="KAT"
/clone="cloning vector pME18SFL3"
1..1614
/note="highly similar to HUMTSLIC Homo sapiens
transcription factor S11 mRNA"
misc_feature
BASE COUNT      557 a      296 c      337 g      424 t
ORIGIN

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Query Match 1.4%; Score 27; DB 9; Length 161;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1871 ACAGCTAAAAAAAAAAAAAAAA 1897
    |||
Db 1581 ACAGCTAAAAAAAAAAAAAAAA 1607

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RESULT 25							PRI 16-MAY-2002
BC028978	Homo sapiens, clone IMAGE:3919084,	2625 bp	MRNA				linear
LOCUS	BC028978						
DEFINITION	Homo sapiens, clone IMAGE:3919084,						
ACCESSION	BC028978						
VERSION	BC028978.1	GI:20810049					
KEYWORDS	.						
SOURCE	Homo sapiens.						

REFERENCE	ORGANISM	SOURCE
1 (bases 1 to 2625)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	Homo sapiens.
Stratopoulos		Homo sapiens.

TIME	Direct Submission
JOURNAL	Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC/DCMP/DRP  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Guaratine, P.H., Garcia, A.M., Lu, X., Huilyr, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/URL at: <http://image.llnl.gov>  
Series: IRAC Plate: 42 Row: b Column: 17.  
Location/Qualifiers

FEATURES  
source 1. 2625

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3919084"  
/issue="type="Skin, melanotic melanoma."  
/clone\_id="NH\_MGC\_72"  
/lab\_host="DH10B"  
/note="vector: pCMV-SPOB6"  
BASE COUNT 860 a 538 c 502 g 725 t  
ORIGIN

Query Match 1.4%; Score 27; DB 9; Length 2625;  
Best local Similarity 100.0%; Pred. No. 0.00092;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAA 1897  
Db 2567 ACAGTGTAAAAA 2593

RESULT 26  
AY094780 3155 bp mRNA linear INV 15-APR-2002  
DEFINITION Drosophila melanogaster full insert cDNA.  
ACCESSION AY094780  
VERSION AY094780.1 GI:20151546  
KEYWORDS FLI-CDNA.  
SOURCE Drosophila melanogaster.  
ORGANISM Drosophila melanogaster.  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 3155)  
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agdayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, Y., Dresnek, D., Fartan, D., Frise, E., George, R., Gonzalez, M., Guartin, H., Krommiller, B., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nuno, J., Paclet, J., Paragas, V., Park, S., Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M. and Celisner, S.  
COMMENT Direct Submission  
Submitted (03-APR-2002) Berkeley Drosophila Genome Project,  
Lawrence Berkeley National Laboratory, One Cyclotron Road,  
Berkeley, CA 94720, USA  
Sequence submitted by:  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Berkeley, CA 94720

FEATURES  
source 1. 3155  
/organism="Drosophila melanogaster"  
/strain="y: cn bw sp"  
/db\_xref="taxon:7227"  
/map="43D3-43D3"  
1. 3155  
Location/Qualifiers  
This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our web site (<http://fruitfly.berkeley.edu>) or send email to [cdna@fruitfly.berkeley.edu](mailto:cdna@fruitfly.berkeley.edu).

FEATURES  
source 1. 3155  
/organism="Drosophila melanogaster"  
/strain="y: cn bw sp"  
/db\_xref="taxon:7227"  
/map="43D3-43D3"  
1. 3155  
Location/Qualifiers  
This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our web site (<http://fruitfly.berkeley.edu>) or send email to [cdna@fruitfly.berkeley.edu](mailto:cdna@fruitfly.berkeley.edu).

/gene="Orcl"  
/note="alignment with genomic scaffold AE003840 and gene has no introns and polyA tail is encoded in the genomic"  
/db\_xref="FlyBase:FBgn0022772"  
112..2886  
/gene="Orcl"  
/note="Longest ORF"  
/codon\_start=1  
/product="lD11626p"  
/db\_xref="GI:20151347"  
/protein\_id="AA01133.1"  
/db\_xref="FlyBase:FBgn0022772"  
/translation="MVKENARSGOQVKKIGSODELPYKLNENKVVYQKCIYCP  
LTVSGDFILSNADAAEPDVTGSCDVARIHMYELRLDREPCRAIVQWSPKAI  
PHNKYDDDEVAIDPSLEVEIHRPYDNDVALGAIKRYCLEGTSKAEILKRAH  
KLSSTACPMVSRVRRKRRASMASSSEFIDVNSFICENKVSPIKTVGRSVRL  
ISARHDTACNKSVEKRRASMASSSEFIDVNSFICENKVSPIKTVGRSVRL  
SEKNAPEINANYLPASPLEKNAKVEPTRRASAAARNLNSLDGADTTADSCIN  
VSIYOQTPDEPTSDMKIKRLSERRSVRLASMDVPLSLAEVQPRNSHLSNV  
VANGDIYHTPTKRSKEPLSAATEQTPTRRSKSIKSAVSRLAEGTPRSILSNIV  
EORVEDEDEIITPRGRSKKTYODNEDYSPKSVQKPTPTRRSSTTKATTPSK  
GITATATPMPSPQMKIRAGELSPSMOORTPLPAKDSKSELALROLHVSVPK  
SLPCREREFENITALEGKIQDCCGCGMYSGVPGCKTATVGVIRTLORMAKONEL  
PAFEYLEINGRILTEPRQAVVQIKQLGTIVSMEQAHALLERFTTPAPRVYTL  
VDEDDILCNRODVYVNLDMPTKSAKLVVITANTMDLPERLKGATYSRGLTRL  
TFQPSYSHKLOEIVTARLGSETEFGCAVOLAVKAAVAGDARRALDLCRRYETAD  
TAAVKCYTLMHVOQALAEIASAKVQAIKNCSEMEQIFLOAIAEYVTRGVETETMG  
VYOOVENTIAAFMGTFFPPPRALRLCKLCAERLIISEHSRNDLFKILLNVSADDIH  
YALVEMENVN"

BASE COUNT 847 a 864 c 821 g 623 t  
ORIGIN

Query Match 1.4%; Score 27; DB 3; Length 3155;  
Best local Similarity 100.0%; Pred. No. 0.00093;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAA 1897  
Db 3127 ACAGTGTAAAAA 3153

RESULT 27  
AL645986 48206 bp DNA linear ROD 19-JUL-2002  
LOCUS AL645986/c  
DEFINITION Mouse DNA sequence from clone DN-35368 on chromosome 1, complete  
ACCESSION AL645986  
VERSION AL645986.6 GI:18855238  
KEYWORDS HTG.  
SOURCE Mus musculus.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 48206)  
AUTHORS Kimberley, A.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Feb 21, 2002 this sequence version replaced gi:117529535.

COMMENT During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following



```

* 12015 13145: contig of 1131 bp in length
* 13146 13245: gap of unknown length
* 13246 14584: contig of 1339 bp in length
* 14585 14684: gap of unknown length
* 14685 16404: contig of 1720 bp in length
* 16405 16504: gap of unknown length
* 16505 17655: contig of 1151 bp in length
* 17656 17755: gap of unknown length
* 17756 19240: contig of 1485 bp in length
* 19341 19340: gap of unknown length
* 19341 20647: contig of 1307 bp in length
* 20648 20747: gap of unknown length
* 20748 22171: contig of 1424 bp in length
* 22172 22271: gap of unknown length
* 22272 23762: contig of 1491 bp in length
* 23763 23862: gap of unknown length
* 23863 25556: contig of 1694 bp in length
* 25557 25656: gap of unknown length
* 25657 26711: contig of 1055 bp in length
* 26712 26811: gap of unknown length
* 26812 28747: contig of 1936 bp in length
* 28748 28847: gap of unknown length
* 28848 30564: contig of 1717 bp in length
* 30565 30664: gap of unknown length
* 30665 32046: contig of 1382 bp in length
* 32047 32146: gap of unknown length
* 32147 33729: contig of 1583 bp in length
* 33730 33829: gap of unknown length
* 33830 35524: contig of 1695 bp in length
* 35525 35624: gap of unknown length
* 35625 37292: contig of 1668 bp in length
* 37293 37392: gap of unknown length
* 37393 38486: contig of 1094 bp in length
* 38487 38586: gap of unknown length
* 38587 40145: contig of 1559 bp in length
* 40146 40245: gap of unknown length
* 40246 41925: contig of 1680 bp in length
* 41926 42025: gap of unknown length
* 42026 43669: contig of 1644 bp in length
* 43670 43769: gap of unknown length
* 43770 45713: contig of 1944 bp in length
* 45714 45813: gap of unknown length
* 45814 47315: contig of 1502 bp in length
* 47316 47415: gap of unknown length
* 47416 48852: contig of 1437 bp in length
* 48853 48952: gap of unknown length
* 48953 50511: contig of 1559 bp in length
* 50512 50611: gap of unknown length
* 50612 52672: contig of 2061 bp in length
* 52673 52772: gap of unknown length
* 52773 54274: contig of 1502 bp in length
* 54275 54374: gap of unknown length
* 54375 55993: contig of 2619 bp in length
* 55994 57093: gap of unknown length
* 57094 59151: contig of 2422 bp in length
* 59152 59616: gap of unknown length
* 59616 61878: contig of 2263 bp in length
* 61879 64520: gap of unknown length
* 64520 64620: contig of 2442 bp in length
* 64621 64620: gap of unknown length
* 64621 67430: contig of 2810 bp in length
* 67431 67530: gap of unknown length
* 67531 68852: contig of 1322 bp in length
* 68853 68952: gap of unknown length
* 68953 70700: contig of 1748 bp in length
* 70701 70800: gap of unknown length
* 70801 72350: contig of 1550 bp in length
* 72351 72450: gap of unknown length
* 72451 74628: contig of 2178 bp in length
* 74629 74728: gap of unknown length
* 74729 76922: contig of 2194 bp in length
* 76923 77022: gap of unknown length
* 77023 79345: contig of 2323 bp in length

```

```

* 79346 79445: gap of unknown length
* 79446 82316: contig of 2871 bp in length
* 82317 82417: gap of unknown length
* 82417 84867: contig of 2450 bp in length
* 84867 84966: gap of unknown length
* 84967 87959: contig of 2993 bp in length
* 87960 88059: gap of unknown length
* 88060 92874: contig of 4815 bp in length.

FEATURES
  source
    1. 92874
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"
    /clone="CH230-286021"

BASE COUNT   23927 a   19653 c   20425 g   23828 t   5041 others

ORIGIN
Query Match      1.4%; Score 27; DB 2; Length 92874;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 GAGAGGAGGAGGATCATGTACGCC 1526
Db 75643 GAGAGGAGGAGGATCATGTACGCC 75669

```

```

RESULT 29
AL807806/c
LOCUS
DEFINITION
  Mus musculus chromosome X clone RP23-67K19, *** SEQUENCING IN
  PROGRESS ***, 2 unordered pieces.
ACCESSION
  AL807806
  AL807806.4 GI:22416117
VERSION
  HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
  house mouse.
SOURCE
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 127524)
REFERENCE
  Whitehead, S.
  Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  humquerry@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
  On Aug 21, 2002 this sequence version replaced gi:21694507.
JOURNAL
  Genome Center
  Center: Wellcome Trust Sanger Institute
  Center code: SC
  Web site: http://www.sanger.ac.uk
  Contact: humquerry@sanger.ac.uk
  Project information
  Center project name: BM67K19
  Summary Statistics
  Assembly program: XGAP4; version 4.5
  Chemistry: Dye-terminator; 100% of reads
  Consensus quality: 127311 bases at least Q40
  Consensus quality: 127389 bases at least Q30
  Consensus quality: 127413 bases at least Q20
  Insert size: 127424; sum-of-ctrls
  Insert size: 142249; 4.2% error; agarose-fp
  Quality coverage: 8.1lx in Q20 bases; sum-of-ctrls Quality
  coverage: 7.35x in Q20 bases; agarose-fp

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 24018: contig of 24018 bp in length
* 24019 24118: gap of 100 bp
* 24119 127524: contig of 103406 bp in length.

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FEATURES
  source
    Location/Qualifiers
      1..127524
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        /db_xref="taxon:10090"
        /chromosome="X"
        /clone_1ID="RPCI-23"
        /clone_1ID="RPCI-23"
        /note="assembly_fragment:00530"
      misc_feature
        24119..127524
          /note="assembly_fragment:00777.0"
      misc_feature
        37921 a 23572 c 23574 g 42574 t 100 others
      BASE COUNT
        37921 a 23572 c 23574 g 42574 t 100 others
      ORIGIN

Query Match
  Best Local Similarity 100.0%; Pred. No. 0.0012;
  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1871 ACAGTGTAACAAAAA 1897
|||||
DB 87560 ACAGTGTAACAAAAA 87534
|||||

RESULT 30
AL645938/C 138851 bp DNA linear ROD 11-APR-2002
LOCUS AL645938
DEFINITION Mouse DNA sequence from clone Rp23-15E24 on chromosome 1, complete
sequence.
ACCESSION AL645938
VERSION AL645938.9 GI:20145949
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
  1
  Corby, N.
  Direct Submission
  Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  humquerry@sanger.ac.uk; clonerequests@sanger.ac.uk
  On Apr 12, 2002 this sequence version replaced gi:20135756.
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one M13 subclone; and the
  assembly was confirmed by restriction digest. The following
  abbreviations are used to associate primary accession numbers given
  in the feature table with their source databases: Em., EMBL; SW.,
  SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information on the WormPEP
  database can be found at
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep/Rp23-15E24.1s
  from the RPCI-23 Mouse PAC Library
  constructed by the group of Pieter de Jong.
  For further details see http://www.chori.org/dacpac/home.htm
  VECTOR: pBAC3.6.
  Location/Qualifiers
    1..138851
      /organism="Mus musculus"
      /db_xref="taxon:10090"
      /chromosome="1"
      /clone="Rp23-15E24"
      /clone_1ID="RPCI-23"
      /clone_1ID="RPCI-23"
  BASE COUNT
    40695 a 25907 c 27333 g 44916 t
  ORIGIN

```

```

Query Match
  Best Local Similarity 100.0%; Pred. No. 0.0012;
  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1871 ACAGTGTAACAAAAA 1897
|||||
DB 31571 ACAGTGTAACAAAAA 31545
|||||

RESULT 31
AC126321/C 151602 bp DNA linear HTG 05-JUL-2002
LOCUS AC126321
DEFINITION Polypertus bichlr clone -22F22, *** SEQUENCING IN PROGRESS ***, 1
ordered piece.
ACCESSION AC126321
VERSION AC126321.1 GI:21699164
KEYWORDS HTG; HTGS_PHASE2; HTGS_FULFILL; HTGS_ACTIVEFIN.
SOURCE Polypertus bichlr.
ORGANISM Polypertus bichlr.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Polypteriformes; Polypteridae; Polypterus.
1
  (bases 1 to 151602)
REFERENCE
  1
  Birren, B., Nusbaum, C. and Lander, E.
  Polypertus bichlr, clone -22F22
  Unpublished
  2 (bases 1 to 151602)
REFERENCE
  1
  Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S.,
  Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Bonkhallier, B.,
  Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
  Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
  Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
  Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
  Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
  Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K.,
  Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
  McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
  Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
  O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
  Plunhach, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
  Roman, J., Roy, A., Schauer, S., Schuppback, R., Seaman, S., Severy, P.,
  Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
  Testaye, S., Theodores, J., Topham, K., Travers, M., Vassiliev, H.,
  Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
  Zembek, L., Zimmer, A. and Zody, M.
  Direct Submission
  Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  All repeats were identified using RepeatMasker:
  Smit, A.F.A. & Green, P. (1996-1997)
  http://ftp.genome.washington.edu/RM/RepeatMasker.html
  ----- Genome Center
  Center: Whitehead Institute/ MIT Center for Genome Research
  Center code: WIBR
  Web site: http://www-seq.wi.mit.edu
  Contact: sequence_submissions@genome.wi.mit.edu
  ----- Project Information
  Center project name: L20497
  Center clone name: 22_F_22
  -----
  * NOTE: This is a 'working draft' sequence. It currently
  * consists of 1 contigs. Gaps between the contigs
  * are represented as runs of N. The order of the pieces
  * is believed to be correct as given, however the sizes
  * of the gaps between them are based on estimates that have
  * provided by the submitter.
  * This sequence will be replaced
  * by the finished sequence as soon as it is available and
  * the accession number will be preserved.
  1 151602: contig of 151602 bp in length.
  Location/Qualifiers
    1..151602
      /organism="Polypertus bichlr"

```

```

/d_b_xref="taxon:31136"
/clone_lib="Bichir"
BASE COUNT      48679 a 27446 c 26903 g 48574 t
ORIGIN

Query Match      1.4%; Score 27; DB 2; Length 151602;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1869 AGCAGCTGTAACAAAAA 1895
Db 80517 AGCAGCTGTAACAAAAA 80491

RESULT 32
AC027118      170255 bp   DNA   linear   PRI 23-APR-2002
LOCUS
DEFINITION     Homo sapiens chromosome 10 clone RP11-573111, complete sequence.
ACCESSION      AC027118
VERSION        AC027118.9   GI:19774390
KEYWORDS       HTG.
SOURCE         Homo sapiens.
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 170255)
AUTHORS        Smith,D.R.
TITLE          Genome Therapeutics Corporation Sequencing Center: Human Genome
                Sequence Data
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 170255)
AUTHORS        Smith,D.R.
TITLE          Direct Submission
JOURNAL        Submitted (27-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
                Street, Waltham, MA 02453, USA
REFERENCE      3 (bases 1 to 170255)
AUTHORS        Smith,D.R.
TITLE          Direct Submission
JOURNAL        Submitted (23-JAN-2002) Genome Therapeutics Corporation, 100 Beaver
                Street, Waltham, MA 02453, USA
REFERENCE      4 (bases 1 to 170255)
AUTHORS        Smith,D.R.
TITLE          Direct Submission
JOURNAL        Submitted (28-MAR-2002) Genome Therapeutics Corporation, 100 Beaver
                Street, Waltham, MA 02453, USA
REFERENCE      5 (bases 1 to 170255)
AUTHORS        Smith,D.R.
TITLE          Direct Submission
JOURNAL        Submitted (23-APR-2002) Genome Therapeutics Corporation, 100 Beaver
                Street, Waltham, MA 02453, USA
COMMENT        On Mar 28, 2002 this sequence version replaced gi:18266621.
FEATURES
    source
        1..170255
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="10"
            /clone="RP11-573111"
            /clone_lib="RP11-573111"
            /clone_lib="RP11-573111"
BASE COUNT      53463 a 30250 c 31205 g 55337 t
ORIGIN

Query Match      1.4%; Score 27; DB 9; Length 170255;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAA 1897
Db 136987 ACAGTGTAAAAA 137013

RESULT 33
AC074245

```

```

LOCUS      AC074245      179364 bp   DNA   linear   HTG 24-AUG-2000
DEFINITION Homo sapiens chromosome 2 clone RP11-341F8, WORKING DRAFT SEQUENCE,
                21 unordered pieces.
ACCESSION   AC074245
VERSION     AC074245.3   GI:9887809
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1 (bases 1 to 179364)
AUTHORS      Waterston,R.H.
TITLE        The sequence of Homo sapiens clone
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 179364)
AUTHORS      Waterston,R.H.
TITLE        Direct Submission
JOURNAL      Submitted (22-JUL-2000) Genome Sequencing Center, Washington
                University School of Medicine, 444 Forest Park Parkway, St. Louis,
                MO 63108, USA
COMMENT      On Aug 24, 2000 this sequence version replaced gi:9665207.

```

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H_NH0341F08
----- Summary Statistics -----
Sequencing vector: MJ3; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-Primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167601 bases at least Q40
Consensus quality: 170488 bases at least Q30
Consensus quality: 171954 bases at least Q20
Insert size: 179000; agarose-fp
Insert size: 177364; sum-of-contigs
Quality coverage: 4.14 in Q20 bases; agarose-fp
Quality coverage: 4.29 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1477: contig of 1477 bp in length
* 1478 1577: gap of unknown length
* 1578 3799: contig of 2222 bp in length
* 3800 3899: gap of unknown length
* 3900 6403: contig of 2504 bp in length
* 6404 6503: gap of unknown length
* 6504 10328: contig of 3825 bp in length
* 10329 10428: gap of unknown length
* 10429 13400: contig of 2972 bp in length
* 13401 13500: gap of unknown length
* 13501 18872: contig of 5372 bp in length
* 18873 18972: gap of unknown length
* 18973 25292: contig of 6320 bp in length
* 25293 25392: gap of unknown length
* 25393 30836: contig of 5444 bp in length
* 30837 30936: gap of unknown length
* 30937 36567: contig of 5631 bp in length
* 36568 36667: gap of unknown length
* 36668 45290: contig of 8623 bp in length
* 45291 45391: gap of unknown length
* 45391 55146: contig of 9756 bp in length
* 55147 55246: gap of unknown length
* 55247 66342: contig of 11096 bp in length

```

```

* 66343 66442: gap of unknown length
* 66443 76462: contig of 10020 bp in length
* 76463 76562: gap of unknown length
* 76563 89099: contig of 12537 bp in length
* 89100 89199: gap of unknown length
* 89200 102001: contig of 12802 bp in length
* 102002 102101: gap of unknown length
* 102102 119488: contig of 17387 bp in length
* 119489 119589: gap of unknown length
* 119589 135844: contig of 16256 bp in length
* 135845 135945: gap of unknown length
* 135945 153641: contig of 17697 bp in length
* 153642 153741: gap of unknown length
* 153742 175739: contig of 21998 bp in length
* 175740 175839: gap of unknown length
* 175840 177387: contig of 1548 bp in length
* 177388 177488: gap of unknown length
* 177488 179364: contig of 1877 bp in length.
Location/Qualifiers
1..179364
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-341F8"
1..1477
/feature="assembly_name:Contig10
clone_end:r7
vector_side:left"
1578..3799
/feature="assembly_name:Contig11"
3900..6403
/feature="assembly_name:Contig12"
6504..10328
/feature="assembly_name:Contig13"
10429..13400
/feature="assembly_name:Contig14"
13501..18872
/feature="assembly_name:Contig15"
18973..25292
/feature="assembly_name:Contig16"
25393..30836
/feature="assembly_name:Contig17"
30937..36567
/feature="assembly_name:Contig18"
36668..45290
/feature="assembly_name:Contig19"
45391..55146
/feature="assembly_name:Contig20"
55247..66342
/feature="assembly_name:Contig21"
66443..76462
/feature="assembly_name:Contig22"
76563..89099
/feature="assembly_name:Contig23"
89200..102001
/feature="assembly_name:Contig24"
102102..119488
/feature="assembly_name:Contig25"
119589..135844
/feature="assembly_name:Contig26
clone_end:sp6
vector_side:left"
135945..153641
/feature="assembly_name:Contig27"
153742..175739
/feature="assembly_name:Contig28"
175840..177387
/feature="assembly_name:Contig8"
177488..179364
/feature="assembly_name:Contig9"

```

```

BASE COUNT 56993 a 32967 c 33013 g 54383 t 2008 others
ORIGIN

```

```

Query Match 1.4%: Score 27; DB 2; Length 179364;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1871 ACAGTGTAACAAAAAAAAAAAAAAAA 1897
Db 166939 ACAGTGTAACAAAAAAAAAAAAAAAA 166965

```

```

RESULT 34
AC074389
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 195782)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074
2 (bases 1 to 195782)
Cordes,M., Doeber,A., Hawkins,M. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-510K8
Unpublished (2002)
3 (bases 1 to 195782)
Waterston,R.H.
Direct Submission
Submitted (30-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 195782)
Waterston,R.H.
Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 195782)
Waterston,R.
Direct Submission
Submitted (10-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 3, 2002 this sequence version replaced gi:14209801.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplin@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0510K08
-----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping







misc_feature	79728..97908	/note="assembly-fragment"
misc_feature	98009..119320	/note="assembly-fragment"
misc_feature	119421..142295	/note="assembly-fragment"
misc_feature	142396..166670	/note="assembly-fragment"
misc_feature	166771..197264	/note="assembly-fragment"
misc_feature	197365..209572	/note="assembly-fragment"
misc_feature	209573..210000	/note="assembly-fragment"
BASE COUNT	63310 a 40377 c 40347 g 63722 t	1806 others
ORIGIN	vector:side:right"	
Query Match	1.4%	Score 27; DB 2; Length 209572;
Best Local Similarity	100.0%	Pred. No. 0.0012;
Matches	27; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1871	ACAGGTGTAACAAAAAAAAAAAAAAAAA 1897
Db	204291	ACAGTGTGTAACAAAAAAAAAAAAAAAAA 204317
RESULT 36	.	
AC110232	AC110232	212690 bp DNA linear HTG-15-MAY-2002
LOCUS	Mus musculus clone RP23-67H24, WORKING DRAFT SEQUENCE, 26 ordered	
DEFINITION	Placens	
AC110232	AC110232.4	GI:20800203
VERSION	HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.	
KEYWORDS	Mus musculus.	
SOURCE	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 212690)	
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.	
TITLE	Mus musculus, clone RP23-67H24	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 212690)	
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukngalter,B., Brown,A., Canarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Deatrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Gades,S., Gordon,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,M., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karats,A., Kells,C., Lacroque,K., Lamazates,R., Landers,T., Lehoczyk,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Margulis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T., Mlenag,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severyl,P., Spencer,B., Stangé-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tophan,K., Travers,M., Travis,N., Triggillo,J., Vassiliou,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
REFERENCE	3 (bases 1 to 212690)	
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Boukngalter,B., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Deatrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Gades,S., Gordon,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,M., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karats,A., Kells,C., Lacroque,K., Lamazates,R., Landers,T., Lehoczyk,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Margulis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T., Mlenag,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severyl,P., Spencer,B., Stangé-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tophan,K., Travers,M., Travis,N., Triggillo,J., Vassiliou,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.	

TITLE  
JOURNAL  
COMMENT

Cook, A., Cooke, P., DeRellano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,  
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
 Hago, B., Horton, L., Huine, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamal, A., Karatas, A., Kells, C., Lahocque, K., Lamazares, R.,  
 Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,  
 Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C.,  
 McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menus, L.,  
 Mihovata, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,  
 Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
 Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P.,  
 Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Schuppach, R.,  
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
 Topham, K., Travers, M., Travis, N., Trifillio, J., Vassiliou, H.,  
 Vriel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G.,  
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, W.  
 Direct Submission  
 Submitted (15-MAY-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 15, 2002 this sequence version replaced g1:20531892.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 -----  
 Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
 -----  
 Project Information  
 Center project name: L22352  
 Center clone name: 67\_LH\_24  
 -----  
 Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 203101 bases at least Q40  
 Consensus quality: 204725 bases at least Q30  
 Consensus quality: 205415 bases at least Q20  
 Insert size: 210000; agarose-fp  
 Insert size: 210190; sum-of-contigs  
 Quality coverage: 14.3 in Q20 bases; agarose-fp  
 Quality coverage: 14.3 in Q20 bases; sum-of-contigs  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 26 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the sizes  
 \* is believed to be correct as given, however the places  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 1 618: contig of 618 bp in length  
 619 718: gap of 100 bp  
 719 1375: contig of 657 bp in length  
 1376 1475: gap of 100 bp  
 1476 2114: contig of 639 bp in length  
 2115 2214: gap of 100 bp  
 2215 2843: contig of 629 bp in length  
 2844 2943: gap of 100 bp  
 2944 3067: contig of 124 bp in length  
 3068 3167: gap of 100 bp  
 3168 3352: contig of 185 bp in length  
 3353 3452: gap of 100 bp  
 3453 4030: contig of 578 bp in length  
 4031 4130: gap of 100 bp  
 4131 4757: contig of 627 bp in length  
 4758 4857: gap of 100 bp  
 4858 5064: contig of 207 bp in length  
 5065 5164: gap of 100 bp  
 5165 6283: contig of 1119 bp in length

```

* 6284 6383: gap of 100 bp
* 6384 7505: contig of 1122 bp in length
* 7506 7605: gap of 100 bp
* 7606 8326: contig of 721 bp in length
* 8327 8426: gap of 100 bp
* 8427 9838: contig of 1412 bp in length
* 9839 9938: gap of 100 bp
* 9939 11695: contig of 11757 bp in length
* 11696 11795: gap of 100 bp
* 11796 15821: contig of 4026 bp in length
* 15822 15921: gap of 100 bp
* 15922 20158: contig of 4237 bp in length
* 20159 20258: gap of 100 bp
* 20259 26711: contig of 6453 bp in length
* 26712 26811: gap of 100 bp
* 26812 35760: contig of 8949 bp in length
* 35761 35860: gap of 100 bp
* 35861 47391: contig of 11531 bp in length
* 47392 47491: gap of 100 bp
* 47492 59604: contig of 12113 bp in length
* 59605 59704: gap of 100 bp
* 59705 74258: contig of 14554 bp in length
* 74259 74358: gap of 100 bp
* 74359 93680: contig of 19322 bp in length
* 93681 93780: gap of 100 bp
* 93781 113564: contig of 19784 bp in length
* 113565 113664: gap of 100 bp
* 11365 134201: contig of 20537 bp in length
* 134202 134501: gap of 100 bp
* 134502 159668: contig of 25367 bp in length
* 159669 159768: gap of 100 bp
* 159769 212690: contig of 52922 bp in length.

```

# FEATURES

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  misc_feature
    1. .618
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      1. .212690
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      /db_xref="taxon:10090"
      /clone="RP23-67H24"
      /clone_11b="RP23-67H24"
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    /note="assembly_fragment"
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    /note="assembly_fragment"
  misc_feature
    1476. .2114
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  misc_feature
    2215. .2843
    /note="assembly_fragment"
  misc_feature
    2944. .3067
    /note="assembly_fragment"
  misc_feature
    3168. .3352
    /note="assembly_fragment"
  misc_feature
    3453. .4030
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    4131. .4757
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    4858. .5064
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  misc_feature
    5165. .6283
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  misc_feature
    6384. .7505
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  misc_feature
    7606. .8326
    /note="assembly_fragment"
  misc_feature
    8427. .9838
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  misc_feature
    9939. .11695
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    15922. .20158
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    26812. .35760

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47492. .59604
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59705. .74258
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74359. .93680
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Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1871 ACAGGTAAAAA 1897
Db 42174 ACAGGTAAAAA 42200

```

```

RESULT 37
AC069297 214411 bp DNA linear HTG 25-MAY-2000
LOCUS Mus musculus chromosome 12 clone RP23-2N7 strain C57BL6/J, WORKING
DEFINITION DRAFT SEQUENCE, 19 unordered pieces.
ACCESSION AC069297
VERSION AC069297.1 GI:8072378
KEYWORDS HTG: HTGS_PHASE1, HTGS_DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 214411)
AUTHORS Bouffard,G.G., Dietrich,N.L., Eagle,W.O., Gupta,J., Ho,S.-L.,
Mastrrian,S.D., McCloskey,J.C., Morse,E., Ojodu,M.A., Pearson,R.,
Stattin,P., Summers,T.J., Thomas,J.W., Thomas,P.J.,
Tlonsky,E.E., Touchman,J.W., Tran,J.T., Vogt,J.L., Walker,M.A.,
Wetherby,K.D., and Green,E.D.
NISC Mouse Sequencing Initiative
Unpublished
2 (bases 1 to 214411)
Green,E.D.
Direct Submission
Submitted (25-MAY-2000) NIH Intramural Sequencing Center, 8717
Groveview Circle, Gaithersburg, MD 20877, USA

```

```

TITLE JOURNAL
REFERENCE JOURNAL
AUTHORS JOURNAL
COMMENT
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.mouse@nih.gov
Project Information
Center project name: us
Center clone name: 002N07

```

```

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 204922 bases at least Q40
Consensus quality: 207590 bases at least Q30
Consensus quality: 209017 bases at least Q20
Insert size: 205000; agarose-fp
Insert size: 248000; pulse-field-gel
Insert size: 212611; sum-of-contrigs
Quality coverage: 5.40x in Q20 bases; agarose-fp
Quality coverage: 4.46x in Q20 bases; pulse-field-gel
Quality coverage: 5.20x in Q20 bases; sum-of-contrigs

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

```

\* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1	2371	contig of 2371 bp in length
2372	2471	gap of unknown length
2472	7036	contig of 4565 bp in length
7037	7136	gap of unknown length
7137	11837	contig of 4701 bp in length
11838	11937	gap of unknown length
11938	16456	contig of 4519 bp in length
16457	16556	gap of unknown length
16557	24064	contig of 7508 bp in length
24065	24164	gap of unknown length
24165	30372	contig of 6208 bp in length
30373	30472	gap of unknown length
30473	38478	contig of 8006 bp in length
38479	38579	gap of unknown length
38579	47748	contig of 9170 bp in length
47749	47848	gap of unknown length
47849	56374	contig of 8526 bp in length
56375	56474	gap of unknown length
56475	68247	contig of 11773 bp in length
68248	68347	gap of unknown length
68348	78809	contig of 10462 bp in length
78810	78909	gap of unknown length
78910	89212	contig of 10303 bp in length
89213	89312	gap of unknown length
89313	99267	contig of 9955 bp in length
99268	99367	gap of unknown length
99368	110419	contig of 11052 bp in length
110420	110519	gap of unknown length
110520	124151	contig of 13632 bp in length
124152	124251	gap of unknown length
124252	141079	contig of 16828 bp in length
141080	141179	gap of unknown length
141180	160980	contig of 19801 bp in length
160981	161080	gap of unknown length
161081	185614	contig of 24534 bp in length
185615	185714	gap of unknown length
185715	214411	contig of 28697 bp in length.

FEATURES  
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 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /chromosome="12"  
 /clone="RP23-2N7"  
 /clone.lib="RPCI mouse BAC library 23"  
 1. 2371  
 /note="assembly-fragment"  
 2472. .7036  
 /note="assembly-fragment"  
 7137. .11837  
 /note="assembly-fragment"  
 11938. .16456  
 /note="assembly-fragment"  
 16557. .24064  
 /note="assembly-fragment"  
 24165. .30372  
 /note="assembly-fragment"  
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 vector.slide:left"  
 30473. .38478  
 /note="assembly-fragment"  
 38579. .47748  
 /note="assembly-fragment"  
 47849. .56374  
 /note="assembly-fragment"  
 56475. .68247  
 /note="assembly-fragment"  
 68348. .78809  
 /note="assembly-fragment"  
 78910. .89212

misc\_feature /note="assembly-fragment"  
 89313. .99267  
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 misc\_feature /note="assembly-fragment"  
 99368. .110419  
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 misc\_feature 110520. .124151  
 /note="assembly-fragment"  
 124252. .141079  
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 misc\_feature /note="assembly-fragment"  
 141180. .160980  
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 misc\_feature 161081. .185614  
 /note="assembly-fragment"  
 185715. .214411  
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 ORIGIN

Query Match 1.4% Score 27; DB 2; Length 214411;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1871 ACAGTGTAAAAA 1897  
 Db 80773 ACAGTGTAAAAA 80799

RESULT 38  
 AL133395/c  
 LOCUS  
 DEFINITION  
 Human DNA sequence from clone RP11-446H13 on chromosome 10.  
 Contains the 3' end of the gene for a novel protein similar to  
 KIAA1059 (ortholog of mouse VPS10 domain receptor protein SORCS),  
 an RPL23A (60S ribosomal protein 23A) pseudogene, ESTs, STS and  
 GSSs, complete sequence.

ACCESSION  
 AL133395  
 VERSION  
 AL133395.21 GI:10045255  
 KEYWORDS  
 HMG; KIAA1059; RPL23A; SORCS; VPS10 domain.  
 SOURCE  
 ORGANISM  
 human.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 Direct Submission  
 Submitted (11-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,  
 Bird, C.  
 1 (bases 1 to 217929)  
 requests: clonerequest@sanger.ac.uk  
 On Sep 9, 2000 this sequence version replaced gi:9943953.

## COMMENT

During sequence assembly data is compared from overlapping clones.  
 Together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information  
 on the WormPEP database can be found at  
 http://www.sanger.ac.uk/projects/C\_elegans/wormpep This sequence  
 was generated from part of bacterial clone configs of human  
 chromosome 10, constructed by the Sanger Centre Chromosome 10  
 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr10  
 This sequence is the entire insert of clone RP11-446H13 The true  
 left end of clone RP11-699H2 is at 128287 in this sequence. The  
 true right end of clone RP11-41D21 is at 75932 in this sequence.  
 This sequence has been finished according to sequence map criteria  
 as follows. An attempt is made to resolve all sequencing problems,  
 such as compressions and repeats, but not necessarily within known  
 annotated repeat sequence elements. Where the sequence is  
 ambiguous, there is an annotation using the 'unsure' feature key.  
 RP11-446H13 is from the library RPCI-11.2 constructed by the group



repeat\_region /note="MIR repeat: matches 160. .250 of consensus"  
 31806. .31957  
 /note="MIR repeat: matches 52. .207 of consensus"  
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 /note="LMC4 repeat: matches 6030. .6135 of consensus"  
 repeat\_region 32274. .32437  
 /note="LMC/D repeat: matches 5559. .5728 of consensus"  
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 /note="match: GSS: Em: A0277814"  
 repeat\_region 32562. .33031

Query Match 1.4%; Score 27; DB 9; Length 217929;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAA 1897  
 DB 204102 ACAGTGTAAAAA 204076

RESULT 39  
 AF297044 1275 bp mRNA linear PLN 10-OCT-2000  
 LOCUS Zea mays homocysteine S-methyltransferase-1 mRNA, complete cds.  
 DEFINITION AF297044  
 ACCESSION AF297044  
 VERSION AF297044.1 GI:10732784  
 KEYWORDS  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 1275)  
 AUTHORS Li, C. and Tarczynski, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-AUG-2000) T&T-D-OT, Pioneer Hi-Bred International  
 Inc., 7300 NW 62nd Ave., Johnston, IA 50131, USA  
 FEATURES  
 source Location/Qualifiers  
 1..1275  
 /organism="Zea mays"  
 /db\_xref="taxon:4577"  
 106..1077  
 /product="homocysteine S-methyltransferase-1"  
 /protein\_id="AA022537.1"  
 /db\_xref="GI:10732785"  
 /translation="MGVLEDLVARAGCAVTDGSGFATOLEALGADINDPLMSACLIT  
 RPLVKEVHMQLKAGADYIISSYQATITFGRKMSVAEADLRTSVKLANEARD  
 EFKSTLRKSPITRNALVANSISGAYIADGSEYSGADITAEKLDLFRRLQ  
 VLASGPDLEFAIPNOMEAQLVLEELKQVQIPMWICFSSVDGNLCSGSFAD  
 LKLNASEKVAIVGVNCTPQFLEIGICEFRKQKALAVYPNGEVDWDRARWLPV  
 ECLGKSFDAKRMQEGASLIGCCRTPTSTIRAVSKILKRGTH"

BASE COUNT 341 a 301 c 356 g 277 t  
 ORIGIN

Query Match 1.4%; Score 26; DB 8; Length 1275;  
 Best Local Similarity 100.0%; Pred. No. 0.0035;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1872 CAGGTGTAAAAA 1897  
 DB 1196 CAGGTGTAAAAA 1221

RESULT 40  
 AF176571 1409 bp mRNA linear PLN 03-NOV-1999  
 LOCUS Alternaria alternata exoglucanase (CI) mRNA, complete cds.  
 DEFINITION AF176571  
 ACCESSION AF176571  
 VERSION AF176571.1 GI:6179888  
 KEYWORDS  
 ORGANISM Alternaria alternata.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria;  
 Alternaria alternata group.  
 1 (bases 1 to 1409)  
 AUTHORS Eshel, D., Prusky, D., and Dinor, A.  
 TITLE Exoglucanase of Alternaria alternata  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1409)  
 AUTHORS Eshel, D., Prusky, D., and Dinor, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-AUG-1999) Postharvest Sciences, Volcani Center, POB  
 6, Bet-Dagan 50250, Israel  
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 ATACPDNKKACANCAVDGADYSGTITGKNSLKIETKSGISTNIGSRITLKKDD  
 TTYEMFRFTGNDFTVDVSNLPCGFNGLFVSDADAGGLKKTSTNKAARKYGTGY  
 CDAQCPRLDKFTINGEGNVEGKRRSSNDANAGVGHSCCAEMDIENANSVPAVPHS  
 CSTIIEQSRCDGCGGTGADRYAGVCDGCDGPNYSRGMVDFYGGKGTVPSTSKFT  
 VVVFISGTGDMGIRKRYVONGKTIQAPASAVGVGNSITTKFDDOKAVRGDYYTF  
 KDGKGNANNAKALANGMVLVMSLMDHYSNMLMDSTYPTDKNPDTDLCTGSGREETS  
 SGVPADVEGSHADATVYSNFKPPLNSTRFG"

BASE COUNT 393 a 325 c 382 g 309 t  
 ORIGIN

Query Match 1.4%; Score 26; DB 8; Length 1409;  
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 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1872 CAGGTGTAAAAA 1897  
 DB 1383 CAGGTGTAAAAA 1408

RESULT 41  
 AX056994 2481 bp DNA linear PAT 17-JAN-2001  
 LOCUS Sequence 11 from Patent WO0075340.  
 DEFINITION AX056994  
 ACCESSION AX056994  
 VERSION AX056994.1 GI:12309857  
 KEYWORDS  
 SOURCE soybean.  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 2481)  
 AUTHORS Butler, K.H., Farnodu, O.O., Gutteridge, S. and Maxwell, C.A.  
 TITLE Magnesium chelatase  
 JOURNAL Patent: WO 0075340-A 11 14-DEC-2000;  
 E.I. DU PONT DE NEMOURS AND COMPANY (US)  
 FEATURES  
 source Location/Qualifiers  
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 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.0037;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGTGTAAAAA 1897  
 DB 2424 CAGTGTAAAAA 2449

RESULT 42  
 AF514845 2745 bp mRNA linear VRT 17-JUN-2002  
 LOCUS Rana catesbeiana epithelial sodium channel ENAC beta subunit mRNA,  
 complete cds.  
 ACCESSION AF514845.1 GI:21435743  
 VERSION AF514845.1  
 KEYWORDS  
 SOURCE bullfrog  
 ORGANISM Rana catesbeiana  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;  
 Aquarana.

REFERENCE  
 1 (bases 1 to 2745)  
 Jentsik, P.J., Holbird, D. and Cox, T.  
 Cloning and partial characterization of an amiloride-sensitive  
 sodium channel (fENaC) from adult bullfrog skin  
 J. Comp. Physiol. B, Biochem. Syst. Environ. Physiol. (2002) In  
 press

JOURNAL  
 2 (bases 1 to 2745)  
 Jentsik, P.J., Holbird, D. and Cox, T.  
 Direct Submission  
 Submitted (22-MAY-2002) Physiology, Southern Illinois University,  
 1135 Lincoln Drive, Carbondale, IL 62901, USA  
 Location/Qualifiers

FEATURES  
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 1..2745  
 /organism="Rana catesbeiana"  
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 168..2135  
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 /product="epithelial sodium channel ENAC beta subunit"  
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 /db\_xref="GI:21435744"  
 /translation="MTTSTNISRSEHSEVIRKTKYTRALHRMKGPGYTKELLVWF  
 CANNTHGKRIVSEGPKRKRVMTLTILFALVFMQGVVLOTLYSGVSLSG  
 NIMVPAVAVCVNPFKSRVHLLHDLVDLADLDRIOFSOHSGICPAVNNNTN  
 VLDPALNVMPLVVIDEHPNNTLVYINFDSTSDYSDIINNATKGNQFVAVKRVAT  
 ELCTNNRQCSYRNFTSGAATKDWYLLOFSNIEPKIEEEKVKKGTGAEDMTLCMF  
 GGQPCSYNFTPIEHODYGNCTIFMAGCBGDLTSANPGADFGKMLVDIDQKYEIP  
 FLQSTAAARITIHQQRSTPEFLDLGITVAMPGETISIAVLEDTQTHLEAPYSSCDVGS  
 DIPVANIYSKENSYSIQCLSCSFQELNMYKCAVYLFPLNGAHYCNQDEPDVY  
 PCYINMDIVSHREQICIMCOQPCNDSNVMTIISADWPSAAEDMIRHVLSYEDTS  
 LDIVNRGIMRLNIYFEFNYRSISESPTNVVLLSLNGGREGFMFGSGVICITTF  
 GEIILDCIMITLIKILAMIRDRORRKRPPYVAVELVEATISNGCFHEDSNQV  
 STRPGTPPPNDRSLKQIDALDIYSSDDE"

BASE COUNT 853 a 581 c 545 g 766 t

ORIGIN

Query Match 1.4%; Score 26; DB 5; Length 2745;  
 Best Local Similarity 100.0%; Pred. No. 0.0037;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGTGTAAAAA 1897  
 DB 2719 CAGTGTAAAAA 2744

RESULT 43  
 BC034500 3889 bp mRNA linear PRI 15-JUL-2002  
 LOCUS Homo sapiens, similar to RIKEN cDNA 0610013117 gene, clone  
 MGC:26926 IMAGE:4838423, mRNA, complete cds.  
 ACCESSION BC034500  
 VERSION BC034500.1 GI:21759790  
 KEYWORDS  
 SOURCE human  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-JUL-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK  
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shrawati  
 Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: [amadan@systemsbiology.org](mailto:amadan@systemsbiology.org)  
 Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha  
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/ILLNL at: <http://image.illnl.gov>  
 Series: IRAC Plate: 34 Row: 0 Column: 3  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Similarity but not  
 identity to protein

FEATURES  
 source  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="MGC:26926 IMAGE:4838423"  
 /tissue\_type="testis"  
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 /lab\_host="DH10B"  
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 /db\_xref="GI:21759791"  
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 LMEWVWVYPOPLPSQVYVYIEMSPYSLIRPLGQVYKRPFLAHITHLAISLM  
 SFSCANVYISGLVAVVHVADIMESAKMFSTAGTQVLCNTLFTFTFTFTSRIL  
 VFPPWILYCTLLPMTWHLPEFSTYFLNQLMGLVYHLVWGYIILKMLNRCIFMKSI  
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BASE COUNT 1072 a 860 c 859 g 1098 t

ORIGIN

Query Match 1.4%; Score 26; DB 9; Length 3889;  
 Best Local Similarity 100.0%; Pred. No. 0.0038;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGTGTAAAAA 1897  
 DB 3844 CAGTGTAAAAA 3869

RESULT 44  
 AF044209 7940 bp mRNA linear PRI 01-SEP-1998  
 LOCUS Homo sapiens nuclear receptor co-repressor N-COR mRNA, complete  
 cds.  
 ACCESSION AF044209  
 VERSION AF044209.1 GI:3510602  
 KEYWORDS  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 7940)  
 AUTHORS Wang, J., Hoshino, T., Redner, R.L., Kajigaya, S. and Liu, J.M.  
 TITLE ETO, fusion partner in t(8;21) acute myeloid leukemia, represses transcription by interaction with the human N-CoR/SMN3/HDAC1 complex  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10860-10865 (1998)  
 MEDLINE 98393736  
 PUBMED 9724795  
 REFERENCES 2 (bases 1 to 7940)  
 AUTHORS Wang, J. and Liu, J.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-JAN-1998) Hematology Branch, National Heart, Lung and Blood Institute, Bldg. 10, Rm. 7C103, 9000 Rockville Pike, Bethesda, MD 20892, USA

FEATURES  
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BASE COUNT 2437 a 1942 c 1894 g 1667 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. NO. 0.0039;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGTGTAACAAAAA 1897  
 Db 7909 CAGTGTAACAAAAA 7934

RESULT 45  
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 LOCUS  
 DEFINITION Homo sapiens BAC clone CTA-318M5 from 7q22, complete sequence.  
 AC005250  
 AC005250.1 GI:3287719  
 HTG.  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 94336)  
 AUTHORS Sulston, J.E. and Waterston, R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 MEDLINE 99063792  
 PUBMED 9847074

REFERENCE 2 (bases 1 to 94336)  
 AUTHORS Courtney, L., Nelson, J., Wohlmann, P., Bauer, C. and Morris, M.  
 TITLE The sequence of Homo sapiens BAC clone CTA-318M5  
 JOURNAL Unpublished (2001)  
 3 (bases 1 to 94336)  
 Waterston, R.

REFERENCE 3 (bases 1 to 94336)  
 AUTHORS Sulston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JUL-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 4 (bases 1 to 94336)  
 Waterston, R.

REFERENCE 4 (bases 1 to 94336)  
 AUTHORS Sulston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 5 (bases 1 to 94336)  
 Waterston, R.

REFERENCE 5 (bases 1 to 94336)  
 AUTHORS Sulston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 6 (bases 1 to 94336)  
 Waterston, R.

REFERENCE 6 (bases 1 to 94336)  
 AUTHORS Sulston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 7 (bases 1 to 94336)  
 Waterston, R.

REFERENCE 7 (bases 1 to 94336)  
 AUTHORS Sulston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 8 (bases 1 to 94336)  
 Waterston, R.

REFERENCE 8 (bases 1 to 94336)  
 AUTHORS Sulston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 9 (bases 1 to 94336)  
 Waterston, R.

REFERENCE 9 (bases 1 to 94336)  
 AUTHORS Sulston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 10 (bases 1 to 94336)  
 Waterston, R.

REFERENCE 10 (bases 1 to 94336)  
 AUTHORS Sulston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 11 (bases 1 to 94336)  
 Waterston, R.

# NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRN/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>



## SOURCE INFORMATION:

Clone CTA-318M5 is from a release of the human BAC library CTRB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).  
VECTOR: pBelOBAC11  
Selection: chloramphenicol

## NEIGHBORING SEQUENCE INFORMATION:

Actual start of this clone is at base position 1 of CTA-318M5.  
Actual end is at base position 94336 of CTA-318M5.

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Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 CAGCTGTAATAAAAAAAAAAAAAAAAAA 1897  
DB 83484 CAGCTGTAATAAAAAAAAAAAAAAAAAA 83459

Search completed: November 7, 2002, 23:53:12  
Job time : 7905.36 secs

Fri Nov 8 18:57:03 2002

us-09-970-966-214.rge

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GenCore version 5.1.3  
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OW nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:52:52 : Search time 2168.96 seconds  
(without alignments)  
12088.965 Million cell updates/sec

Title: US-09-970-966-211  
Perfect score: 1619  
Sequence: 1 ggcacatttcgcatgt.....aaaaaaaaaaaaaaaaaa 1619

Scoring table: IDENTITY-NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estlun:\*  
5: em\_estlun:\*  
6: em\_estlun:\*  
7: em\_estlun:\*  
8: em\_estlun:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estfun:\*  
17: gb\_est5:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_hum:\*  
20: em\_gss\_hum:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_vrt:\*  
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24: em\_gss\_vrt:\*  
25: em\_gss\_vrt:\*  
26: em\_gss\_vrt:\*  
27: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	787.8	48.7	888	14	B0689771 AGENCOURT
2	754.2	46.6	814	9	AL567376
3	704	43.5	821	12	BG752329
4	687.8	42.5	702	14	B0006545
5	668.6	41.3	1490	11	AK012406
6	661.4	40.9	678	9	AI936826

Result No.	Score	Query Match	Length	ID	Description
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10	640.2	39.5	690	10	AM149665
11	613.8	38.0	649	10	AM590950
12	613.4	37.9	627	13	BM69397
13	602.8	37.2	743	10	BE395797
14	600.2	37.1	616	9	AI990500
15	599.4	37.0	666	12	BF439382
16	597.4	36.9	645	12	BF432379
17	589.2	36.4	879	14	B0689033
18	578	35.7	843	12	BF125134
19	576.4	35.6	591	12	BF125134
20	566.4	35.0	759	12	BF126050
21	549.4	33.9	578	9	AI742092
22	548.8	33.9	699	10	BE395581
23	538.4	33.3	551	12	BE585216
24	527.4	32.6	540	12	BF939693
25	526	32.5	537	12	BF594242
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27	522.8	32.3	538	13	BM667957
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29	521.2	32.2	670	12	BG753617
30	519.8	32.1	534	10	BE350014
31	518.8	32.0	540	10	AM954549
32	515.8	31.9	561	10	AM150789
33	515.8	31.9	589	9	AI859538
34	514.4	31.8	527	10	AM338938
35	514.2	31.8	920	9	AL538562
36	509.8	31.5	652	10	BE392412
37	509.2	31.5	570	13	BE181919
38	502.8	31.1	885	10	BE378674
39	502.4	31.0	515	9	AI336858
40	484.2	29.9	500	10	AM075558
41	474.2	29.3	640	10	AM148557
42	463.4	28.6	530	12	BF726459
43	462.6	28.6	480	9	AI423162
44	456	28.2	475	9	AI363261
45	455.4	28.1	457	9	AI459805

## ALIGNMENTS

RESULT 1  
LOCUS B0689771  
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ACCESSION AGENCOURT\_8344092 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6248684  
VERSION B0689771.1 GI:21815087  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 888)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LCM2388 row: c column: 21  
High quality sequence stop: 665.  
Location/Qualifiers  
I. 888

FEATURES  
source



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Qy 1055 GCTGTGCGTGTGTGAGTGGCATGTACGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1114
Db 390 GCTGTGCGTGTGTGAGTGGCATGTACGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 331
Qy 1115 GCACAGGCGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1174
Db 330 GCACAGGCGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 272
Qy 1175 TGTACAGAGAGGCTGTGATGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1234
Db 271 TGTACAGAGAGGCTGTGATGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 212
Qy 1235 GATCATGTACGCGCGGAGAGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1294
Db 211 GATCATGTACGCGCGGAGAGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 152
Qy 1295 TGTATCTCGGATCTGTGTGGGCTGACATGACAGCAGCAGCAGCAGCAGCAGCAGCAGC 1354
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Qy 1355 GCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1414
Db 91 GCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 32
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VERSION Bg752229.1 GI:14062882
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 821)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbsr.nlm.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1755 row: 0 column: 18
High quality sequence stop: 770.
Location/Qualifiers
1..821

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FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4875113"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"

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BASE COUNT 194 a 201 c 248 g 178 t
ORIGIN
Query Match 43.5%; Score 704; DB 12; Length 821;
Best Local Similarity 95.1%; Pred. No. 3.8e-126;
Matches 782; Conservative 0; Mismatches 30; Indels 10; Gaps 5;
Note: this is a NIH-MGC library.

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Qy 555 GAAAGAGCTCGGTAAAGCAATTCGATTAATTAATTCAGCTGATGATTAATTAATTAATTA 614
Db 2 GAAAGAGCTCGGTAAAGCAATTCGATTAATTAATTCAGCTGATGATTAATTAATTAATTA 61
Qy 615 TGAAGGAAGAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 674
Db 62 TGAAGGAAGAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 121
Qy 675 GCGTGGCAGAGTCAAGTCTTGAAGTCAAGTCTTGAAGTCAAGTCTTGAAGTCAAGTCTTGAAG 734
Db 122 GCGTGGCAGAGTCAAGTCTTGAAGTCAAGTCTTGAAGTCAAGTCTTGAAGTCAAGTCTTGAAG 181
Qy 735 CAGTGTCCATTCATCCCTGTATGGGGCATAGTTGAGACTGAGAGTGAAGTGAAGTGAAGTGA 794
Db 182 CAGTGTCCATTCATCCCTGTATGGGGCATAGTTGAGACTGAGAGTGAAGTGAAGTGAAGTGA 241
Qy 795 TTTCTTAAAGGCTGGAGGGGAGTCCCACTCAAGGCTCCCTGCTGATTCATTAATTCATTA 854
Db 242 TTTCTTAAAGGCTGGAGGGGAGTCCCACTCAAGGCTCCCTGCTGATTCATTAATTCATTAATTC 301
Qy 855 TGTCTCTTAAAGCAATTCCTGACAGCAAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 914
Db 302 TGTCTCTTAAAGCAATTCCTGACAGCAAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 361
Qy 915 AGTACTCGAAGCTCA---TGACTGGGACTTGAAGTGGGCTGGCTGGCTGGCTGGCTGGCTGG 967
Db 362 AGTACTCGAAGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 421
Qy 968 AAAAGTCTTAAAGAA-AATCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTT 1026
Db 422 AAAAGTCTTAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 481
Qy 1027 AGAGCAAGGCGGCTGCAAAAGGCGGCTGCTGGTGGTGGAGTGGCATGTACGGCA 1086
Db 482 AGAGCAAGGCGGCTGCAAAAGGCGGCTGCTGGTGGTGGAGTGGCATGTACGGCA 541
Qy 1087 GCGCTTCTGCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1146
Db 542 GCGCTTCTGCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 601
Qy 1147 ACCGCCGAAGTCTGCGAGAGACAGCTGTACAGAGAGCGGCTGGTGGTGGTGGTGGTGGTGG 1206
Db 602 ACCGCCGAAGTCTGCGAGAGACAGCTGTACAGAGAGCGGCTGGTGGTGGTGGTGGTGGTGG 661
Qy 1207 TAGAAAAAGCTCTCCGAGAGGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 1266
Db 662 TAGAAAAAGCTCTCCGAGAGGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 721
Qy 1267 CAGTGTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1326
Db 722 CAGTGTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Qy 1327 ACGCCAATGTACAAATATGACGCTGGCAGACAGCAGCA 1368
Db 781 ACGCCAATGTACAAATATGACGCTGGCAGACAGCAGCA 821

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RESULT 4
BQ006545/c 702 bp mRNA linear EST 26-MAR-2002
LOCUS UI-H-EII-aza-n-21-0-UI-s1.NCI-CGAP-EII Homo sapiens cDNA clone
DEFINITION IMAGE:5846228 3', mRNA sequence.
ACCESSION BQ006545
VERSION BQ006545.1 GI:19731445
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM human.
Mammalia: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 702)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5846228"
/clone_lib="NCI-CGAP-EII"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: p7773-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI-CGAP-EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p7773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ACACTTGCAC.
TAG_LIB-UI-H-EII
TAG_TISSUE="chondrosarcoma"
TAG_SEQ="ACACTTGCAC"

BASE COUNT 137 a 200 c 163 g 202 t
ORIGIN
Query Match 42.5%; Score 687.8; DB 14; Length 702;
Best Local Similarity 99.6%; Pred. No. 5.3e-123;
Matches 700; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 522 TCGTGCTGGCGCTTGTGAGCGACGACGGCGACGACACACC-TCGACGAACACCCCGC 464
Oy 1155 AAACCTGTCGAGACGACACCGTGTACAGAGCGGGTGTGACCGAGGTGAGTGA 1214
Db 463 AAACGTCTGCAGAGACACCGTGTACAGAGCGGGTGTGACCGAGGTGAGTGA 404
Oy 1215 CGTTCGAGAGAGGAGAGAGATCATGTAGCCCGGAATGAGACCTGCTCCAGTGTG 1274
Db 403 CGTTCGAGAGAGGAGAGAGATCATGTAGCCCGGAATGAGACCTGCTCCAGTGTG 344
Oy 1275 CTGGGTTTGGCCCGAGCCATGATCTCCGAATCTGTTGGGCGATCCAGATACGCCAA 1334
Db 343 CTGGGTTTGGCCCGAGCCATGATCTCCGAATCTGTTGGGCGATCCAGATACGCCAA 284
Oy 1335 TGTCAACAATTCAGCCCTGGCGACACGACGACGAGGAGAGACAGAGAGAGAGAA 1394
Db 283 TGTCAACAATTCAGCCCTGGCGACACGACGACGAGGAGAGAGAGAGAGAGAGAA 224
Oy 1395 CACAGCATGAGACACAGTAATGATTAACATTAATTAATTAATTAATTAATTAATTA 1454
Db 223 CACAGCATGAGACACAGTAATGATTAACATTAATTAATTAATTAATTAATTAATTA 164
Oy 1455 GCTTACTGGCCGAGAGAAATGTACCAATTTTCACTGTTGGACTTGACAGCTTTTGGC 1514
Db 163 GCTTACTGGCCGAGAGAAATGTACCAATTTTCACTGTTGGACTTGACAGCTTTTGGC 104
Oy 1515 ACAAGCAAGAGAGAAATTTACACTGTTTCAAAACCCGGGGAGTTGGCTGTTAAGAA 1574
Db 103 ACAAGCAAGAGAGAAATTTACACTGTTTCAAAACCCGGGGAGTTGGCTGTTAAGAA 44
Oy 1575 GACCATTAATGCTTTAGACAGTGTAAACCAACCAACCAACCAACCAACCAACCA 1617
Db 43 GACCATTAATGCTTTAGACAGTGTAAACCAACCAACCAACCAACCAACCAACCA 1

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RESULT 5
AK012406
LOCUS Mus musculus 11 days embryo whole body cDNA, RIKEN full-length
DEFINITION enriched library, clone:270050C12:BRAIN cDNA, CLONE MNCB-0671,
full insert sequence.
ACCESSION AK012406
VERSION AK012406.1 GI:12849129
KEYWORDS HNC: CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 11 days embryo cDNA to mRNA,
clone:lib:RIKEN full-length enriched mouse cDNA library
clone:270050C12.
ORGANISM Mus musculus
Mammalia: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sclurognathu; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 2049374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneida, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

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QY 1581 TAAATGCTTTAGACATG 1598
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|
|
Db 18 TAAATGCTTTAGACATG 1

RESULT 7
LOCUS BM547680 696 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6507108 NIH_MGC_124 Homo sapiens CDNA clone IMAGE:5727798
5', RNA sequence.
ACCESSION BM547680
VERSION BM547680.1 GI:18781656
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM12722 row: h column: 07
High quality sequence stop: 641.
Location/Qualifiers
1..696
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5727798"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; EcoRV
(destroyed); Site: 2; NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT 188 a 160 c 197 g 134 t 17 others
ORIGIN
Query Match 40.9%; Score 661.4; DB 13; Length 696;
Best Local Similarity 98.5%; Pred No. 6.6e-118;
Matches 673; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 931 ATGACTGGACTTAGACTGGGCTCGGCTCGCTGGAAGAAGCTTTAGAAATCTTCT 990
|
|
|
Db 4 ATGACTGGACTTAGACTGGGCTCGGCTCGCTGGAAGAAGCTTTAGAAATCTTCT 63

QY 991 CAGTTCTCTTGCAGAGCACTGGCGCGGAGCGCAAGAGCAAGGGCCCTGCACAAAC 1050
|
|
|
Db 64 CAGTTCTCTTGCAGAGCACTGGCGCGGAGCGCAAGAGCAAGGGCCCTGCACAAAC 123

QY 1051 GGGCGCTGTGCTGTGAGTGCATGTACGCGAGCGCTTCTGCTGTTGGCGTGTCT 1110
|
|
|
Db 124 GGGCGCTGTGCTGTGAGTGCATGTACGCGAGCGGCTTCTGCTGTTGGCGTGTCT 183

QY 1111 GCAGCAGCAGGGGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1170
|
|
|
Db 184 GCAGCAGCAGGGGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 242

QY 1171 ACCGTGTACAGGAGCGGCTTGTGATGACCGAGCTGAGTAAAAAGCTCTCCAGAAAGGG 1230
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Db 243 ACCGTGTACAGGAGCGGCTTGTGATGACCGAGCTGAGTAAAAAGCTCTCCAGAAAGGG 302
QY 1231 AGAGATCATGTATACGCCCGGAGTAGAGCTCGACAGCTGCTGGTGGCGGCA 1290
|
|
|
Db 303 AGAGATCATGTATACGCCCGGAGTAGAGCTCGACAGCTGCTGGTGGCGGCA 362
QY 1291 GCCATGATCTCTCCGATCTGTTGGGATCCAGCATACGCGCAATGTCTACAAATCAGC 1350
|
|
|
Db 363 GCCATGATCTCTCCGATCTGTTGGGATCCAGCATACGCGCAATGTCTACAAATCAGC 422
QY 1351 CCTGGGCGAGACAGCAGCGAGGAGGAGAGACAGAGAAAAAACAACAGCATGAAACAC 1410
|
|
|
Db 423 CCTGGGCGAGACAGCAGCGAGGAGGAGAGACAGAGAAAAAACAACAGCATGAAACAC 482
QY 1411 AGTAATGATAAAAACCTAAATATTATAGCCCTCTGCTGTGCTTACAGGCGAGAA 1470
|
|
|
Db 483 AGTAATGATAAAAACCTAAATATTATAGCCCTCTGCTGTGCTTACAGGCGAGAA 542
QY 1471 ATGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAAGCAAGAGAAAT 1530
|
|
|
Db 543 ATGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAAGCAAGAGAAAT 602
QY 1531 TTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACCATTAATGCTTT 1550
|
|
|
Db 603 TTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACCATTAATGCTTT 662
QY 1591 AGACAGTGTAAAAAANAAAAA 1613
|
|
|
Db 663 AGACAGTGTAAAAAANAAAAA 685

RESULT 8
LOCUS BE271770 799 bp mRNA linear EST 26-OCT-2000
DEFINITION 601141674F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3141450 5',
RNA sequence.
ACCESSION BE271770
VERSION BE271770.1 GI:9145793
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 799)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM111 row: c column: 19
High quality sequence stop: 721.
Location/Qualifiers
1..799
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3141450"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pORF7; Site: 1; XhoI; Site: 2;
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald W. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT      171 a      225 c      199 g      204 t
ORIGIN
Query Match      40.7%; Score 659.6; DB 10; Length 799;
Best Local Similarity 96.9%; Pred. No. 1.4e-117;
Matches 769; Conservative 0; Mismatches 14; Indels 11; Gaps 9;

OY 215 ATGCGCTCTGCGGGGACAGTCTTCTGCTCCCAAGGGAACGACATTTGGCATC 274
    |||||||
DB 1 ATGCGCTCTGCGGGGACAGTCTTCTGCTCCCAAGGGAACGACATTTGGCATC 59
    |||||||

OY 275 AGCTGTGCAACACCCCTTTTGAACGGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCC 334
    |||||||
DB 60 AGCTGTGCAACACCCCTTTTGAACGGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCC 119
    |||||||

OY 335 TGGGCGCTGAGGCGCA-GGCTTCGCGACACCATCTGTTCTCAAAATTAAGCCCTTCTCG 394
    |||||||
DB 120 TGGGCGCTGAGGCGCA-GGCTTCGCGACACCATCTGTTCTCAAAATTAAGCCCTTCTCG 178
    |||||||

OY 395 GCACACTGCTGAAGCTGAAGGAGATGCCACG--CCCTCTGCAATGTTCTTCAGCCCTC 452
    |||||||
DB 179 GCACACTGCTGAAGCTGAAGGAGATGCCACG--CCCTCTGCAATGTTCTTCAGCCCTC 238
    |||||||

OY 453 GCGCCCAACCCCGCCACCTCCCTGAGTGAATTTCTTCTGGGTCTCTTATTTCTGGTAG 512
    |||||||
DB 239 GCGCCCAACCCCGCCACCTCCCTGAGTGAATTTCTTCTGGGTCTCTTATTTCTGGTAG 298
    |||||||

OY 513 GGAAGCGGAGTCCGTCTCTTTTGTCTTCTGCAATATGAAGAGCTCGTAAAGC 572
    |||||||
DB 299 GGAAGCGGAGTCCGTCTCTTTTGTCTTCTGCAATATGAAGAGCTCGTAAAGC 358
    |||||||

OY 573 ATTCGTAATTAATTCAGCTGAGTGAATTTCTGATGATGACTTGAAGAGAGGCTGGAG 632
    |||||||
DB 359 ATTCGTAATTAATTCAGCTGAGTGAATTTCTGATGATGACTTGAAGAGAGGCTGGAG 418
    |||||||

OY 633 TGAAGCTTACCCCGCCATGCTGTGTAAACCGGAGTCAAGGCGGCTGGCAGAGTCAGTCC 692
    |||||||
DB 419 TGAAGCTTACCCCGCCATGCTGTGTAAACCGGAGTCAAGGCGGCTGGCAGAGTCAGTCC 478
    |||||||

OY 693 TTGAAGTACAGTGGGCGCATCTGCCCTTTTGTAAAGCTCCAGTGTCCATTCATGCC 752
    |||||||
DB 479 TTGAAGTACAGTGGGCGCATCTGCC--TTTGTAAAGCTCCAGTGTCCATTCATGCC 537
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OY 753 TGAATGGGCGCATAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 812
    |||||||
DB 538 TGAATGGGCGCATAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 596
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OY 813 CAGTTCCTCACTCAAGGCTCCCT-CGCTTGACATTCAAACCTTCATGCTCGTGAACCAT 871
    |||||||
DB 597 CAGTTCCTCACTCAAGGCTCCCTCAAGCTTGACATTCAAACCTTCATGCTCGTGAACCAT 656
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OY 872 CTCTGAGAGAAATTTGGCTGGTTCGCGCTGAGTGAAGTGGGCTCTAG-TGACTGGAAGTCA 930
    |||||||
DB 657 CTCTGAGAGAAATTTGGCTGGTTCGCGCTGAGTGAAGTGGGCTCTAGTGAAGTCA 716
    |||||||

OY 931 ATGA-CTGGAGACTTGAAGTGGGCTGGCTGCTGCTGAAAGTGGTGAAGAAATCTTC 989
    |||||||
DB 717 ATGACTTGGGACTTAAACTTGGGCTGGCTTCG--TCTGAAGTGGCTTAAGCAATCTTC 774
    |||||||

OY 990 TCAGTTCTCTCTTC 1003
    |||||||
DB 775 TCAGTTCTCTCTTC 788
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RESULT 9
BE385990 676 bp mRNA linear EST 21-JUL-2000
LOCUS 601276636f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617696 5',
DEFINITION MRNA sequence.
ACCESSION BE385990
VERSION BE385990.1 GI:9331355
KEYWORDS EST.
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 676)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcraps-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov
Plate: LICM285 row: 9 column: 09
High quality sequence stop: 653.
Location/Qualifiers
1..676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3617696"
/clone_1b="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pORF7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAAGAG(g). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      168 a      172 c      199 g      137 t
ORIGIN
Query Match      39.9%; Score 646.6; DB 10; Length 676;
Best Local Similarity 99.0%; Pred. No. 4.8e-115;
Matches 672; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

OY 830 TCCCTGCTGACATTCNAACCTTCCTCTGAAACCATCTCTGACAGCAATTTGCC 889
    |||||||
DB 1 TCCCTGCTGACATTCNAACCTTCCTCTGAAACCATCTCTGACAGCAATTTGCC 60
    |||||||

OY 890 TGGTTTGGCGCTGAGTTGGGCTCTAGGACTGAGACTGAATGACTGGGACTTAGACTG 949
    |||||||
DB 61 TGGTTTGGCGCTGAGTTGGGCTCTAGGACTGAGACTGAATGACTGGGACTTAGACTG 120
    |||||||

OY 950 GGGCTGGCGCTGCTGAAAGTGTAAAGTCTTCAAGTCTCTCAAGTCTCTCTGAGAGGA 1009
    |||||||
DB 121 GGGCTGGCGCTGCTGAAAGTGTAAAGTCTTCAAGTCTCTCAAGTCTCTCTGAGAGGA 180
    |||||||

OY 1010 CTGGCGCCGGGAGCGGAAGCAACGGGCGCTGCACAAAGCGGGCGCTGCGGTGTGA 1069
    |||||||
DB 181 CTGGCGCCGGGAGCGGAAGCAACGGGCGCTGCACAAAGCGGGCGCTGCGGTGTGA 240
    |||||||

OY 1070 GTGGGCAATGTACGGGCGGCTCTGCTGTTGGGCTGTGTCGACGAGGAGGGGAGCA 1129
    |||||||
DB 241 GTGGGCAATGTACGGGCGGCTCTGCTGTTGGGCTGTGTCGACGAGGAGGGGAGCA 300
    |||||||

OY 1130 CAGCAGCTTGCAGCAACCGCGCGGAAGTGTGCGAGGACACCGTGTACAGAGCGGGT 1189
    |||||||
DB 301 CAGCAGC-TGCAGCAACCGCGCGGAAGTGTGCGAGGACACCGTGTACAGAGCGGGT 359
    |||||||

OY 1190 TGATGACCGAGCTGAGTGAAGAAAGCTTCCGAGAAAGGAGAGGATCATGTAGCCCC 1249
    |||||||
DB 360 TGATGACCGAGCTGAGTGAAGAAAGCTTCCGAGAAAGGAGAGGATCATGTAGCCCC 419
    |||||||

OY 1250 GGAGTGGAGACTGCTCAGTGTGCTGTTGGTGGCGGAGGACATATCTCGAATCT 1309
    |||||||
DB 420 GGAAGTGGAGACTGCTCAGTGTGCTGTTGGTGGCGGAGGACATATCTCGAATCT 479
    |||||||

OY 1310 GGTGGGATCAGCAGATACGCGCAATGTCAACAAATCAGCCCTGGGCAAGAGAGCAG 1369
    |||||||

```

Db 480 GGTGGGATCAGCAGGATGATGACAAATGACCCCTGGGACAGACAGACAG 539

QY 1370 GAGGAGAGACAGAGAAAGAAAACACAGATGAGAAACAGTAATGATTAACCAT 1429

Db 540 GAGGAGAGACAGAGAAAGAAAACACAGATGAGAAACAGTAATGATTAACCAT 599

QY 1430 AAAATATTATGACCCCTGCTGTCTGCTTACTGCGCAGAAATGTAACCAATTTTCAGT 1489

Db 600 AAAATATTATGACCCCTGCTGTCTGCTTACTGCGCAGAAATGTAACCAATTTTCAGT 657

QY 1490 GTTGACTGACAGCTTCT 1508

Db 658 GTTGACTGACAGCTTCT 676

RESULT 10  
AW149665/c  
LOCUS  
DEFINITION x140105.x1 NCI CGAP Brn50 Homo sapiens cDNA clone IMAGE:2620569 3' similar to SW:GP39\_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.

ACCESSION AW149665  
VERSION AW149665.1  
KEYWORDS GI:6197561  
SOURCE EST.  
ORGANISM human.

REFERENCE  
AUTHORS  
TITLE  
Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
1 (bases 1 to 690)  
NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbp/image/image.html

JOURNAL  
COMMENT  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Glibco  
High quality sequence stop: 402.  
Location/Qualifiers  
1.690  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2620569"  
/clone\_1ib="NCI CGAP Brn50"  
/tissue\_type="medulloblastoma"  
/lab\_host="DH10B (phage resistant)"  
/note="Organ: brain; Vector: pRT30-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from medulloblastoma tumor tissue, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT30 vector. This library is normalized. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 142 a 196 c 160 g 191 t 1 others

ORIGIN

Query Match 39.5% Score 640.2 DB 10; Length 690;  
Best Local Similarity 96.4% Pred No. 8.3e-114;  
Matches 665; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

QY 921 TCGAGACTGAATGACTGAGCTGGGCTGGCTCGTGAAGAAGTGTAG 980  
||||| ||||||||| ||| ||||||||| ||| ||||||||| ||| |||||||||

Db 689 TCGAATTCGAATGACTGATTAAGACTTGGGCTGGCTTCGTCGAAAGTGTAAAG 630

QY 981 AAAATCTTCAGTCTCTCTTCGAGAGACTGGCCCGGAGACCGAAGCAAGCGGCC 1040

Db 629 AAAATCTTCAGTCTCTCTTCGAGAGACTGGCCCGGAGACCGAAGCAAGCGGCC 570

QY 1041 TGCACAAACGGGCGCTGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1100

Db 569 TGCACAAACGGGCGCTGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 510

QY 1101 TTGGCGTCTGACGACAGCGGCGGACGACAGCACACCTTGCAGCAACCGCGGAACTG 1160

Db 509 TTGGCGTCTGACGACAGCGGCGGACGACAGCACACCTTGCAGCAACCGCGGAACTG 451

QY 1161 CTGGCGGACCGCTGTATAGAGAGGGGTTGATGACCGAGCTGAGTGAAGAAACGTCTC 1220

Db 450 CTGGCGGACCGCTGTATAGAGAGGGGTTGATGACCGAGCTGAGTGAAGAAACGTCTC 391

QY 1221 CGAAGAGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1280

Db 390 CGAAGAGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 331

QY 1281 TTGGCGGACCGCTGTATAGAGAGGGGTTGATGACCGAGCTGAGTGAAGAAACGTCTC 1340

Db 330 TTGGCGGACCGCTGTATAGAGAGGGGTTGATGACCGAGCTGAGTGAAGAAACGTCTC 271

QY 1341 AACATTCAGCCCTGGGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1400

Db 270 AACATTCAGCCCTGGGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 211

QY 1401 ATGAGACACAGTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1460

Db 210 ATGAGACACAGTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 151

QY 1461 TGGCCAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1520

Db 150 TGGCCAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 91

QY 1521 AAGAGAGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1580

Db 90 AAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 31

QY 1581 TAAATGCTTTAGACAGTGTAAAAAAAAA 1610

Db 30 TAAATGCTTTAGACAGTGTATTTATACCA 1

RESULT 11  
AW590950/c  
LOCUS  
DEFINITION h51e12.x1 NCI CGAP G66 Homo sapiens cDNA clone IMAGE:2949166 3' similar to SW:GP39\_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.

ACCESSION AW590950  
VERSION AW590950.1  
KEYWORDS GI:7278094  
SOURCE EST.  
ORGANISM human.

REFERENCE  
AUTHORS  
TITLE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
1 (bases 1 to 649)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: [image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 457.

## FEATURES

## Source

1. 649

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2949166"

/clone\_lib="NCI CGAP GC6"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 132 a 189 c 155 g 173 t

## ORIGIN

Query Match 38.0%; Score 615.8; DB 10; Length 649;  
Best Local Similarity 98.6%; Pred. No. 4.3e-109;

Matches 642; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

949 GGGGCTGGCCCTCGCTGAAAGTCTTAGAATAATCTCTCAGTTCTCTTCAGAGG 1008  
|||||  
649 GGGGCTGGCCCTCGCTG-AAAAGCTTTTAAACAATCTCTCAGTTCTCTTCAGAGG 591  
|||||  
1009 ACTGGCGCGGAGCGAAGAGCAAGCGCGCTGCACAAAGCGGCGCTGTGCGTGTGG 1068  
|||||  
590 ACTGGCGCGGAGCGAAGATCAACGGCGCTGCACAAAGCGGCGCTGTGCGTGTGG 531  
|||||  
1069 AGTGGCGATGACGGGAGGCGGCTTCTGTGTGGCTGTGCAGCAGCAGCGGCGGCG 1128  
|||||  
530 AGTGGCGATGACGGGAGGCGGCTTCTGTGTGGCTGTGCAGCAGCAGCGGCGGCG 471  
|||||  
1129 ACAGCAGCTTGCAGCAACACCGCGCAAGCTGTCGAGCAGCAGCTGTACAGAGCGGG 1188  
|||||  
470 ACAGCAGC-TGCAGCAACACCGCGCAAGCTGTCGAGCAGCAGCTGTACAGAGCGGG 412  
|||||  
1189 TTGATGACCGAGCTGAGTAAAGAACTCTCCGAGAAAGGAGAGGAGATCATGTAGCGC 1248  
|||||  
411 TTGATGACCGAGCTGAGTAAAGAACTCTCCGAGAAAGGAGAGGAGATCATGTAGCGC 352  
|||||  
1249 CGGAGTGGAGGAGCTGTCAGTGTGGCTTGGCGGAGCGATGATCTCCGAAATC 1308  
|||||  
351 CGGAGTGGAGGAGCTGTCAGTGTGGCTTGGCGGAGCGATGATCTCCGAAATC 292  
|||||  
1309 TGGTTGGCGATCCAGCATACGGCCCAATGTCAACAATCAGCCCTGGGAGAGAGCA 1368  
|||||  
291 TGGTTGGCGATCCAGCATACGGCCCAATGTCAACAATCAGCCCTGGGAGAGAGCA 232  
|||||  
1369 GGAGGAG 1428  
|||||  
231 GGAGGAG 172  
|||||  
1429 TAAATATTATTACCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1488  
|||||  
171 TAAATATTATTACCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 112  
|||||  
1489 TGTGGAGCTTGCAGCTTCTTGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1548  
|||||  
111 TGTGGAGCTTGCAGCTTCTTGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 52  
|||||  
1549 CGGGGAGTGTGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1599  
|||||

DB 51 CGGGGAGTGTGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1

## RESULT 12

BM669397/c

627 bp

mRNA linear EST 27-FEB-2002

## LOCUS

UI-E-DWI-and-c-11-0-UI-s1 UI-E-DWI Homo sapiens cDNA clone

## DEFINITION

UI-E-DWI-and-c-11-0-UI 3', mRNA sequence.

## ACCESSION

BM669397

## VERSION

BM669397.1

GI:18979294

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 627)

## AUTHORS

Bonaldo,M.F., Lennon,G. and Soares,M.B.

## TITLE

Normalization and subtraction: two approaches to facilitate gene discovery

## JOURNAL

Genome Res. 6 (9), 791-806 (1996)

## COMMENT

97044477

## MEDLINE

Contact: Soares, MB

## PROGRAM

Program for Rat Gene Discovery and Mapping

## UNIVERSITY

University of Iowa

## TEL

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

## FAX

Tel: 319 335 8250

## EMAIL

Fax: 319 335 9565

## TISSUE

Email: msoares@blue.weeg.uiowa.edu

## CDNA

Tissue Procurement: Dr. Gregg Hageman

## LIBRARY

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

## DNA

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

## GENETICS

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

## SEQ

Seq primer: M13 Forward

## POLY

PolyA+yes.

## FEATURES

## source

Location/Qualifiers

## 1. 627

## /organism="Homo sapiens"

## /db\_xref="taxon:9606"

## /clone="UI-E-DWI-and-c-11-0-UI"

## /clone\_lib="UI-E-DWI"

## /tissue\_type="adult"

## /dev\_stage="adult"

## /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

## /note="Organ: eye; Vector: pTR73-Pac (Pharmacia) with a modified polylinker. Site 1: EcoR I; Site 2: Not I; UI-E-DWI is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTR73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program 'Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

BASE COUNT 118 a 180 c 145 g 183 t 1 others

## ORIGIN

Query Match 37.9%; Score 613.4; DB 13; Length 627;

Best Local Similarity 99.5%; Pred. No. 1.3e-108;

Matches 625; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

990 TCAATTTCTCTTGCAGAGAGCTGGCGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1049  
|||||  
627 TCAATTTCTCTTGCAGAGAGCTGGCGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAG 568  
|||||

```

QY 1050 CCGGCGCTGTGGTGGAGTGCATGATGACGAGCGCTTCTGTTGGCGTGC 1109
      |||
Db 567 CCGGCGCTGTGGTGGAGTGCATGATGACGAGCGCTTCTGTTGGCGTGC 508
QY 1110 TCGAGGACAGGCGGACGACACACCTCTGACGAAACCCCGCAACTGCTGCAGGA 1169
      |||
Db 507 TCGAGGACAGGCGGACGACACACCTCTGACGAAACCCCGCAACTGCTGCAGGA 449
QY 1170 CACCGTGTACAGAGCGGGTGTGATGACCGAGTGTGAAAACGTCCTCCGAGAGGG 1229
      |||
Db 448 CACCGTGTACAGAGCGGGTGTGATGACCGAGTGTGAAAACGTCCTCCGAGAGGG 389
QY 1230 GAGGAGATCATGTACGCGCCGGAAGTAGACCTGCTCAGTGTGCTTGGTGGCCGC 1289
      |||
Db 388 GAGGAGATCATGTACGCGCCGGAAGTAGACCTGCTCAGTGTGCTTGGTGGCCGC 329
QY 1290 AGCCATGATCTCCGAAATCTGTTGGGCACTCCAGCATAGCGCAATGTCAACAATCAG 1349
      |||
Db 328 AGCCATGATCTCTCGAATCTGTTGGGCACTCCAGCATAGCGCAATGTCAACAATCAG 269
QY 1350 CCCTGGGACAGACGACGAGAGGAGAGACAGAGAAAAGAAAACACAGCATGAGAAC 1409
      |||
Db 268 CCCTGGGACAGACGACGAGAGGAGAGACAGAGAAAAGAAAACACAGCATGAGAAC 209
QY 1410 CAGTAAATGATTAACCAATTAATATTTAGCCCTCTGCTTGTGCTTACTGCGCAGGA 1469
      |||
Db 208 CAGTAAATGATTAACCAATTAATATTTAGCCCTCTGCTTGTGCTTACTGCGCAGGA 149
QY 1470 AATGATACCAATTTTCACTGTTGGCTGACAGCTTCTTTGCCACAGAGAGAGAA 1529
      |||
Db 148 AATGATACCAATTTTCACTGTTGGCTGACAGCTTCTTTGCCACAGAGAGAGAA 89
QY 1530 TTTTACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTT 1589
      |||
Db 88 TTTTACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTT 29
QY 1590 TTAGACAGTGTAAAAAAGAAAAA 1617
      |||
Db 28 TTAGACAGTGTAAAAAAGAAAAA 1

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RESULT 13  
 BE395797 743 bp mRNA linear EST 21-JUL-2000  
 LOCUS 6031002861 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3631543 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BE395797  
 VERSION BE395797.1 GI:9341162  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 743)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: csapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM321 row: h column: 08  
 High quality sequence stop: 600.  
 Location/Qualifiers  
 1..743  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

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/clone="IMAGE:3631543"
/clone_lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOTB7; Site:1; XhoI; Site:2;
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Library constructed by Ling Hong
in the Laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT 160 a 189 c 214 g 180 t  
 ORIGIN

Query Match	Score	DB	Length
Best Local Similarity	92.3%	Pred. No. 1,4e-106	743
Matches 668; Conservative 0; Mismatches 52; Indels 4; Gaps 3;			
QY 410 TGAAGAGATGACACCCCTCCGATGTTCTTCCAGCCCTCGCCGACCCGACCCGAC			468
Db 1 TGAAGAGATGACACCCCTCCGATGTTCTTCCAGCCCTCGCCGACCCGACCCGAC			60
QY 468 CTCCTGAGTGAATTTCTTGGGTGCTCTTTATTTGAGGAGAGAGCGGAGTCCGTG			528
Db 61 CTCCTGAGTGAATTTCTTGGGTGCTCTTTATTTGAGGAGAGAGCGGAGTCCGTG			120
QY 529 TTTCTTTTGTTCCTGCTGCAATATGAAGAGTCCGTTAAAGCATTTCTGAATTAATCA			588
Db 121 TTTCTTTTGTTCCTGCTGCAATATGAAGAGTCCGTTAAAGCATTTCTGAATTAATCA			180
QY 589 GCTGACTGAAATTTTCAATATGATCTTGAAGAGAGAGTGAAGTGAAGTCAACCCCA			648
Db 181 GCTGACTGAAATTTTCAATATGATCTTGAAGAGAGAGTGAAGTGAAGTCAACCCCA			240
QY 649 TGTCTGTTAAACCGAGATCAAGGCGAGCTGGCAGAGTCACTCTTGAAGTCACTAGG			708
Db 241 TGTCTGTTAAACCGAGATCAAGGCGAGCTGGCAGAGTCACTCTTGAAGTCACTAGG			300
QY 709 TGGGATCTGCTTTTGTAAAGCCTCCAGTGTCCATTCCTGATTTGGGGATAGTT			768
Db 301 TGGGATCTGCTTTTGTAAAGCCTCCAGTGTCCATTCCTGATTTGGGGATAGTT			360
QY 769 TGAAGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG			828
Db 361 TGAAGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG			420
QY 829 CTCCTGCTGATGATTAACCTTCAATGCTCTGTAAGAAACATTTCTGACAGCAATGG			888
Db 421 CTCCTGCTGATGATTAACCTTCAATGCTCTGTAAGAAACATTTCTGACAGCAATGG			480
QY 889 CTGTTTGGCGCTGAGTGTGGCTCTGATGACCTGAGACTCAATGACTGAGTACT			948
Db 481 CTGTTTGGCGCTGAGTGTGGCTCTGATGACCTGAGACTCAATGACTGAGTACT			540
QY 949 GGGGCTGGGCTGCTGTAAGAGTGTAAAGAAATCTTCTAGTTCCTCTTGCAGAGG			1008
Db 541 GGGGCTGGGCTGCTGTAAGAGTGTAAAGAAATCTTCTAGTTCCTCTTGCAGAGG			599
QY 1009 ACTGGCGCGGAGGACCAAGAGCAAGCGGCGCTGCAAAAGCGGCGCC--TGTGCTGT			1066
Db 600 ACTGGCGCGGAGGACCAAGAGCAAGCGGCGCTGCAAAAGCGGCGCC--TGTGCTGT			659
QY 1067 GGAATGCGATGTGCGGAGAGCGCTTCTGCTGTTGGTGGCTGCGAGAGAGGGGCA			1126
Db 660 GGAATGCGATGTGCGGAGAGCGCTTCTGCTGTTGGTGGCTGCGAGAGAGGGGCA			719
QY 1127 GCAC 1130			
Db 720 ACAC 723			

RESULT 14  
 A1990500/c

LOCUS AI990500 616 bp mRNA linear EST 08-MAR-2000  
 DEFINITION WS40007.x1 NCI\_CGAP\_G6 Homo sapiens CDNA clone IMAGE:2499661.3'  
 similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39. ; mRNA sequence.  
 ACCESSION AI990500  
 VERSION AI990500.1 GI:5837381  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 616)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/dbfp/image/image.html  
 Insert Length: 1212 Std Error: 0.00  
 Seq primer: -400p from Gibco  
 High quality sequence stop: 459.  
 Location/Qualifiers  
 1. 616  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2499661"  
 /clone\_1ib="NCI\_CGAP\_G6"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="Vector: pT73D-pac (Pharmacia) with a modified  
 polylinker. Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
 from the normalized library NCI\_CGAP\_G64 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clonids  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 120 a 182 c 147 g 167 t  
 ORIGIN  
 Query Match 37.1%; Score 600.2; DB 9; Length 616;  
 Best Local Similarity 99.4%; Pred. NO. 4.5e-106;  
 Matches 613; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1283 TGGCCGACCATGATCTCCGATCTGGTGGGCATCCAGCATCGGCCAATGTCACAA 1342  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 317 TGGCCGACCATGATCTCCGATCTGGTGGGCATCCAGCATCGGCCAATGTCACAA 258  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1343 CATCAGCCCTGGGACAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1402  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 257 CATCAGCCCTGGGACAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 198  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1403 GAGAACACAGTAAATGAATAAACATAAATATTTAGCCCTCTGTTCTGCTTACTG 1462  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 197 GAGAACACAGTAAATGAATAAACATAAATATTTAGCCCTCTGTTCTGCTTACTG 138  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1463 GCCAGGAATGTGATCAATTTTTCAGTGTGGACCTTGACAGCTTTTGGCACAGCAA 1522  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 137 GCCAGGAATGTGATCAATTTTTCAGTGTGGACCTTGACAGCTTTTGGCACAGCAA 78  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1523 GAGAGATTTTAACTGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTA 1582  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 77 GAGAGATTTTAACTGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTA 18  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1583 AATGCTTTAGACAGTGT 1599  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 17 AATGCTTTAGACAGTGT 1  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 15  
 BF439382 696 bp mRNA linear EST 30-MAR-2001  
 BF439382/c  
 LOCUS nab63906.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P.S1 Homo sapiens CDNA clone  
 DEFINITION IMAGE:327627 3' similar to SW:GP39\_HUMAN O43194 PUTATIVE G  
 PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.  
 ACCESSION BF439382  
 VERSION BF439382.1 GI:11451899  
 EST.  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 696)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seg primer: -400p from Gibco  
 High quality sequence stop: 459.  
 Location/Qualifiers  
 1. 696  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:327627"  
 /clone\_1ib="Soares\_NSF\_F8\_9W\_OT\_PA\_P.S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled. Vector: pT73D-pac (Pharmacia) with  
 a modified polylinker. Site\_1: Not I; Site\_2: Eco RI;  
 Equal amounts of plasmid DNA from five normalized  
 libraries were mixed, and ss circles were made in vitro.  
 Following HAP purification, this DNA was used as tracer in  
 a subtractive hybridization reaction. The driver was  
 PCR-amplified cDNAs from pools of 5,000 clones made from  
 the same 5 libraries. The pools consisted of the following  
 libraries and clones: Soares NBHF pool 1:  
 309384-310919, 323208-325895 Soares NB2HP pool 1:  
 145032-147335, 147720-148103, 148872-149255, 15002 -  
 150407, 151176-152327 Soares NB2HP-9W pool 1:  
 758280-760583, 772104-774407 Soares NBHPA pool 1:  
 304776-306311, 320136-322823, 326280-326663 Soares NBHOT  
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento  
 Soares and M. Fatima Bonaldo."



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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 15:03:08 ; Search time 373.511 Seconds  
(without alignments)  
11437.514 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897

Sequence: 1 gccaaactccgagagctctg.....aaaaaaaaaaaaaaaa 1897

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1368953

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
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22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1897	100.0	1897	24	ABT03284
2	1897	100.0	1897	24	ABT03284
3	1897	100.0	1897	24	ABT03284
4	1897	100.0	1897	24	ABT03284
5	1897	100.0	1897	24	ABT03284
6	1897	100.0	1897	24	ABT03284
7	1897	100.0	1897	24	ABT03284
8	1897	100.0	1897	24	ABT03284
9	1897	100.0	1897	24	ABT03284

10	1344	70.8	1890	22	AAE93845	Human CDNA encoding
11	1218	64.2	2528	22	AAO18690	Human G protein co
12	1150	60.6	1608	24	ABO54231	Human ovarian anti
13	606	31.9	625	24	ABT03280	Human ovarian carc
14	606	31.9	625	24	ABT03280	Human ovarian carc
15	606	31.9	625	24	ABT03280	Human ovarian carc
16	511	26.9	591	22	AAE94044	Human ovarian carc
17	506	26.7	1362	22	ABT03279	Human ovarian carc
18	506	26.7	1362	22	ABT03279	Human ovarian carc
19	425	22.4	480	24	ABT03283	Human ovarian carc
20	425	22.4	480	24	ABT03283	Human ovarian carc
21	366	19.3	587	22	AAE94186	Human ovarian carc
22	364	19.2	444	22	AAH50766	Human ovarian carc
23	316	16.7	396	22	AAE94818	Human ovarian carc
24	316	16.7	396	22	AAE94818	Human ovarian carc
25	316	16.7	396	22	AAE94818	Human ovarian carc
26	315	16.6	369	22	AAE95007	Human ovarian carc
27	315	16.6	369	22	AAE95007	Human ovarian carc
28	315	16.6	369	22	AAE95007	Human ovarian carc
29	315	16.6	369	22	AAE95007	Human ovarian carc
30	307	16.2	349	24	ABT03282	Human ovarian carc
31	271	14.3	1010	24	ABT03282	Human ovarian carc
32	271	14.3	1010	24	ABT03282	Human ovarian carc
33	264	13.9	409	24	ABT03282	Human ovarian carc
34	166	8.8	201	24	ABT03282	Human ovarian carc
35	154	8.1	390	24	ABT03282	Human ovarian carc
36	125	6.6	381	24	ABT03282	Human ovarian carc
37	120	6.3	430	24	ABT03282	Human ovarian carc
38	120	6.3	430	24	ABT03282	Human ovarian carc
39	60	3.2	60	24	ABT03282	Human ovarian carc
40	27	1.4	50	22	AAE94186	Human ovarian carc
41	26	1.4	50	22	AAE94186	Human ovarian carc
42	26	1.4	50	22	AAE94186	Human ovarian carc
43	26	1.4	50	22	AAE94186	Human ovarian carc
44	26	1.4	50	22	AAE94186	Human ovarian carc
45	25	1.3	51	22	AAE94186	Human ovarian carc

## ALIGNMENTS

RESULT 1	ABT03284	standard; CDNA; 1897 BP.
ID	ABT03284	
XX	ABT03284	
AC	ABT03284	
XX	ABT03284	
DT	05-SEP-2002	(first entry)
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.	
XX	Human: ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;	
KW	Cyclostatic; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200239885-A2.	
PD	23-MAY-2002.	
XX		
FF	13-NOV-2001; 2001MO-US45395.	
XX		
PR	14-NOV-2000; 2000US-0713550.	
PR	03-APR-2001; 2001US-0825294.	
XX	02-OCN-2001; 2001US-0970966.	
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;	
XX	WPI; 2002-500186/53.	
DR		
XX		
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for	



XX	RESULT 2
ABL40352	ID ABL40352 standard; cDNA; 1897 BP.
AC	ABL40352;
DT	28-JUN-2002 (first entry)
XX	Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.
DE	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer; ss.
KM	Homo sapiens.
OS	
XX	
FH	Key Location/Qualifiers
FT	CDS 260..685
FT	/tag= a
FT	/product= "Ovarian carcinoma protein O1034C/O591S"
PN	US2002004491-A1.
XX	
PD	10-JAN-2002.
XX	
PF	03-APR-2001; 2001US-0825294.
PR	10-SEP-1999; 99US-0394374.
PR	01-MAY-2000; 2000US-0561778.
PR	15-AUG-2000; 2000US-0640173.
PR	07-SEP-2000; 2000US-0656668.
PR	14-NOV-2000; 2000US-0713550.
PA	(XUJ/) XU J.
PA	(STOL/) STOLK J A.
PA	(ALGA/) ALGATE P A.
PA	(FLIN/) FLING S P.
PI	XU J, STOLK JA, ALGATE PA, FLING SP;
XX	
DR	WPI: 2002-171027/22.
XX	P-PSDB: ABB09417.
PT	Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
PT	prevention and/or treatment of cancer, especially ovarian cancer .
XX	
PS	Claim 1a; Page 127-128; 131pp; English.
XX	
CC	The invention relates to ovarian tumour polynucleotides and polypeptides
CC	that may be utilised in cancer therapy, for example in a vaccine or
CC	gene therapy. Polypeptides and polynucleotides of the invention are
CC	useful for detecting a cancer in a patient, for stimulating and/or
CC	expanding T-cells specific for a tumour protein, and for inhibiting the
CC	development of a cancer in a patient. They are also useful for
CC	stimulating an immune response in a patient, and for treating a cancer in
CC	a patient and for determining the presence of a cancer in a patient.
CC	The isolated polynucleotides of the invention are useful for their
CC	ability to selectively form duplex molecules with complementary stretches
CC	of the entire desired gene or gene fragments, and for designing and
CC	preparing ribozyme molecules for inhibiting expression of tumour
CC	polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC	invention are also useful in recombinant DNA molecules to direct
CC	expression of a polypeptide in appropriate host cells. The current
CC	sequence represents the ovarian carcinoma O1034C/O591S consensus
CC	nucleotide sequence.
XX	
SQ	Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other:
	Query Match 100.0%; Score 1897; DB 24; Length 1897;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1897; Conservative 0; Mismatches 0; Indels 0; Gaps 0
0Y	1 GCCAACCTCGGAGGCCTGTGCTCGCCCCGGGAGCCGAGGAGAGACAGACCCG 60 

Db	1	GCACACTCCGGAGAGGCTGTGTGCTCGGCGCGGGAGCGCGAGCGGGAGAGACAGACACCGG	60
QY	61	CAGCCGGGAGGCCCAAGCCGGGGGCATGCAAGGCTCCGCGAGCGCCACTGCGGCTCTCTTA	120
Db	61	CAGCCGGGAGGCCCAAGCGCGGGGCATGCAAGGCTCCGCGAGCGCCACTGCGGCTCTCTTA	120
QY	121	AGCTACGACCGCTGCTTCGCCGGCAGCAGCGCGGGGCCCGCAGACCTCGGCACCCACAGC	180
Db	121	AGCTACGACCGCTGCTTCGCCGGCAGCAGCGCGGGGCCCGCAGACCTCGGCACCCACAGC	180
QY	181	CGCTACACCGGGGAGGCTTCGCTGTCGCTCTGTATGCGCTTGGCCCTCCCG	240
Db	181	CGCTACACCGGGGAGGCTTCGCTGTCGCTCTGTATGCGCTTGGCCCTCCCG	240
QY	241	GGCCCCGGGAGCTCCGGGAGAAATGTGGGTCTAGAGCATGCGGGCAACTTTTGGGGATTTT	300
Db	241	GGCCCCGGGAGCTCCGGGAGAAATGTGGGTCTAGAGCATGCGGGCAACTTTTGGGGATTTT	300
QY	301	CTTGTCTCAGGCTTTGGCGTGCAGAAATCCAGTGCATACAGTGTGAAGAAATTCACAGTGA	360
Db	301	CTTGTCTCAGGCTTTGGCGTGCAGAAATCCAGTGCATACAGTGTGAAGAAATTCACAGTGA	360
QY	361	CAAGCAGCTGCTTCCTCCCGGAGTTGATTGTGAATTGCAGGCTAACGTTCAAGACATGTG	420
Db	361	CAAGCAGCTGCTTCCTCCCGGAGTTGATTGTGAATTGCAGGCTAACGTTCAAGACATGTG	420
QY	421	TCAGAAAGAAATGTATGAGAGCAAAATGCGCGGGATCATGTATCCGCAATCCTGTGACATATC	480
Db	421	TCAGAAAGAAATGTATGAGAGCAAAATGCGCGGGATCATGTATCCGCAATCCTGTGACATATC	480
QY	481	AGCGGCGTGTCTCATCGCTTCGCGGGATACAGTCCCTTCTGCTCCCGAGGAAATGTAA	540
Db	481	AGCGGCGTGTCTCATCGCTTCGCGGGATACAGTCCCTTCTGCTCCCGAGGAAATGTAA	540
QY	541	CTCAGTTTGCATCAGCTGCTGCGCAACACCCCTCTTGTAAACGGGCCAAGGCCCAAGAAAG	600
Db	541	CTCAGTTTGCATCAGCTGCTGCGCAACACCCCTCTTGTAAACGGGCCAAGGCCCAAGAAAG	600
QY	601	GGGAAATTCGTCGCTCGGCGCTCAGGCGCAGGGCTCGCACACCATCTCTTCTCAAAAT	660
Db	601	GGGAAATTCGTCGCTCGGCGCTCAGGCGCAGGGCTCGCACACCATCTCTTCTCAAAAT	660
QY	661	AGCCCTCTTTCGCGCACAGCTGAGAAAGCTAAAGAAATGCAACCCCTCTCTCATTTGTC	720
Db	661	AGCCCTCTTTCGCGCACAGCTGAGAAAGCTAAAGAAATGCAACCCCTCTCTCATTTGTC	720
QY	721	TTTCAGAGCCCTCGCCCAACCCCGCAACCTCCGATGAGTTTCTTGCGGTCTCTTT	780
Db	721	TTTCAGAGCCCTCGCCCAACCCCGCAACCTCCGATGAGTTTCTTGCGGTCTCTTT	780
QY	781	ATTCTGGGTAGGAGACGGGAGTCCGTTCTCTTTGTTCTGTGCAATAATTAAGAAAG	840
Db	781	ATTCTGGGTAGGAGACGGGAGTCCGTTCTCTTTGTTCTGTGCAATAATTAAGAAAG	840
QY	841	CTCGGTAAAGCATCTCAATAAATTCAGCTGAGCTAAATTTTCAGTATGTACTTAAGGA	900
Db	841	CTCGGTAAAGCATCTCAATAAATTCAGCTGAGCTAAATTTTCAGTATGTACTTAAGGA	900
QY	901	AGGAGGTGAGTGAAGTTTCAACCCCATGTCTGTGTAAACCGGAGTCAAGGCCAGGCTGGC	960
Db	901	AGGAGGTGAGTGAAGTTTCAACCCCATGTCTGTGTAAACCGGAGTCAAGGCCAGGCTGGC	960
QY	961	AGAGTCMGTCCTTGAAGTACTGAGGTGGGCAATTCGCTTTTGTGAAGCCCTCCAGTGTG	1020
Db	961	AGAGTCMGTCCTTGAAGTACTGAGGTGGGCAATTCGCTTTTGTGAAGCCCTCCAGTGTG	1020
QY	1021	CATTCCATCCCTGATGGGGGCAATAGTTTGAAGTGCAGAGTGAAGTACGTTTCTTAG	1080
Db	1021	CATTCCATCCCTGATGGGGGCAATAGTTTGAAGTGCAGAGTGAAGTACGTTTCTTAG	1080
QY	1081	GGCTGGAGGGGCAAGTTTCCCACTAAAGGCTCCCTGCTTACATTTAAACTTCATGCTCTT	1140
Db	1081	GGCTGGAGGGGCAAGTTTCCCACTAAAGGCTCCCTGCTTACATTTAAACTTCATGCTCTT	1140



QY 259 AATGGGCTCTTAAAGCATCGCGCAACTTTTGGAGATGTTCTGCTTCAGGCTTTC 318  
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 Db 1695 AATGGGCTCTTAAAGCATCGCGCAACTTTTGGAGATGTTCTGCTTCAGGCTTTC 1636  
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 QY 319 GGTGCAATTCAGTGTACCAAGTGTGAAGAAATTCAGCTTAACAAGACTGCTCTCC 378  
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 Db 1635 GGTGCAATTCAGTGTACCAAGTGTGAAGAAATTCAGCTTAACAAGACTGCTCTCC 1576  
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 QY 379 CGAGTTCATTTGTAATTCAGAGTGAAGCTTCAAGACATGTGTCAAGAAATGTATGA 438  
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 QY 439 GCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTATCG 498  
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 QY 499 CTCTGCGGGGTACAGTCTTCTGCTCCCGAGGAAATGAACTCATGTTGCTACGCTG 558  
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 Db 1455 CTCTGCGGGGTACAGTCTTCTGCTCCCGAGGAAATGAACTCATGTTGCTACGCTG 1396  
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 QY 559 CTGCAACACCCCTCTTGTAAACGGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGG 618  
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 Db 1395 CTGCAACACCCCTCTTGTAAACGGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGG 1336  
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 QY 619 CCTCAGGCGAGGGCTCCGACACCACTCTTCTTCAAAATTAAGCCCTCTTCTCGGACA 678  
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 Db 1335 CCTCAGGCGAGGGCTCCGACACCACTCTTCTTCAAAATTAAGCCCTCTTCTCGGACA 1277  
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 Db 1276 CTGCTAGAGTGAAGAGATGCCACCCCTCTGATGTTCTTCTTCCAGGCTCTGCGGCA 1217  
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 QY 739 ACCCCACCTCTCTAGTGAAGTCTTCTGCTCTTAAATTCGTGGAAGGAGCGG 798  
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 Db 1216 ACCCCACCTCTCTAGTGAAGTCTTCTGCTCTTAAATTCGTGGAAGGAGCGG 1157  
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 QY 919 TCACCCCATGCTGTGTAAACCGGAGTCAAGGCGAGGCTGCGAGAGTCTTGAAG 978  
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 Db 1036 TCACCCCATGCTGTGTAAACCGGAGTCAAGGCGAGGCTGCGAGAGTCTTGAAG 977  
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 QY 979 TCACGAGGTGGGATCTGCTTTTGTAAAGCTCAGTGCATTTCCATCCCTATGG 1038  
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 Db 976 TCACGAGGTGGGATCTGCTTTTGTAAAGCTCAGTGCATTTCCATCCCTATGG 917  
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 Db 676 TTGCAAGAGACTGGGCGGAGAGCAAGGCGCTGCAAAAGGCGGCTGT 617  
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Db 616 CGGTGGTGAAGTGCAGATTAAGCGAGCGCTTCTGCTGTTGGCTGTGACAGCACA 557  
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 QY 1399 GCGGCGAGCAGACACCTTGACAGAACACCGCGGAAGTGTGCGAGAGACCGGTGACA 1458  
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 Db 556 GCGGCGAGCAGACACCTTGACAGAACACCGCGGAAGTGTGCGAGAGACCGGTGACA 497  
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 Db 496 GAGGCGGTTGATGACCGAGTGTGAGTGAAGAAACGTCTCGAGAAAGGAGAGATCA 437  
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 QY 1519 TGTAGCCCGGAAGTGAAGACCTGCTCAAGTGTGCTTGGGTTGGCCGACCATGATCC 1578  
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 Db 436 TGTAGCCCGGAAGTGAAGACCTGCTCAAGTGTGCTTGGGTTGGCCGACCATGATCC 377  
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 QY 1579 TCCGAATCTGTTGGGATCCAGATACAGGCGCAATGTCAACAATCAGCCCTGGGACA 1638  
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 Db 376 TCCGAATCTGTTGGGATCCAGATACAGGCGCAATGTCAACAATCAGCCCTGGGACA 317  
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 QY 1639 CACGAGCAGAGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1698  
 |||||  
 Db 316 CACGAGCAGAGGAG 257  
 |||||  
 QY 1699 TAAACCATTAATTAATTAAGCCCTCTGCTGCTTACTGAGGCGCAATGGTACCA 1758  
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 Db 256 TAAACCATTAATTAATTAAGCCCTCTGCTGCTTACTGAGGCGCAATGGTACCA 197  
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 QY 1759 TTTTTCAGTGTGACCTTGACAGCTTCTTTTGCACAAGAGAGAGATTTAACACTGT 1818  
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 Db 196 TTTTTCAGTGTGACCTTGACAGCTTCTTTTGCACAAGAGAGAGATTTAACACTGT 137  
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 QY 1819 TTCAACCCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGA 1878  
 |||||  
 Db 136 TTCAACCCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTAGACAGTGA 77  
 |||||  
 RESULT 4  
 AAF64188/c  
 ID AAF64188 standard; cDNA; 1956 BP.  
 XX  
 AC AAF64188;  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human secreted protein gene I3 SRQ ID NO:23.  
 XX  
 KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
 KW nootropic; neuroprotective; antibacterial; virucide; fungicide;  
 KW ophthalmological; vulnary; autoimmune disease; cardiovascular disorder;  
 KW hyperproliferative disorders; cerebrovascular disorder; wound healing;  
 KW nervous system disorder; ocular disorder; skin aging; chemotaxis;  
 KW food additive; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200077026-A1.  
 PN  
 PD 21-DEC-2000.  
 PD  
 XX 01-JUN-2000; 2000WO-US14973.  
 PF  
 PR 11-JUN-1999; 99US-0138630.  
 PR  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 PA  
 PI Rosen CA, Ruben SM, Komatsoulis GA;  
 PI  
 XX WPI: 2001-071258/08.  
 DR P-PSDB; AAB75518.  
 DR  
 XX Nucleic acid molecules encoding human secreted proteins, used in  
 PT

PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
 PT Parkinson's diseases and cancers -  
 PS Claim 1, Page 443-444, 542pp; English.

XX Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide  
 CC sequences AAF64176 - AAF64224. The specification includes amino acid  
 CC sequences AAB75555 - AAB75606 which represent fragments of the human  
 CC secreted proteins, and protein sequences with which they share homology.  
 CC The proteins and polynucleotides, their agonists and antagonists have  
 CC activities dependent on the tissues and cells in which they are  
 CC expressed, examples of these activities include; immunosuppressive;  
 CC antirheumatic; antirheumatic; antiproliferative; cyostatic; cardiac;  
 CC vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;  
 CC virucide; fungicide; ophtalmological; and vulnerary. The proteins,  
 CC polynucleotides, agonists and antagonists can be used to treat or detect  
 CC or diagnose various diseases and disorders including; autoimmune  
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders  
 CC e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angioneuosis, nervous system disorders e.g. Alzheimer's disease,  
 CC infections caused by bacteria, viruses and fungi and ocular disorders  
 CC e.g. corneal infection. The polypeptides can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin ageing due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities. Included in the invention are  
 CC polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which  
 CC are used in the isolation, identification and characterisation of the  
 CC proteins of the invention.

SO Sequence 1956 BP: 430 A: 543 C: 524 G: 456 T: 3 other:

Query Match 83.6%; Score 1586; DB 22; Length 1956;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1856; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 19 GGTGCTCGCCCGGAGGCGGAGGAGAGACCCGCGGAGCCGGAACG 78  
 DB 1935 GGTGCTCGCCCGGAGGCGGAGGAGAGACCCGCGGAGCCGGAACG 1876  
 QY 79 CGGGGAGTCAAGGCTCCGAGACGCGACCTGGGCTCTCTAAAGCTACGACGCTGTC 138  
 DB 1875 GGGGGAGTCAAGGCTCCGAGACGCGACCTGGGCTCTCTAAAGCTACGACGCTGTC 1816  
 QY 139 CGGGGAGTCAAGGCTCCGAGACGCGACCTGGGCTCTCTAAAGCTACGACGCTGTC 198  
 DB 1815 CGGGGAGTCAAGGCTCCGAGACGCGACCTGGGCTCTCTAAAGCTACGACGCTGTC 1756  
 QY 199 CTCGGCTGTGCGCTCTCTGATGCGGCTTCCCTCCGCGCCCGGAGCTCGGAG 258  
 DB 1755 CTCGGCTGTGCGCTCTCTGATGCGGCTTCCCTCCGCGCCCGGAGCTCGGAG 1696  
 QY 259 AATGTGGTCTAGAGCANTCGGCAACTTTTGGGATTTGTTCTTCCAGGCTTTGC 318  
 DB 1695 AATGTGGTCTAGAGCANTCGGCAACTTTTGGGATTTGTTCTTCCAGGCTTTGC 1636  
 QY 319 GGTGCAATTCAGTGTACCACTGTGAAGAAATTCAGCTGAACAGCATGCTCTCC 378  
 DB 1635 GGTGCAATTCAGTGTACCACTGTGAAGAAATTCAGCTGAACAGCATGCTCTCC 1576  
 QY 379 CGAGTTCATTGTAATTCAGGTAAGCTTCAAGACATGTGTCAAGAAAGAGATGATGA 438  
 DB 1575 CGAGTTCATTGTAATTCAGGTAAGCTTCAAGACATGTGTCAAGAAAGAGATGATGA 1516  
 QY 439 GCAAAAGTCCGGGAGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCG 498  
 DB 1515 GCAAAAGTCCGGGAGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCG 1456  
 QY 499 CTCGCGGGGTACCACTCTTCTGCTCCCGAGGAAAGCACTGATGATCAGGTC 558  
 DB 1455 CTCGCGGGGTACCACTCTTCTGCTCCCGAGGAAAGCACTGATGATCAGGTC 1396

QY 559 CTGCAACACCCCTCTTGTGTAAGCGGCGCCAGGCCCAAGAAAGGAGTGTGCTCGGC 618  
 DB 1395 CTGCAACACCCCTCTTGTGTAAGCGGCGCCAGGCCCAAGAAAGGAGTGTGCTCGGC 1336  
 QY 619 CCGACGCGGAGGCTCCGACACACATCTGTGCTCAAAATTAAGCCCTTCTCGGACA 678  
 DB 1335 CCGACGCGGAGGCTCCGACACACATCTGTGCTCAAAATTAAGCCCTTCTCGGACA 1277  
 QY 679 CTGCTAAGCTGAAGAGATGCCACCCCTCTGCACTTGTCTTCCAGGCTCGCCCA 738  
 DB 1276 CTGCTAAGCTGAAGAGATGCCACCCCTCTGCACTTGTCTTCCAGGCTCGCCCA 1217  
 QY 739 ACCCGCACCTCCCTGAGAGATGTTCTTGTGGGTGCTTTTATCTGGGTAGGAGCG 798  
 DB 1216 ACCCGCACCTCCCTGAGAGATGTTCTTGTGGGTGCTTTTATCTGGGTAGGAGCG 1157  
 QY 799 GAGTCGGTCTCTTGTGCTGCAATTAAGAGCTCGGTAAAGCATTTCTGA 858  
 DB 1156 GAGTCGGTCTCTTGTGCTGCAATTAAGAGCTCGGTAAAGCATTTCTGA 1097  
 QY 859 ATAAATTCACCTGAGTGAATTTCAATGTAAGAGAGAGAGTGAAGT 918  
 DB 1096 ATAAATTCACCTGAGTGAATTTCAATGTAAGAGAGAGTGAAGT 1037  
 QY 919 TCACCCCATGCTGTGTAACCGAGTCAAGGCGAGCTGCGAGTCTGCTTAAGA 978  
 DB 1036 TCACCCCATGCTGTGTAACCGAGTCAAGGCGAGCTGCGAGTCTGCTTAAGA 977  
 QY 979 TCACGAGTGGGCAATCTGCTTTTGAAGCTCCAGTCTCATTCCTGATGG 1038  
 DB 976 TCACGAGTGGGCAATCTGCTTTTGAAGCTCCAGTCTCATTCCTGATGG 917  
 QY 1039 GGCATATTTGAGACGTGACAGAGTGAAGTGAAGTCTTGAAGGCTGAGGCGCAATTCC 1098  
 DB 916 GGCATATTTGAGACGTGACAGAGTGAAGTGAAGTCTTGAAGGCTGAGGCGCAATTCC 857  
 QY 1099 CACTCAAGGCTCCCTGCTTGTGATTCAAACTTCATGCTCTGAAACATTTCTGCA 1158  
 DB 856 CACTCAAGGCTCCCTGCTTGTGATTCAAACTTCATGCTCTGAAACATTTCTGCA 797  
 QY 1159 CAGAAATGCTGTTTGGCGCTGAGTGGGCTTGTGATGCTGAGACATCAATGATGG 1218  
 DB 796 CAGAAATGCTGTTTGGCGCTGAGTGGGCTTGTGATGCTGAGACATCAATGATGG 737  
 QY 1219 ACTTAGACTGGGCTCGGCTCTGCTGAAAGTGTAAAGAAATCTTCTCAGTTCTCC 1278  
 DB 736 ACTTAGACTGGGCTCGGCTCTGCTGAAAGTGTAAAGAAATCTTCTCAGTTCTCC 677  
 QY 1279 TTGCAAGAGACTGGCGCCGAGAGCGCAAGAGCAACGGGCTGCAACAGGGGCTGT 1338  
 DB 676 TTGCAAGAGACTGGCGCCGAGAGCGCAAGAGCAACGGGCTGCAACAGGGGCTGT 617  
 QY 1339 CGGTGTGAGTGTGCGATGTACGCGGAGGCGCTTCTGCTTGGGCTGTGAGGAGCA 1398  
 DB 616 CGGTGTGAGTGTGCGATGTACGCGGAGGCGCTTCTGCTTGGGCTGTGAGGAGCA 557  
 QY 1399 GCGCGAGCAGCAGCAGCTGCAAGCAACCCGCAAACTCTCGAGAGCACCTGTACA 1458  
 DB 556 GCGCGAGCAGCAGCAGCTGCAAGCAACCCGCAAACTCTCGAGAGCACCTGTACA 497  
 QY 1459 GGAGCGGTTGATACCGAGCTGAGGTAGAAAACGTCCTCGAAGAGGAGAGATCA 1518  
 DB 496 GGAGCGGTTGATACCGAGCTGAGGTAGAAAACGTCCTCGAAGAGGAGAGATCA 437  
 QY 1519 TGTACGCGCGGAATGAGAGCTGTCAGTGTGCTTGGGTTGGCGGAGCATGTC 1578  
 DB 436 TGTACGCGCGGAATGAGAGCTGTCAGTGTGCTTGGGTTGGCGGAGCATGTC 377  
 QY 1579 TCCGAATCTGTTGGGATCCAGCATACGAGCAATGTACAAACATCAGCCTTGCGAGA 1638  
 DB 376 TCCGAATCTGTTGGGATCCAGCATACGAGCAATGTACAAACATCAGCCTTGCGAGA 317

QY 1639 CACGACGAGGAGGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATGAA 1698  
 DB 316 CACGACGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATGAA 257  
 QY 1699 TAAACCATTAATATTTATTTGCCCCCTCTGTTCTGTCTACTGGCCAGGAATGTAACCA 1758  
 DB 256 TAAACCATTAATATTTATTTAGCCCCCTCTGTTCTGTCTACTGGCCAGGAATGTAACCA 197  
 QY 1759 TTTTTCAGTGTGAGCTTGACACTTCTTTTGGCACAGCAGAGAGAAATTAACCTGT 1818  
 DB 196 TTTTTCAGTGTGAGCTTGACACTTCTTTTGGCACAGCAGAGAGAAATTAACCTGT 137  
 QY 1819 TTTAAACCCGCGGAGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAGACAGTGA 1878  
 DB 136 TTTAAACCCGCGGAGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAGACAGTGA 77  
 RESULT 5  
 ABR33543  
 ID ABR33543 standard; cDNA; 1524 BP.  
 AC ABR33543;  
 XX 08-MAY-2002 (first entry)  
 DE CDNA encoding human PRO protein, Seq ID No 15.  
 XX  
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha; gene; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200208288-A2.  
 PD 31-JAN-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-US21066.  
 XX  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220585P.  
 PR 25-JUL-2000; 2000US-220605P.  
 PR 25-JUL-2000; 2000US-220607P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220638P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 26-JUL-2000; 2000US-220893P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-253646P.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001WO-US17092.  
 XX  
 PA (GENE) GENENTECH INC.  
 PI Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WL;  
 PI WPI; 2002-172001/22.  
 DR P-PSDB; AAU83599.  
 XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumours  
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal

PT tumour or liver tumour -  
 XX  
 PS Claim 2; Figure 15; 359pp; English.  
 XX  
 CC The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. ABR33543-ABR33567 represent human  
 CC PRO protein coding sequences of the invention.  
 CC  
 SQ Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;  
 Query Match 75.0%; Score 1422; DB 24; Length 1524;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 140 GCGGACGAGCGCGGCGCCGACAGCCTGCGGACGACGCGGTGACGCGGCGAGCC 199  
 DB 1 GCGGACGAGCGCGGCGCCGACAGCCTGCGGACGACGCGGTGACGCGGCGAGCC 60  
 QY 200 TCCGCTGCTGCGCTCCTCTGATGCGCTTGCCTCCGCGCGCGGACTCGGGAGA 259  
 DB 61 TCCGCTGCTGCGCTCCTCTGATGCGCTTGCCTCCGCGCGCGGACTCGGGAGA 120  
 QY 260 ATGTGGGTCTAGGACATGCGGCACTTTTGGGATGTTCTTCCAGGCTTGGC 319  
 DB 121 ATGTGGGTCTAGGACATGCGGCACTTTTGGGATGTTCTTCCAGGCTTGGC 180  
 QY 320 CTGCAATCCAGTCTGACAGTGTGAAGAAATTCAGTGAACAAGACTCTCTCCCC 379  
 DB 181 CTGCAATCCAGTCTGACAGTGTGAAGAAATTCAGTGAACAAGACTCTCTCCCC 240  
 QY 380 GAGTTCATTGTAATTCAGAGTGTGAAGAAATTCAGTGAACAAGACTCTCTCCCC 439  
 DB 241 GAGTTCATTGTAATTCAGAGTGTGAAGAAATTCAGTGAACAAGACTCTCTCCCC 300  
 QY 440 CAAAGTCCGCGGATCATGATCCGCAAGTCTGTGCATCATCAGGCGCTGTCTATGCC 499  
 DB 301 CAAAGTCCGCGGATCATGATCCGCAAGTCTGTGCATCATCAGGCGCTGTCTATGCC 360  
 QY 500 TCTGCGGAGTACGAGTCTCTGCTCCGCGGAGAAATGTAATTCAGTGAACAAGACTCTCT 559  
 DB 361 TCTGCGGAGTACGAGTCTCTGCTCCGCGGAGAAATGTAATTCAGTGAACAAGACTCTCT 420  
 QY 560 TGCAACACCCCTTTTGAACGGGCGCAAGGCCCAAGAAAGGGAAAGTTTGTCTCGGCG 619  
 DB 421 TGCAACACCCCTTTTGAACGGGCGCAAGGCCCAAGAAAGGGAAAGTTTGTCTCGGCG 480  
 QY 620 CTCAGGCGAGGCGTCCGACACCATCTCTTCTCAATTAAGCCCTCTTCTGCGGACAC 679  
 DB 481 CTCAGGCGAGGCGTCCGACACCATCTCTTCTCAATTAAGCCCTCTTCTGCGGACAC 540  
 QY 680 TGCTGAAGCTGAAGGAATGCAACCCCTCTGATGTTCTTCCAGGCGCTCGCCGCCA 739  
 DB 541 TGCTGAAGCTGAAGGAATGCAACCCCTCTGATGTTCTTCCAGGCGCTCGCCGCCA 600  
 QY 740 CCCCCACCTCCCTGAGTGAAGTTCTTCTGAGTGTCTTTATTCAGGAGGAGCGGG 799  
 DB 601 CCCCCACCTCCCTGAGTGAAGTTCTTCTGAGTGTCTTTATTCAGGAGGAGCGGG 660  
 QY 800 AGTCCGTTCTCTTTGTTCTCTGCAATTAAGAAAGCTCGGTAAGCAATTCGAA 859  
 DB 660 AGTCCGTTCTCTTTGTTCTCTGCAATTAAGAAAGCTCGGTAAGCAATTCGAA 859



Db	661	AGTCCGTTCTCTTTTGTGTCCTGCGCAAAATPATGAAAGAGCTCGGTAAAGCAATTTCGA	720
Qy	860	TAAATTCAGCTYACACGAAATTTTCAGTATGTACTTGAAGGAAGAGGTGGAGTGAAGTT	919
Db	721	TAAATTCAGCTYACACGAAATTTTCAGTATGTACTTGAAGGAAGAGGTGGAGTGAAGTT	780
Qy	920	CACCCCATCTCTGTATTAACCCGAGACAAGGGCAGGAGTGGCAGAGTGCCTTAGAAGT	979
Db	781	CACCCCATCTCTGTATTAACCCGAGACAAGGGCAGGAGTGGCAGAGTGCCTTAGAAGT	840
Qy	980	CACGTAGGTGGGCATCTGCCCTTTTGTAAAGCCTCCAGTGTCCATTCCATCCCTGATGGG	1039
Db	841	CACGTAGGTGGGCATCTGCCCTTTTGTAAAGCCTCCAGTGTCCATTCCATCCCTGATGGG	900
Qy	1040	GCATAGTTTGAAGCTGAGAGTGAAGTGAAGTCTTTTCTTAGGGCTGGAAGGCCAGTTGCC	1099
Db	901	GCATAGTTTGAAGCTGAGAGTGAAGTGAAGTCTTTTCTTAGGGCTGGAAGGCCAGTTGCC	960
Qy	1100	ACTCMAAGGCTCCCTCGCTGTGACATTCMAAATTCATGCTCTGTGAACCATTCTCTGCAGC	1159
Db	961	ACTCMAAGGCTCCCTCGCTGTGACATTCMAAATTCATGCTCTGTGAACCATTCTCTGCAGC	1020
Qy	1160	AGAAATGGCTGTGTTTGCCGCTGAGTTGGGGCTCTAGTGCACGACACATGTACTGGGA	1219
Db	1021	AGAAATGGCTGTGTTTGCCGCTGAGTTGGGGCTCTAGTGCACGACACATGTACTGGGA	1080
Qy	1220	CTTAGACTGGGGCTCGGCTCTCGCTGTGAAGATGCTTAAAGAAATCTTCTCAGTTCTCT	1279
Db	1081	CTTAGACTGGGGCTCGGCTCTCGCTGTGAAGATGCTTAAAGAAATCTTCTCAGTTCTCT	1140
Qy	1280	TGCAAGAGACTGTGCGCCGGGACGCGAAGGAACAAAGGGGCTGCACAAAGGGGGCTGTGC	1339
Db	1141	TGCAAGAGACTGTGCGCCGGGACGCGAAGGAACAAAGGGGCTGTGCACAAAGGGGGCTGTGC	1200
Qy	1340	GGTGGTGGAGTGCACATGTACGGCGAGGGCTTCTGTGTGGTTGGCGTCTCAGCAGACAG	1399
Db	1201	GGTGGTGGAGTGCACATGTACGGCGAGGGCTTCTGTGTGGTTGGCGTCTCAGCAGACAG	1260
Qy	1400	GGCGACGACACAGCACTGTGCACAAACACCCGGGAAATGCTCTCGAGACACCCGTGTACAG	1459
Db	1261	GGCGACGACACAGCACTGTGCACAAACACCCGGGAAATGCTCTCGAGACACCCGTGTACAG	1320
Qy	1460	GAGCGGGTGTGATGCACGAGCTGAGGTGAAGAAAAAGCTCTCCGAGAAGGGAGAGAGATCAT	1519
Db	1321	GAGCGGGTGTGATGCACGAGCTGAGGTGAAGAAAAAGCTCTCCGAGAAGGGAGAGAGATCAT	1380
Qy	1520	GTAAGCCCGGAAGTGAAGCACTCGTCCAGTCTGTCTTGGCTTTGGCCGACAGCATGATCTCT	1579
Db	1381	GTAAGCCCGGAAGTGAAGCACTCGTCCAGTCTGTCTTGGCTTTGGCCGACAGCATGATCTCT	1440
Qy	1580	CCGAATCTGTTTGGGCAATCCAGCATACGGGCAATGTCAACAACATCAGCCCTGGGCAAC	1639
Db	1441	CCGAATCTGTTTGGGCAATCCAGCATACGGGCAATGTCAACAACATCAGCCCTGGGCAAC	1500
Qy	1640	ACGAGCAGAGGAGAGACAGAGA 1663	
Db	1501	ACGAGCAGAGGAGAGACAGAGA 1524	
RESULT 6			
ABT03277			
ID	ABT03277	standard; cdNA; 1619 BP.	
AC	ABT03277;		
XX	05-SEP-2002	(first entry)	
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.		
XX	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;:		
KM	cytostatic; gene: ss.		
XX			
OS	Homo sapiens.		

PX	
PN	WO200239885-A2.
XX	
PD	23-MAY-2002.
XX	
PE	13-NOV-2001; 2001WO-US45395.
XX	
PR	14-NOV-2000; 2000US-0713550.
PR	03-APR-2001; 2001US-0825294.
PR	02-OCT-2001; 2001US-0970966.
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesn DA;
DR	WPI; 2002-500186/53.
XX	
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for
PT	detecting the presence of ovarian cancer in a patient, and in
PT	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT	-
XX	
XS	Claim 2; Page 189-190; 197pp; English.
XX	
CC	The present invention provides human ovarian cancer associated proteins
CC	and coding sequences. The sequences can be used in the diagnosis and
CC	treatment of ovarian cancers. The present sequence is a coding sequence
CC	of the invention.
XX	
SQ	Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match	73.6%	Score 1396	DB 24	Length 1619
Best Local Similarity	99.8%	Pred. No. 0	Mismatches 2	Indels 1
Matches 1616	Conservative	0		Gaps
QY 280	GGCACTTTTTCGGGATTTGTTCTTCTTCACAGGCTTTTGCGGTGCAAAATCCAGTGTACCA	339		
DB 1	GGCACTTTTTCGGGATTTGTTCTTCTTCACAGGCTTTTGCGGTGCAAAATCCAGTGTACCA	60		
QY 340	GGTGAAGAAATTCACAGCTGCAACAGAGCTGCTCCGCCGAGTTCATTGTGAATTTGCAC	399		
DB 61	GGTGAAGAAATTCACAGCTGCAACAGAGCTGCTCCGCCGAGTTCATTGTGAATTTGCAC	120		
QY 400	GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGACAAAGTCCGGATCATGTGA	459		
DB 121	GGTGAACGTTCAAGACATGTGTGAGAAAGATGATGAGACAAAGTCCGGATCATGTGA	180		
QY 460	CGGCAAGTCTGTGCACTCATCAGCGGCTGTGTATCATCGGCTGTGCGGGTACAGTCTT	519		
DB 181	CGGCAAGTCTGTGCACTCATCAGCGGCTGTGTATCATCGGCTGTGCGGGTACAGTCTT	240		
QY 520	CTGCTCTCCAGGAAATCTAGTCTGATCTGATCTGTCACACCCCTCTTTGTGA	579		
DB 241	CTGCTCTCCAGGAAATCTAGTCTGATCTGATCTGTCACACCCCTCTTTGTGA	300		
QY 580	CGGGCCAAAGGCCAAGAAAAGGGAAGTTCTGCTCTGCGGCTCAGGCCAGGGCTCCGCAC	639		
DB 301	CGGGCCAAAGGCCAAGAAAAGGGAAGTTCTGCTCTGCGGCTCAGGCCAGGGCTCCGCAC	360		
QY 640	CACCATCTGTTCTCTCAATTAGCCCTCTTCTTGCGCACACTGTGAAAGCTGAAGGAGAG	699		
DB 361	CACCATCTGTTCTCTCAATTAGCCCTCTTCTTGCGCACACTGTGAAAGCTGAAGGAGAG	420		
QY 700	CCACCCCTCTCGCATGTTGTTTCCAGCCCTCGGCCCCCAACCCCACTCCCTCGATGA	759		
DB 421	CCACCCCTCTCGCATGTTGTTTCCAGCCCTCGGCCCCCAACCCCACTCCCTCGATGA	480		
QY 760	GTTTCTTCTGGGTGTCCTTTTATTCTTGCGGTAGGAGCGGAGTCCGTCTTTTGT	819		
DB 481	GTTTCTTCTGGGTGTCCTTTTATTCTTGCGGTAGGAGCGGAGTCCGTCTTTTGT	540		
QY 820	CGGTGCAATATGAAGAGCTCGGTAAGCAATTCGAAATAAATCAGCTACTGAAT	879		



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Db 541 CTTGTGCAATAATGAAAGAGCTCGGTAAAGCATTCCTGATAATTAATTCAGCCCTGATGAAT 600
Qy 880 TTTCAGTATGTTACTTGAAGAGAGAGGTGGAGTGAAGTTCCACCCCAATGCTGTGTAAAC 939
Db 601 TTTCAGTATGTTACTTGAAGAGAGAGGTGGAGTGAAGTTCCACCCCAATGCTGTGTAAAC 660
Qy 940 CGAGTCAAGGCGGAGCTGGCAGAGTCTGCTTGAAGTCACTGAGTGGGATGTGCC 999
Db 661 CGAGTCAAGGCGGAGCTGGCAGAGTCTGCTTGAAGTCACTGAGTGGGATGTGCC 720
Qy 1000 TTTTGTAAAGCCCTCCAGTGTCCATTCCTCATTCCTGATGGGGCATAGTTTGAAGTGCAGA 1059
Db 721 TTTTGTAAAGCCCTCCAGTGTCCATTCCTCATTCCTGATGGGGCATAGTTTGAAGTGCAGA 780
Qy 1060 GTGAGAGTGCAGTTTCTTGAAGGCTGGAGGGCCAGTTCCCACTCAAGGGCTCCCTGCTTG 1119
Db 781 GTGAGAGTGCAGTTTCTTGAAGGCTGGAGGGCCAGTTCCCACTCAAGGGCTCCCTGCTTG 840
Qy 1120 ACATTCAAACTTCATGCTCTCTGAAAACATTCCTGACAGCAGAAATGGCTGGTTGCGGC 1179
Db 841 ACATTCAAACTTCATGCTCTCTGAAAACATTCCTGACAGCAGAAATGGCTGGTTGCGGC 900
Qy 1180 CTGAGTTGGGCTCTAGTACTGAGACATCAATGACTGGGACTTAACTGGGCTGGGCT 1239
Db 901 CTGAGTTGGGCTCTAGTACTGAGACATCAATGACTGGGACTTAACTGGGCTGGGCT 960
Qy 1240 CGCTGTGAAAAGTGTCTTGAAGAAATCTCTCAGTTCTCTCTGACAGAGACCTGGCGCGG 1299
Db 961 CGCTGTGAAAAGTGTCTTGAAGAAATCTCTCAGTTCTCTCTGACAGAGACCTGGCGCGG 1020
Qy 1300 AGCGGAAGGCAAGGCGGCTGCAACAAGCGGCGCTGCTGCTGTGAGTGCAGATGA 1359
Db 1021 AGCGGAAGGCAAGGCGGCTGCAACAAGCGGCGCTGCTGCTGTGAGTGCAGATGA 1080
Qy 1360 CCGCGAGGCGCTTCTCTGCTGTGGGCTGTGCGAGCAGCAGGCGGAGCAGACACACC-TGC 1418
Db 1081 CCGCGAGGCGCTTCTCTGCTGTGGGCTGTGCGAGCAGCAGGCGGAGCAGACACACC-TTGC 1140
Qy 1419 AGCAACACCCCGCGGAAGTGTCTGCGAGCAGCAGCAGTGTACAGAGCGGGTGTGATGACCGAG 1478
Db 1141 AGCAACACCCCGCGGAAGTGTCTGCGAGCAGCAGCAGTGTACAGAGCGGGTGTGATGACCGAG 1200
Qy 1479 CTGAGGTAGAAAAGTGTCCGGAAGGAGAGAGATCATGTACGCCCGGGAAGTAGAGAC 1538
Db 1201 CTGAGGTAGAAAAGTGTCCGGAAGGAGAGAGATCATGTACGCCCGGGAAGTAGAGAC 1260
Qy 1539 CTGCTCAGTGTGCTGTGGGCTTGGCCGAGCCATGATCTCCGAATCTGGTTGGGCATC 1598
Db 1261 CTGCTCAGTGTGCTGTGGGCTTGGCCGAGCCATGATCTCCGAATCTGGTTGGGCATC 1320
Qy 1599 CAGCATACGGCCCATATGTACAAACATCAGCCCTGGGAGACAGCAGAGAGAGAGAGAC 1658
Db 1321 CAGCATACGGCCCATATGTACAAACATCAGCCCTGGGAGACAGCAGAGAGAGAGAGAC 1380
Qy 1659 AGAGAAAAGAAAACAGACATGAGACACAGTAATTAATTAATTAATTAATTTAG 1718
Db 1381 AGAGAAAAGAAAACAGACATGAGACACAGTAATTAATTAATTAATTAATTTAG 1440
Qy 1719 CCCCTCTGTTCTGTGCTTACTGAGCCAGGAAATGTATCCAAATTTTCACTGTGTGACCTTGA 1778
Db 1441 CCCCTCTGTTCTGTGCTTACTGAGCCAGGAAATGTATCCAAATTTTCACTGTGTGACCTTGA 1500
Qy 1779 CAGCTTCTTTTGGCCAGCAGAGAGAGAAATTTAACACTGTTTCAAAACCCCGGGGAGTTGG 1838
Db 1501 CAGCTTCTTTTGGCCAGCAGAGAGAGAAATTTAACACTGTTTCAAAACCCCGGGGAGTTGG 1560
Qy 1839 CTGTGTTAAAGAAAGACCATTAATGCTTTTGAAGAGTGTAAATTAATTAATTAATTAATTAAT 1897
Db 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTTGAAGAGTGTAAATTAATTAATTAATTAATTAAT 1619
```

RESULT 7  
ABT03281

```
ID ABT03281 standard: cDNA: 1619 BP.
XX
AC ABT03281;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX cytosolic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
PR 03-APR-2001; 2001US-0825294.
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;
XX
DR WPI: 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
PS
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention.
SQ
Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;
Query Match 73.6%; Score 1396; DB 24; Length 1619;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 280 GGCACATTTTGGCGATTGTTCTTGTCCAGGCTTGGCTGCAATCCAGTGTACCA 339
Db 1 GGCACATTTTGGCGATTGTTCTTGTCCAGGCTTGGCTGCAATCCAGTGTACCA 60
Qy 340 GTGTGAAGAAATTCAGCTGAACAACGACTCTCTCCCGAGTTCATTGTGAATTCAC 399
Db 61 GTGTGAAGAAATTCAGCTGAACAACGACTCTCTCCCGAGTTCATTGTGAATTCAC 120
Qy 400 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGAAGGAGGCGGAGTCAATGTA 459
Db 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGAGTGAAGGAGGCGGAGTCAATGTA 180
Qy 460 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGGCGGGATCAAGTCTT 519
Db 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGGCGGGATCAAGTCTT 240
Qy 520 CTGTCTCCCGAGGGAATGAACTCAGTTTCATCAGCTGTGCGGAGTCAAGTCTTGA 579
Db 241 CTGTCTCCCGAGGGAATGAACTCAGTTTCATCAGCTGTGCGGAGTCAAGTCTTGA 300
Qy 580 CGGGCCAAAGCCCAAGAAAGGGAAGTTCTGCTGGCCCTCAGGCGAGGCTCCGCGAC 639
Db 301 CGGGCCAAAGCCCAAGAAAGGGAAGTTCTGCTGGCCCTCAGGCGAGGCTCCGCGAC 360
Qy 640 CACCATCTTCTTCTCAATTAAGCCTCTTTCGAGACACTGCTGAAGTGAAGAGATG 699
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Db 361 CACATCTCTTCTCTCAATTAGCCCTCTTCGGGACACTGTAAGCTGAAGGATG 420  
 QY 700 CACACCCCTCTGATGTTTCTTCAGCCCTGCCCCAACCCCTCCCTGATGTA 759  
 Db 421 CACACCCCTCTGATGTTTCTTCAGCCCTGCCCCAACCCCTCCCTGATGTA 480  
 QY 760 GTTTCCTCTGGGTCCTTTTATTCGGGTAGGAGGAGTCCGTTTCTTTTGT 819  
 Db 481 GTTTCCTCTGGGTCCTTTTATTCGGGTAGGAGGAGTCCGTTTCTTTTGT 540  
 QY 820 CTTGTCAATTAATGAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGTAAT 879  
 Db 541 CTTGTCAATTAATGAAGAGCTCGTAAAGCATTTCTGAATTAATTCAGCTGTAAT 600  
 QY 880 TTTTCAGTATGTTCTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATCTCTGTGAAC 939  
 Db 601 TTTTCAGTATGTTCTTGAAGAGAGAGTGAAGTGAAGTTCACCCCATCTCTGTGAAC 660  
 QY 940 CGGAGTCAGGCGCAGGCTGGGAGAGTGMGTCTTGAAGTCACTGAGGTGGCATCGCC 999  
 Db 661 CGGAGTCAGGCGCAGGCTGGGAGAGTGMGTCTTGAAGTCACTGAGGTGGCATCGCC 720  
 QY 1000 TTTTGTAAAGCCTCAGTGTCCATTCCTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 1059  
 Db 721 TTTTGTAAAGCCTCAGTGTCCATTCCTCATCCCTGATGGGGCATAGTTTGAAGTGCAGA 780  
 QY 1060 GTGAGAGTGAAGTCTTCTTGAAGGCTGAGGCGCATCCCATCAAGGCTCCCTCGCTTG 1119  
 Db 781 GTGAGAGTGAAGTCTTCTTGAAGGCTGAGGCGCATCCCATCAAGGCTCCCTCGCTTG 840  
 QY 1120 ACATTTCAAACTTCATGCTCTCGAAGAACATTCCTGACAGAGAAATTTGGCTTTCGCG 1179  
 Db 841 ACATTTCAAACTTCATGCTCTCGAAGAACATTCCTGACAGAGAAATTTGGCTTTCGCG 900  
 QY 1180 CTGAGTGGCTCTTGAAGTCTGAGACTCAATGACTGAGACTGAGACTGGGCTCGGCT 1239  
 Db 901 CTGAGTGGCTCTTGAAGTCTGAGACTCAATGACTGAGACTGAGACTGGGCTCGGCT 960  
 QY 1240 CGCTCTGAAGTCTTGAAGAAATCTTCTGAGTCTCTTCTGAGAGAGTGGGCGCGG 1299  
 Db 961 CGCTCTGAAGTCTTGAAGAAATCTTCTGAGTCTCTTCTGAGAGAGTGGGCGCGG 1020  
 QY 1300 ACGGAGAGAGCAGGCGCTGACAAAGCGGCGCTGCTGGTGGTGGATGCGCATGTA 1359  
 Db 1021 ACGGAGAGAGCAGGCGCTGACAAAGCGGCGCTGCTGGTGGTGGATGCGCATGTA 1080  
 QY 1360 CGCGCAGCGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1418  
 Db 1081 CGCGCAGCGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1140  
 QY 1419 ACGAAGACCGCGCGAATGCTGCGAGAGACCGGTGACAGAGCGGGTGTATGACGAG 1478  
 Db 1141 ACGAAGACCGCGCGAATGCTGCGAGAGACCGGTGACAGAGCGGGTGTATGACGAG 1200  
 QY 1479 CTGAGTGAAGAAACGCTCTCGAGAGAGGAGAGATCATGTACGCCGGAAGTAGAC 1538  
 Db 1201 CTGAGTGAAGAAACGCTCTCGAGAGAGGAGAGATCATGTACGCCGGAAGTAGAC 1260  
 QY 1539 CTGCTCCAGTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1598  
 Db 1261 CTGCTCCAGTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1320  
 QY 1599 CAGCATACGCGCAATGTACAAACATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1658  
 Db 1321 CAGCATACGCGCAATGTACAAACATCAGCCCTGGGACAGACAGAGAGAGAGAGAC 1380  
 QY 1659 AG 1718  
 Db 1381 AG 1440  
 QY 1719 CCGCTCTGTTCTGCTTACCTGCGAGAGAAATGTACCAATTTTTCAGTGGTGGACTTGA 1778  
 Db 1441 CCGCTCTGTTCTGCTTACCTGCGAGAGAAATGTACCAATTTTTCAGTGGTGGACTTGA 1500

QY 1779 CAGCTTCTTTTCCACAGAGAGAGATTTAACACTGTTTCAAAACCCGGGGAGTTGG 1838  
 Db 1501 CAGCTTCTTTTCCACAGAGAGAGATTTAACACTGTTTCAAAACCCGGGGAGTTGG 1560  
 QY 1839 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTT 1897  
 Db 1561 CTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGTAAAAAATTTTTTTTTT 1619  
 RESULT 8  
 ABL40345  
 ID ABL40345 standard: cDNA; 1619 BP.  
 AC ABL40345;  
 XX 28-JUN-2002 (first entry)  
 DT  
 DE Ovarian carcinoma sequence isolate 57887 extended cDNA.  
 XX  
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KW SS.  
 XX Homo sapiens.  
 OS  
 PN US2002004491-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PE 03-APR-2001; 2001US-0825294.  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PA (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALGM/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 DR WPI; 2002-171027/22.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 XX prevention and/or treatment of cancer, especially ovarian cancer.  
 PS Claim 1a: Page 119-120; 131pp; English.  
 XX  
 CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the extended cDNA sequence of ovarian carcinoma  
 CC isolate 57887 given in record ABL48956.  
 CC  
 XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;  
 SQ  
 Query Match 73.6%; Score 1396; DB 24; Length 1619;  
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 280 GGCACATTTTGGGATGTTGTTGCTTCCAGGCTTTGGCCTCAATCATGATGCTACCA 339
    |||||
Db 1 GGCACATTTTGGGATGTTGTTGCTTCCAGGCTTTGGCCTCAATCATGATGCTACCA 60
QY 340 GTTGAAGATTTCCAGCTGAACAAGACTGCTTCCCGAGTTTCATTTGTAAATTCAC 399
    |||||
Db 61 GTTGAAGATTTCCAGCTGAACAAGACTGCTTCCCGAGTTTCATTTGTAAATTCAC 120
QY 400 GGTGAAGCTTCAAGACATGTCAGAAAAGAGTGAAGCAAAAGTCCGGGATCATGTA 459
    |||||
Db 121 GGTGAAGCTTCAAGACATGTCAGAAAAGAGTGAAGCAAAAGTCCGGGATCATGTA 180
QY 460 CCGCAAGTCTGTGATCATACAGGCTGTCTCATGCTGCGGGGTACCAAGCTT 519
    |||||
Db 181 CCGCAAGTCTGTGATCATACAGGCTGTCTCATGCTGCGGGGTACCAAGCTT 240
QY 520 CTGCTCCCAAGGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 579
    |||||
Db 241 CTGCTCCCAAGGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 580 CCGGCAAGGCCCCAAGAAAAGGGAGTTCTGCTGCGGCTTCAGGCTCAGGCTCCGAC 639
    |||||
Db 301 CCGGCAAGGCCCCAAGAAAAGGGAGTTCTGCTGCGGCTTCAGGCTCAGGCTCCGAC 360
QY 640 CACCATCTGTTCTCCTCAATTAAGCTCTTCTGCGACACTGTAAGCTGAAGAGATG 699
    |||||
Db 361 CACCATCTGTTCTCCTCAATTAAGCTCTTCTGCGACACTGTAAGCTGAAGAGATG 420
QY 700 CCAACCCCTTCGATGTTGTTTTCACAGCCCTGCCCCAACCCCTCCCTGAGTGA 759
    |||||
Db 421 CCAACCCCTTCGATGTTGTTTTCACAGCCCTGCCCCAACCCCTCCCTGAGTGA 480
QY 760 GTTCTTCTGGGATGCTTTTATTCGGGTAGGAGGCGGAGTCCGTTCTTTGTT 819
    |||||
Db 481 GTTCTTCTGGGATGCTTTTATTCGGGTAGGAGGCGGAGTCCGTTCTTTGTT 540
QY 820 CCTGTCAAAATATGAAGAGCTCGGTAAAGCATTCGTGAATTAATTCAGCTGATGAT 879
    |||||
Db 541 CCTGTCAAAATATGAAGAGCTCGGTAAAGCATTCGTGAATTAATTCAGCTGATGAT 600
QY 880 TTTCAATATGATCTTGAAGAGAGGAGTGAAGTTCACCCCATGCTGTGTATAC 939
    |||||
Db 601 TTTCAATATGATCTTGAAGAGAGGAGTGAAGTTCACCCCATGCTGTGTATAC 660
QY 940 CCGAGTCAAGGCGCAGGCTGCGAGAGTCTGCTTGAAGATCCTGAGGGGATCTGCG 999
    |||||
Db 661 CCGAGTCAAGGCGCAGGCTGCGAGAGTCTGCTTGAAGATCCTGAGGGGATCTGCG 720
QY 1000 TTTTGTAAAGCTCCAGTGTCCATTCATCCGTGATGGGGCATAGTTGAGATGACGA 1059
    |||||
Db 721 TTTTGTAAAGCTCCAGTGTCCATTCATCCGTGATGGGGCATAGTTGAGATGACGA 780
QY 1060 GTGAGAGTACGTTTCTTAAAGGCTGAGAGGCTCCCATCAAGGCTCCCTGCTTG 1119
    |||||
Db 781 GTGAGAGTACGTTTCTTAAAGGCTGAGAGGCTCCCATCAAGGCTCCCTGCTTG 840
QY 1120 ACATTCAAATCTCATGCTCTGAAAACATCTCTGACAGACAAATTTGGTGTTCGGCG 1179
    |||||
Db 841 ACATTCAAATCTCATGCTCTGAAAACATCTCTCTGACAGACAAATTTGGTGTTCGGCG 900
QY 1180 CTGAGTGGGGCTCTAGTGAAGTCAAGTCAATGACTGGGACTTAGACTGGGGCTCGGCT 1239
    |||||
Db 901 CTGAGTGGGGCTCTAGTGAAGTCAAGTCAATGACTGGGACTTAGACTGGGGCTCGGCT 960
QY 1240 CGCTCGAAAAGTGTGAAGAAATCTTCTCAGTTCTCTTCAAGAGACTGCGCGGG 1299
    |||||
Db 961 CGCTCGAAAAGTGTGAAGAAATCTTCTCAGTTCTCTTCAAGAGACTGCGCGGG 1020
QY 1300 ACGCAAGAGCAAGCGGCGCTCACAAGCGGCGCTGCGGTGAGTGGATGCGCATGTA 1359
    |||||
Db 1021 ACGCAAGAGCAAGCGGCGCTCACAAGCGGCGCTGCGGTGAGTGGATGCGCATGTA 1080

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QY 1360 GCGCAGGCGCTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1418
    |||||
Db 1081 GCGCAGGCGCTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1419 ACGAAGACCCCGGCAAACTGCTGCGAGAGACACCGGTACAGAGAGCGGGTATGACCGAG 1478
    |||||
Db 1141 ACGAAGACCCCGGCAAACTGCTGCGAGAGACACCGGTACAGAGAGCGGGTATGACCGAG 1200
QY 1479 CTGAGTGAAGAAAGCTTCCGAGAAAGGAGAGAGATCATGACGCCCGGAAGTAGAGAC 1538
    |||||
Db 1201 CTGAGTGAAGAAAGCTTCCGAGAAAGGAGAGAGATCATGACGCCCGGAAGTAGAGAC 1260
QY 1539 CTGCTTCAGTGTGCTTGGGTTTGGCCGACCATGATCTCCGAAATCTGTTGGCATC 1598
    |||||
Db 1261 CTGCTTCAGTGTGCTTGGGTTTGGCCGACCATGATCTCCGAAATCTGTTGGCATC 1320
QY 1599 CAGCATAGGCGCAATGTCAACAACATCAGCCCTGGGAGAGACAGAGAGAGAGAC 1658
    |||||
Db 1321 CAGCATAGGCGCAATGTCAACAACATCAGCCCTGGGAGAGACAGAGAGAGAGAGAC 1380
QY 1659 AGAGAAAAGAAAACACAGCATGAGACACAGTAATGATTAATTAATTAATTAATTAAT 1718
    |||||
Db 1381 AGAGAAAAGAAAACACAGCATGAGAACACAGTAATGATTAATTAATTAATTAATTAAT 1440
QY 1719 CCCCCTGTTGCTGCTTACGAGGCGCAGAAATGATTAATTTTCACTGTTGACCTTGA 1778
    |||||
Db 1441 CCCCCTGTTGCTGCTTACGAGGCGCAGAAATGATTAATTTTCACTGTTGACCTTGA 1500
QY 1779 CAGCTTCTTTTGCACAAGAGAGAAATTAACACTGTTTCAACCCGGGAGAGTTGG 1838
    |||||
Db 1501 CAGCTTCTTTTGCACAAGAGAGAAATTAACACTGTTTCAACCCGGGAGAGTTGG 1560
QY 1839 CTGCTTAAAGAAAGCATTAATGCTTTAGACAGTCTAATTAATTAATTAATTAATTAAT 1897
    |||||
Db 1561 CTGCTTAAAGAAAGCATTAATGCTTTAGACAGTCTAATTAATTAATTAATTAATTAAT 1619

```

RESULT 9  
 ABL40349  
 ID ABL40349 standard; cDNA; 1619 BP.  
 ABL40349;  
 AC 28-JUN-2002 (first entry)  
 DE Ovarian carcinoma O591S nucleotide sequence.  
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 OS ss.  
 XX Homo sapiens.  
 PN US2002004491-A1.  
 PD 10-JAN-2002.  
 PE 03-APR-2001; 2001US-0825294.  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 PA (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 XX WPI; 2002-171027/22.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
PT prevention and/or treatment of cancer, especially ovarian cancer -  
XX  
XX  
XX Claim 1a: Page 125-126; 131pp: English.

The invention relates to ovarian tumour polynucleotides and polypeptides that may be utilised in cancer therapy, for example in a vaccine or gene therapy. Polypeptides and polynucleotides of the invention are useful for detecting a cancer in a patient, for stimulating and/or expending T-cells specific for a tumour protein, and for inhibiting the development of a cancer in a patient. They are also useful for stimulating an immune response in a patient, and for treating a cancer in a patient and for determining the presence of a cancer in a patient. The isolated polynucleotides of the invention are useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumour polypeptides in tumour cells. Polypeptides and polynucleotides of the invention are also useful in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. The current sequence represents the ovarian carcinoma 05915 nucleotide sequence.

Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 73.6%; Score 1396; DB 24; Length 1619;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 2; Indels 1; Gaps 1;

Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 280 GGCACATTTTTCGCGATTGCTTCTTCACAGCTTTGGCTGCAATTCACAGCTACCA 339  
DB 1 GGCACATTTTTCGCGATTGCTTCTTCACAGCTTTGGCTGCAATTCACAGCTACCA 60  
QY 340 GTGTGAAGAAATTCACAGCTAACAAGACGCTGCTCTCCCGGATTCATTGTATGAC 399  
DB 61 GTGTGAAGAAATTCACAGCTAACAAGACGCTGCTCTCCCGGATTCATTGTATGAC 120  
QY 400 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 459  
DB 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180  
QY 460 CCGCAAGCTCTGCTGATCATACAGCGGCTGTCTCATCGCTTGGCGGGATCAGCTCTT 519  
DB 181 CCGCAAGCTCTGCTGATCATACAGCGGCTGTCTCATCGCTTGGCGGGATCAGCTCTT 240  
QY 520 CTGCTCCGAGGAAATCACTAGTTGATCAGCTGCTGCAACACCCCTTTGTAA 579  
DB 241 CTGCTCCGAGGAAATCACTAGTTGATCAGCTGCTGCAACACCCCTTTGTAA 300  
QY 580 CCGGCCAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 639  
DB 301 CCGGCCAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGAC 360  
QY 640 CACCATCTGTTCTCAAAATAGCCCTTCTGCGACACTGCTCAAGCTGAGAGATG 699  
DB 361 CACCATCTGTTCTCAAAATAGCCCTTCTGCGACACTGCTCAAGCTGAGAGATG 420  
QY 700 CACACCCCTCTGATGTTCTTCAAGCCCTGCGCCCAACCCCACTCCCTAGAGA 759  
DB 421 CACACCCCTCTGATGTTCTTCAAGCCCTGCGCCCAACCCCACTCCCTAGAGA 480  
QY 760 GTTCTTCTGCGGTCCTTTTATTCGTAGAGAGCGGAGTCCGTGTTCTTTGTT 819  
DB 481 GTTCTTCTGCGGTCCTTTTATTCGTAGAGAGCGGAGTCCGTGTTCTTTGTT 540  
QY 820 CCTGTCAAAATTAAGAGAGCTCGGTAAAGCATTCGTAATTAATTCAGCTGAGT 879  
DB 541 CCTGTCAAAATTAAGAGAGCTCGGTAAAGCATTCGTAATTAATTCAGCTGAGT 600  
QY 880 TTTTCAATATGATCTGAAGAGAGAGTGAAGAAATTCACCCCACTGCTGTGTAAC 939  
DB 601 TTTTCAATATGATCTGAAGAGAGAGTGAAGAAATTCACCCCACTGCTGTGTAAC 660

QY 940 CGAGTCAGAGCCAGGCTGCGACAGCTCMTGCTTGAAGTCACTGAGTGGCATCTGCC 999  
DB 661 CGAGTCAGAGCCAGGCTGCGACAGCTCMTGCTTGAAGTCACTGAGTGGCATCTGCC 720  
QY 1000 TTTTGAAGCCCTCAGTGTTCATTCATTCCTGATGGGGGATTAATTGAGACTCAAA 1059  
DB 721 TTTTGAAGCCCTCAGTGTTCATTCATTCCTGATGGGGGATTAATTGAGACTCAAA 780  
QY 1060 GTGAGATGACGTTTCTTGAAGGCTGAGGCGAGTTCACACCAAGGCCCTGCTTG 1119  
DB 781 GTGAGATGACGTTTCTTGAAGGCTGAGGCGAGTTCACACCAAGGCCCTGCTTG 840  
QY 1120 ACATTCAAATTCATGCTCTCTGAAACCATTCCTGACAGCAATTTGGCTGTTGGCC 1179  
DB 841 ACATTCAAATTCATGCTCTCTGAAACCATTCCTGACAGCAATTTGGCTGTTGGCC 900  
QY 1180 CTGAGTTGGGCTCTGATGACTCGAGACTCAATGACTGAGCTTAACTGAGGCTCGGCT 1239  
DB 901 CTGAGTTGGGCTCTGATGACTCGAGACTCAATGACTGAGCTTAACTGAGGCTCGGCT 960  
QY 1240 CGCTCTGAAAGTCTTAAGAAATCTTCTCAGTCTCTTTCAGAGAGACTGGCGCGGG 1299  
DB 961 CGCTCTGAAAGTCTTAAGAAATCTTCTCAGTCTCTTTCAGAGAGACTGGCGCGGG 1020  
QY 1300 ACGGAGAGAGCAAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGAGTGGCATGTA 1359  
DB 1021 ACGGAGAGAGCAAGCGGCGCTGCAAAAGCGGCGCTGCTGCTGAGTGGCATGTA 1080  
QY 1360 CGCGAGGCGCTTCTGCTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1418  
DB 1081 CGCGAGGCGCTTCTGCTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
QY 1419 ACGAAGACCCGCGCAACCTGCTGAGAGACACCGCTGTAAGAGAGCGGCTGATGACGAG 1478  
DB 1141 ACGAAGACCCGCGCAACCTGCTGAGAGACACCGCTGTAAGAGAGCGGCTGATGACGAG 1200  
QY 1479 CTGAGGTAGAAAACGCTCTCGAAGAGGAGAGAGATCATGTACGCCGGAATGAGAC 1538  
DB 1201 CTGAGGTAGAAAACGCTCTCGAAGAGGAGAGAGATCATGTACGCCGGAATGAGAC 1260  
QY 1539 CTGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1598  
DB 1261 CTGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
QY 1599 CAGCATACGGCATGTCTACAAATCAGCCCTGCGAGACAGAGAGGAGAGAGAC 1658  
DB 1321 CAGCATACGGCATGTCTACAAATCAGCCCTGCGAGACAGAGAGGAGAGAGAC 1380  
QY 1659 AGAGAAAAGAAAACACAGCATGAGAACAGTAATGAATTAATTAATTAATTAAT 1718  
DB 1381 AGAGAAAAGAAAACACAGCATGAGAACAGTAATGAATTAATTAATTAATTAAT 1440  
QY 1719 CCCCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1778  
DB 1441 CCCCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
QY 1779 CAGCTCTCTTTCGACAAAGCAAGAGAAATTAACACTGTTTCAAAACCCGCGGAGTTGG 1838  
DB 1501 CAGCTCTCTTTCGACAAAGCAAGAGAAATTAACACTGTTTCAAAACCCGCGGAGTTGG 1560  
QY 1839 CTGTGTTAAGAAAGACATTAATTAATGCTTTAGACAGTGTAAAAAATTAATTAAT 1897  
DB 1561 CTGTGTTAAGAAAGACATTAATTAATGCTTTAGACAGTGTAAAAAATTAATTAAT 1619

RESULT 10

AAF93845 ID AAF93845 standard; cDNA; 1890 BP.

XX AAF93845:

XX 23-MAY-2001 (first entry)

DE Human cDNA encoding a membrane or secretory protein clone PSEC0181.  
 XX  
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; ss.  
 OS Homo sapiens.  
 PN EP1067182-A2.  
 XX  
 PD 10-JAN-2001.  
 XX  
 PE 07-JUL-2000; 2000EP-0114090.  
 XX  
 PR 08-JUL-1999; 99JP-0194179.  
 PR 11-JAN-2000; 2000JP-0118775.  
 PR 02-MAY-2000; 2000JP-0183766.  
 XX  
 PA (HELI-) HELIX RES INST.  
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 DR WPI: 2001-093989/71.  
 DR P-PSDB: AAB88418.  
 XX  
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 gene therapy or as candidate target molecules in drug development -  
 XX  
 PS Claim 1; SEQ ID 203; 609pp + CD ROM; English.  
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by  
 CC AAB88419. Included in the invention are primers  
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
 CC cDNA sequences of the invention. The invention also includes methods for  
 CC the production of antibodies directed against the proteins, and cDNA  
 CC sequences, which can be used in vaccines. The polynucleotide sequences  
 CC can be used in gene therapy. The polynucleotide sequences and the  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate secretory  
 CC protein/membrane protein expression. The nucleic acids and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays  
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples. They may also be  
 CC used to study the expression and function of secretory proteins/membrane  
 CC polypeptides and their role in metabolism. The polypeptides may be used  
 CC as antigens in the production of antibodies against them and in assays to  
 CC identify modulators (agonists and antagonists) of expression and  
 CC activity. The antibodies and antagonists may also be used as therapeutic  
 CC agents to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of the  
 CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
 CC (ELISA). Examples of diseases which may be treated include rheumatoid  
 CC arthritis and diabetes.  
 XX  
 SQ Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other;  
 Query Match 70.8%; Score 1344; DB 22; Length 1890;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1854; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Db 213 CTCGCTGCTGTCGCCCTCTGATGGGCTTGCCTCCCGGAGCCGCGGAG 272  
 QY AATGGGCTCTAGGCTATCGCGGCACCTTTTGGATGTTGCTTCTCCAGGCTTGC 318  
 QY 259 AATGGGCTCTAGGCTATCGCGGCACCTTTTGGATGTTGCTTCTCCAGGCTTGC 332  
 Db 273 AATGGGCTCTAGGCTATCGCGGCACCTTTTGGATGTTGCTTCTCCAGGCTTGC 332  
 QY 319 GCTGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAAACGAGCTCTCC 378  
 Db 333 GCTGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAAACGAGCTCTCC 392  
 QY 379 CGAGTTATTTGTGAATTCACAGGTTGAAGAGATGTCAGAAAGATGATGA 438  
 Db 393 CGAGTTATTTGTGAATTCACAGGTTGAAGAGATGTCAGAAAGATGATGA 452  
 QY 439 GCAAGTGGCGGGGATCATATGACGCAAGTCTGTGATCATACGCGGCTCATGCG 498  
 Db 453 GCAAGTGGCGGGGATCATATGACGCAAGTCTGTGATCATACGCGGCTCATGCG 512  
 QY 499 CTCTGCGGGGTACAGTCTTCTGCTCCAGGGAACCTGACATGTTGATCAGCTG 558  
 Db 513 CTCTGCGGGGTACAGTCTTCTGCTCCAGGGAACCTGACATGTTGATCAGCTG 572  
 QY 559 CTGCAACACCCCTCTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTTCTCGGC 618  
 Db 573 CTGCAACACCCCTCTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTTCTCGGC 632  
 QY 619 CCTAGGCGAAGGGGTCCGCGACACCAATCCGTCTTCAATTAATGACCTCTCTCCGAC 678  
 Db 633 CTTAGGCGAAGGGGTCCGCGACACCAATCCGTCTTCAATTAATGACCTCTCTCCGAC 691  
 QY 679 CTGCTGAAGCTGAAGAGATGACCAACCCCTCTGATTTGTTCCAGCCCTGCCCCCA 738  
 Db 692 CTGCTGAAG-CTGAAGAGATGACCAACCCCTCTGATTTGTTCCAGCCCTGCCCCCA 750  
 QY 739 ACCCCCAACCTCTCTGAGTGTCTTCTGCGGTCTTTTATTTGGGTAGGAGCGG 798  
 Db 751 ACCCCCAACCTCTCTGAGTGTCTTCTGCGGTCTTTTATTTGGGTAGGAGCGG 810  
 QY 799 GAGTCGCTGTTCTTTTGTTCCTGTCGAATATATGAAGAGCGGTAAAGCATTTCTGA 858  
 Db 811 GAGTCGCTGTTCTTTTGTTCCTGTCGAATATATGAAGAGCGGTAAAGCATTTCTGA 870  
 QY 859 ATAAATTCAGCTGATGAATTTTCACTATGTACTTGAAGAGAGGTGAGTGAAGT 918  
 Db 871 ATAAATTCAGCTGATGAATTTTCACTATGTACTTGAAGAGAGGTGAGTGAAGT 930  
 QY 919 TCACCCCAATGTCGTGTAAACCGAGTCAAGGCCAGGCTGCGAGAGTCACTCTTGAAG 978  
 Db 931 TCACCCCAATGTCGTGTAAACCGAGTCAAGGCCAGGCTGCGAGAGTCACTCTTGAAG 990  
 QY 979 TCACCTGAAGTGGGATGTCGCTTTTGAAGCCGTCGATTCATTCATTCCTGATGGG 1038  
 Db 991 TCACCTGAAGTGGGATGTCGCTTTTGAAGCCGTCGATTCATTCATTCCTGATGGG 1050  
 QY 1039 GGCATAGTTTGAAGTCTCAGAGTGAAGTGAAGTTCCTTGAAGGCTGAGGCGCAGTTCC 1098  
 Db 1051 GGCATAGTTTGAAGTCTCAGAGTGAAGTGAAGTTCCTTGAAGGCTGAGGCGCAGTTCC 1110  
 QY 1099 CACTCAAGGCTCTCTGCTTGAATTCATTCATTCATTCCTTGAAGGCTCTCTGACAG 1158  
 Db 1111 CACTCAAGGCTCTCTGCTTGAATTCATTCATTCATTCCTTGAAGGCTCTCTGACAG 1170  
 QY 1159 CAGAAATGGGCTGTTGGGCGCTGAGTGTGGGCTCTAGTGAAGTGAAGTGAAGTGGG 1218  
 Db 1171 CAGAAATGGGCTGTTGGGCGCTGAGTGTGGGCTCTAGTGAAGTGAAGTGAAGTGGG 1230  
 QY 1219 ACTTAGACTGGGCTCGGCTCTGTAAGAGTGTCTTAAGAAATCTTCTCAGTTCT-C 1277  
 Db 1231 ACTTAGACTGGGCTCGGCTCTGTAAGAGTGTCTTAAGAAATCTTCTCAGTTCTC 1290  
 QY 1278 CTTGCAAGAGACTGGGCGCGGAGCGGAGACGAGCAAGCGGCGCTGACAAAGCGGCGCTG 1337  
 |||||||

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Db 1291 CTTCAGAGAGACTGGCCGCGGAGCGGAAGACACAGGCGCTGACAAAGCGGCGCTG 1350
QY 1338 TCCGTGTGAGAGTGGCATGTACGCGCAGCGCGTTCGTGGTGGCCGTGTGACAGCGAC 1397
Db 1351 TCCGTGTGAGAGTGGCATGTACGCGCAGCGCGTTCGTGGTGGCCGTGTGACAGCGAC 1410
QY 1398 AGCGGCGAGACAGACACTGTGACAGAACACCGCCGGAACCTGCTGGAGAGACACCGTGTAC 1457
Db 1411 AGCGGCGAGACAGACACTGTGACAGAACACCGCCGGAACCTGCTGGAGAGACACCGTGTAC 1470
QY 1458 AGAGCGGGGTGTATGACCCAGCTGAGAGTGAAGAAACGTCTCCGAGAGGGAGAGAGATC 1517
Db 1471 AGAGCGGGGTGTATGACCCAGCTGAGAGTGAAGAAACGTCTCCGAGAGGGAGAGAGATC 1530
QY 1518 ATGTACGCCCGGAAGTGAAGACCTGCTCAGTGTGCTGGTGGTGGCCGACCATGATC 1577
Db 1531 ATGTACGCCCGGAAGTGAAGACCTGCTCAGTGTGCTGGTGGTGGCCGACCATGATC 1590
QY 1578 CTCGGAATCTGTTGGGCAATCCAGCATAGCGCAATGTCAACAATCAGCCCTGGGCGAG 1637
Db 1591 CTCGGAATCTGTTGGGCAATCCAGCATAGCGCAATGTCAACAATCAGCCCTGGGCGAG 1650
QY 1638 ACACGAGCAGAGAGAGAGACAGAGAAAGAAACACAGCATGAGAACACAGTAAATGA 1697
Db 1651 ACACGAGCAGAGAGAGAGACAGAGAAAGAAACACAGCATGAGAACACAGTAAATGA 1710
QY 1698 ATAAACCATATAATATTAGCCCTCTGTCTGTCTTACTGAGGCGAGAAATGTACCA 1757
Db 1711 ATAAACCATATAATATTAGCCCTCTGTCTGTCTTACTGAGGCGAGAAATGTACCA 1770
QY 1758 ATTTTCAAGTGTGAGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAAATTTAACACTG 1817
Db 1771 ATTTTCAAGTGTGAGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAAATTTAACACTG 1830
QY 1818 TTTCAAACCCGGGGGAGTGGCTGTGTAAAGAAAGACCATTAATTCCTTACAGAGTCT 1877
Db 1831 TTTCAAACCCGGGGGAGTGGCTGTGTAAAGAAAGACCATTAATTCCTTACAGAGTCT 1890

RESULT 11
AAD18690/c
ID AAD18690 standard; cDNA; 2528 BP.
XX
AC AAD18690;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human G protein coupled receptor (GPCR) 4941 cDNA.
XX
KW Human; cardiovascular; tumorigenic disorder; aberrant angiogenesis;
KW gene therapy; aberrant vascularisation; atherosclerosis; ovarian cancer;
KW ischaemia/reperfusion injury; hypertension; arterial inflammation;
KW psoriasis; endothelial cell disorder; diabetic retinopathy; restenosis;
KW myocardial infarction; Grave's disease; G protein coupled receptor;
KW GPCR 4941; vasodilator; hypotensive; antiinflammatory; cytosolic;
KW antidiabetic; antipsoriatic; leukemia; ss.
XX
OS Homo sapiens.
XX
FH Key 42.1403 Location/Qualifiers
FT CDS
FT /tag= a
FT /product= "Human GPCR 4941"
FT /note= "The CDS is specifically claimed in claim 1 of
FT the specification."
XX
PN WO200181634-A2.
XX
PD 01-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US13788.
XX
PR 26-APR-2000; 2000US-19908P.

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PR 09-AUG-2000; 2000US-0635521.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Galvin KA, Rudolph-owen LA;
XX
XX WPI; 2001-611743/70.
XX
XX P-PSDB; AAE11751.
XX
XX Identifying nucleic acids for the diagnosis and treatment of
XX cardiovascular and tumorigenic disorders, comprises identifying G
XX protein coupled receptor (GPCR)-4941
XX
XX Example 1; Fig 1; 118pp; English.
XX
XX The present invention relates to a method for identifying a nucleic acid
XX molecule (G protein coupled receptor gene, GPCR 4941) associated with a
XX cardiovascular or tumorigenic disorder. The method comprising contacting
XX a sample containing a nucleic acid molecule with a hybridisation probe or
XX amplification primers and detecting the presence. The invention is used
XX in gene therapy. The method of the invention is used for identifying
XX nucleic acids or polypeptides associated with a cardiovascular or
XX tumorigenic disorder such as aberrant angiogenesis, aberrant
XX vascularisation, atherosclerosis, or ovarian cancer, ischaemia/
XX reperfusion injury, hypertension, restenosis, arterial inflammation,
XX endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial
XX infarction, Grave's disease and leukemia. The methods can also detect
XX mRNA or genomic DNA in a sample. The present sequence is G protein
XX coupled receptor (GPCR) 4941 cDNA.
XX
XX Sequence 2528 BP; 516 A; 766 C; 677 G; 567 T; 2 other;
XX
XX Query Match 64.2%; Score 1218; DB 22; Length 2528;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 1318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 310 AGGCTTGGCGGTGCAATTCACAGTCTACAGTGTGAAGAAATTCAGGTGAACAAGCACTG 369
XX 2217 AGGCTTGGCGGTGCAATTCACAGTCTACAGTGTGAAGAAATTCAGGTGAACAAGCACTG 2158
XX
XX 370 CTCCTCCCCCGAGTTCATTTGATTTGACGCGTGAACGTTCAAGACATGTGTGAGAAAGA 429
XX 2157 CTCCTCCCCCGAGTTCATTTGATTTGACGCGTGAACGTTCAAGACATGTGTGAGAAAGA 2098
XX
XX 430 AGTATGAGCAAGAGTGGCGGATCATGTACCGCAAGTCTCTGATCATCAGCGGCTG 489
XX 2097 AGTATGAGCAAGAGTGGCGGATCATGTACCGCAAGTCTCTGATCATCAGCGGCTG 2038
XX
XX 490 TGTGATCGCTCTGCGGGATACAGTCTCTGCTGCCAGGGAAGTGAATCACTGTTG 549
XX 2037 TGTGATCGCTCTGCGGGATACAGTCTCTGCTGCCAGGGAAGTGAATCACTGTTG 1978
XX
XX 550 CATGAGCTGCTGCAACACCCCTTTTAAACGGGCGCAAGGCCCAAGAAAGGGAAGTTC 609
XX 1977 CATGAGCTGCTGCAACACCCCTTTTAAACGGGCGCAAGGCCCAAGAAAGGGAAGTTC 1918
XX
XX 610 TGCCTGGCCCTCAAGGCGAGGGCTCCGACACCATCTCTTCCCAATTAAGCCCTCT 669
XX 1917 TGCCTGGCCCTCAAGGCGAGGGCTCCGACACCATCTCTTCCCAATTAAGCCCTCT 1858
XX
XX 670 CTGGGACACTGTGAAAGTGAAGAGATGCCACCCCTCTGATTTGTTTCCAGCC 729
XX 1857 CTGGGACACTGTGAAAGTGAAGAGATGCCACCCCTCTGATTTGTTTCCAGCC 1798
XX
XX 730 TCGCCCCCAACCCCGCACTCCGATGAGTGTCTTCTGGGTGCTTTTATTCGGGT 789
XX 1797 TCGCCCCCAACCCCGCACTCCGATGAGTGTCTTCTGGGTGCTTTTATTCGGGT 1738
XX
XX 790 AGGAGCGGAGTCCGTTCTTTTGTCTCTGTGCAATTAATGAAGAGTCCGTA 849
XX 1737 AGGAGCGGAGTCCGTTCTTTTGTCTCTGTGCAATTAATGAAGAGTCCGTA 1678
XX
XX 850 GCATTCGTAATTAATTCAGCTGACTGAATTTTCAGTATGTACTGAAGAGAGGTGG 909

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Db 1677 GCATTCCTGAAATTAATTCACCTTGACGTAATTTTCAATATGTACTTGAAGAGAGAGGTGG 1618
OY 910 AGTGAAGATTCACCCCAATGCTGTGTACCGAGTCAAGGCGAGCGAGTCCAGTACGT 969
Db 1617 AGTGAAGATTCACCCCAATGCTGTGTGTACCGAGTCAAGGCGAGCGAGTCCAGTACGT 1558
OY 970 CCTTGAAGATTCACGAGTGGGATCTGCTTTTGTAAAGCTCCAGTGTCCATTCATC 1029
Db 1557 CCTTGAAGATTCACGAGTGGGATCTGCTTTTGTAAAGCTCCAGTGTCCATTCATC 1498
OY 1030 CCTGATGGGGGATAGTGTGACACTGACAGTGAAGTGAAGTCTTTTCTTAAAGGCTGAGG 1089
Db 1497 CCTGATGGGGGATAGTGTGACACTGACAGTGAAGTGAAGTCTTTTCTTAAAGGCTGAGG 1438
OY 1090 GCGAGTCCCACTCAAGGCTCCCTGCTGACATTCAAACTCAAGCTCCCTCAAAACCAT 1149
Db 1437 GCGAGTCCCACTCAAGGCTCCCTGCTGACATTCAAACTCAAGCTCCCTCAAAACCAT 1378
OY 1150 TCTGTGACAGCAGAAATTTGGCTGTTCGCGCTGAGTTGGGCTCTAGTACCTGACATCA 1209
Db 1377 TCTGTGACAGCAGAAATTTGGCTGTTCGCGCTGAGTTGGGCTCTAGTACCTGACATCA 1318
OY 1210 ATGACTGGGACTTACAGTGGGCTGCGCTGCTGAAAGTGGTTAAGAAATCTTCT 1269
Db 1317 ATGACTGGGACTTACAGTGGGCTGCGCTGCTGAAAGTGGTTAAGAAATCTTCT 1258
OY 1270 CAGTTCTCTCTGACAGAGAGCTGGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1329
Db 1257 CAGTTCTCTCTGACAGAGAGCTGGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
OY 1330 GGGGCTGTGCTGTGTGTGAGAGTGCAGTGTACCGCGAGCGCTTCTGCTGCTGCTGCT 1389
Db 1197 GGGGCTGTGCTGTGTGTGAGAGTGCAGTGTACCGCGAGCGCTTCTGCTGCTGCTGCT 1138
OY 1390 GAGGAGACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1449
Db 1137 GAGGAGACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1078
OY 1450 CCGTGTACAGAGAGCGGCTGTGATGACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1509
Db 1077 CCGTGTACAGAGAGCGGCTGTGATGACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1018
OY 1510 GAGGATCATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
Db 1017 GAGGATCATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
OY 1570 CCATGATCCTCCGAAATGCTGTTGGGATTCACGACATTCACGACATTCACGACATTCAC 1629
Db 957 CCATGATCCTCCGAAATGCTGTTGGGATTCACGACATTCACGACATTCACGACATTCAC 898

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## RESULT 12

AB054231  
ID AB054231 standard; cDNA: 1608 BP.

AC AB054231;

DT 22-AUG-2002 (first entry)

DE Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.

Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
ovarian cancer; breast cancer; tumour; reproductive system disorder;  
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
inflammatory condition; immune disorder; blood disorder;  
cardiovascular disorder; respiratory disorder; neurological disorder;  
gastrointestinal disorder; urinary system disorder; drug screening;  
gene therapy; chromosome mapping; forensic analysis;  
antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
antiinflammatory; gynaecological; reproductive; chromosome 2q21-22;  
gene; ss.

XX Homo sapiens.  
OS  
PN W0200200677-A1.  
XX  
PD 03-JAN-2002.  
XX  
PF 07-JUN-2001; 2001MO-US18569.  
XX  
PR 07-JUN-2000; 2000US-209467P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Blaise CE, Rosen CA;  
XX  
DR WPI: 2002-147878/19.  
XX  
DR P-PSDB: ABP41154.  
XX  
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
PT ovarian cancer), immune disorders, cardiovascular disorders and  
PT neurological diseases -  
XX  
PS  
XX  
PS Claim 1; SEQ ID NO 111; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-  
ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents cDNA encoding a human ovarian antigen of the  
CC invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

Sequence 1608 BP; 402 A; 402 C; 417 G; 381 T; 6 other;

Query Match 60.6%; Score 1150; DB 24; Length 1608;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 627 CAGGCGTCCGACACCATCTGTCTCAAAATTAAGCCCTCTGCGACACTGCTGA 686
Db 281 CAGGCGTCCGACACCATCTGTCTCAAAATTAAGCCCTCTGCGACACTGCTGA 340
OY 687 GCTGAAGAGATGCACACCCCTCTGATTTCTTCAGACCCCTCCCAACCCCA 746
Db 341 GCTGAAGAGATGCACACCCCTCTGATTTCTTCAGACCCCTCCCAACCCCA 400
OY 747 CTTCCCTGATGATTTCTTCTGCTGCTCTTTTATTTGAGGAGAGGAGGCTCGT 806
Db 401 CTTCCCTGATGATTTCTTCTGCTGCTCTTTTATTTGAGGAGAGGAGGAGGCTCGT 460

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QY 807 GTTCTCTTTTGTCTCTGCAATAATGAAGAGCTCGGTAAGCATTCGATAAATTC 866  
 DB 461 GTTCTCTTTTGTCTCTGCAATAATGAAGAGCTCGGTAAGCATTCGATAAATTC 520  
 QY 867 AGCTGACTGAATTTTTCAGTATGTAAGGAAGAGAGTGAAGTGAACCTCCACC 926  
 DB 521 AGCTGACTGAATTTTTCAGTATGTAAGGAAGAGAGTGAAGTGAACCTCCACC 580  
 QY 927 ATGCTGTGTAAACCGAGATCAAGGCGAGTGGCAGAGTCTGCTTGAAGTCACTGAG 986  
 DB 581 ATGCTGTGTAAACCGAGATCAAGGCGAGTGGCAGAGTCTGCTTGAAGTCACTGAG 640  
 QY 987 GTGGGCACTCTGCTTTTAAAGCCTCCAGTGTCCATCCCTGATGGGGGCAATAGT 1046  
 DB 641 GTGGGCACTCTGCTTTTAAAGCCTCCAGTGTCCATCCCTGATGGGGGCAATAGT 700  
 QY 1047 TTGAGACTGAGAGTGAAGTGAAGTCTTTCTAGGCGTGAAGGCGAGTCCCACTCAAG 1106  
 DB 701 TTGAGACTGAGAGTGAAGTGAAGTCTTTCTAGGCGTGAAGGCGAGTCCCACTCAAG 760  
 QY 1107 GCTCCCTGCTTGACATTTCAAACTTCATGCTGTAAGAAACCATTCCTGACAGCAATTG 1166  
 DB 761 GCTCCCTGCTTGACATTTCAAACTTCATGCTGTAAGAAACCATTCCTGACAGCAATTG 820  
 QY 1167 GCTGCTTTCGGGCTGAGTGTGGGCTCTAGTACTGACATCAATGACTGGGACTTGAAC 1226  
 DB 821 GCTGCTTTCGGGCTGAGTGTGGGCTCTAGTACTGACATCAATGACTGGGACTTGAAC 880  
 QY 1227 TGGGGCTGGGCTGCTGTAAGAAAGTGTCTGTAAGAAATCTTCTCAGTCTCTTTCAGAG 1286  
 DB 881 TGGGGCTGGGCTGCTGTAAGAAAGTGTCTGTAAGAAATCTTCTCAGTCTCTTTCAGAG 940  
 QY 1287 GACTGGGCGGGGAGCGCAAGAGCAAGCGGCTGACAAAGCGGCGCTGCTGCTGCTG 1346  
 DB 941 GACTGGGCGGGGAGCGCAAGAGCAAGCGGCTGACAAAGCGGCGCTGCTGCTGCTG 1000  
 QY 1347 GAGTGGGAGTGAAGGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1406  
 DB 1001 GAGTGGGAGTGAAGGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1060  
 QY 1407 CACAGCAGCTGACAGCAACCGCGGAAAGTCTGCGAGAGACCGTGTACAGAGCGGG 1466  
 DB 1061 CACAGCAGCTGACAGCAACCGCGGAAAGTCTGCGAGAGACCGTGTACAGAGCGGG 1120  
 QY 1467 TTGATGACCGAGCTGAGTGAAGAAAGTCTTCCGAGAGGAGGAGAGATATGATGCC 1526  
 DB 1121 TTGATGACCGAGCTGAGTGAAGAAAGTCTTCCGAGAGGAGGAGATATGATGCC 1180  
 QY 1527 CGGAGTGAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1586  
 DB 1181 CGGAGTGAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240  
 QY 1587 TGGTTGGGAGTCAAGCATACGCGCAATGTCACAAACATCAGCGCTGGGCGAGACAGACA 1646  
 DB 1241 TGGTTGGGAGTCAAGCATACGCGCAATGTCACAAACATCAGCGCTGGGCGAGACAGACA 1300  
 QY 1647 GAGGAGAGAGACAGAGAAAGAAACACAGCATGAGAACACAGTAAATGAATAAACCA 1706  
 DB 1301 GAGGAGAGAGACAGAGAAAGAAACACAGCATGAGAACACAGTAAATGAATAAACCA 1360  
 QY 1707 TAAATATTTAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1766  
 DB 1361 TAAATATTTAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1420  
 QY 1767 TGTGGAGTGAAGCATCTTTTTCACAGAGAGAGAGATTTTAACTGTTTCAACC 1826  
 DB 1421 TGTGGAGTGAAGCATCTTTTTCACAGAGAGAGAGATTTTAACTGTTTCAACC 1480  
 QY 1827 CGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 1878  
 DB 1481 CGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 1532

RESULT 13  
 ID ABT03280 standard; cDNA; 625 BP.  
 XX  
 AC ABT03280;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 210.  
 XX  
 KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
 KW cytostatic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200239885-A2.  
 PD 23-MAY-2002.  
 XX  
 PF 13-NOV-2001; 2001MO-US45395.  
 XX  
 PR 14-NOV-2000; 2000US-0713550.  
 PR 03-APR-2001; 2001US-0825294.  
 PR 02-OCT-2001; 2001US-0970966.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Xu J, Skolk JA, Algate PA, Fling SP, Molesch DA;  
 DR WPI; 2002-500186/53.  
 XX  
 PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
 PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
 PT  
 XX  
 PS Claim 2; Page 194; 197pp; English.  
 XX  
 CC The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.  
 XX  
 SQ Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;  
 Query Match 31.9%; Score 606; DB 24; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-234;  
 Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1271 AGTCTCTTGGAGGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1330  
 DB 1 AGTCTCTTGGAGGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60  
 QY 1331 GCGGCTGCGGTGGTGGAGTGGCGCATGTACGCGAGGCGCTTCTGCTGCTGCTGCTGCTG 1390  
 DB 61 GCGGCTGCGGTGGTGGAGTGGCGCATGTACGCGAGGCGCTTCTGCTGCTGCTGCTGCTG 120  
 QY 1391 CAGCGAGGCGGCGAGCAGACACCTGACGAACACCGCGGAACTGCTGCGAGACAC 1450  
 DB 121 CAGCGAGGCGGCGAGCAGACACCTGACGAACACCGCGGAACTGCTGCGAGACAC 180  
 QY 1451 CGGTATAGAGAGCGGCTTGAATGACCGAGCTGAGGTGAAGAAAGTCTCCGAGAGGAGGAG 1510  
 DB 181 CGGTATAGAGAGCGGCTTGAATGACCGAGCTGAGGTGAAGAAAGTCTCCGAGAGGAGGAG 240  
 QY 1511 GAGGATCATGAGACCGCGGAGAGTGAAGACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTG 1570  
 DB 241 GAGGATCATGAGACCGCGGAGAGTGAAGACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTG 300  
 QY 1571 CATGATCTCCGAATCTGTTGGGAGTCAAGATACGCGGCAATGTCAACAATCAAGCC 1630  
 DB 301 CATGATCTCCGAATCTGTTGGGAGTCAAGATACGCGGCAATGTCAACAATCAAGCC 360









DE	Ovarian carcinoma GPR39 cDNA.
XX	
KW	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX	ss.
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
CDS	1..1362
FT	/tag= a
FT	/product= "Ovarian carcinoma protein GPR39"
PN	US2002004491-A1.
PD	10-JAN-2002.
XX	
PF	03-APR-2001; 2001US-0825294.
XX	
PR	10-SEP-1999; 99US-0394374.
PR	01-MAY-2000; 2000US-0561778.
PR	15-AUG-2000; 2000US-0640173.
PR	07-SEP-2000; 2000US-0656668.
PR	14-NOV-2000; 2000US-0713550.
XX	
PA	(XUJ/) XU J.
PA	(STOLK/) STOLK J A.
PA	(ALGA/) ALGATE P A.
PA	(FLIN/) FLING S P.
XX	
PI	Xu J, Stolk JA, Algate PA, Fling SP;
DR	WPI: 2002-171027/22.
XX	P-PSDB: ABB09416.
PT	Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX	prevention and/or treatment of cancer, especially ovarian cancer -
PS	Claim 1a; Page 123-124; 131pp; English.
XX	
CC	The invention relates to ovarian tumour polynucleotides and polypeptides
CC	that may be utilised in cancer therapy, for example in a vaccine or
CC	gene therapy. Polypeptides and polynucleotides of the invention are
CC	useful for detecting a cancer in a patient, for stimulating and/or
CC	expanding T-cells specific for a tumour protein, and for inhibiting the
CC	development of a cancer in a patient. They are also useful for
CC	stimulating an immune response in a patient, and for treating a cancer in
CC	a patient and for determining the presence of a cancer in a patient.
CC	The isolated polynucleotides of the invention are useful for their
CC	ability to selectively form duplex molecules with complementary stretches
CC	of the entire desired gene or gene fragments, and for designing and
CC	preparing ribozyme molecules for inhibiting expression of tumour
CC	polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC	invention are also useful in recombinant DNA molecules to direct
CC	expression of a polypeptide in appropriate host cells. The current
CC	sequence represents the ovarian carcinoma GPR39 cDNA.
XX	
SQ	Sequence 1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other:
Query Match	26.7%; Score 506; DB 24; Length 1362;
Best Local Similarity	100.0%; Pred. No. 7.8e-194;
Matches 506; Conservative	0; Mismatches 0; Indels 0; Gaps 0.0;
OY	1124 TCMAACTTCATCTCCTCGTAAACCATTTCTCTGCAGAGAAGATTGGCTGTTCGCCGCTGA 1183
Db	1362 TCMAACTTCATCTCCTCGTAAACCATTTCTCTGCAGAGAAGATTGGCTGTTCGCCGCTGA 1303
OY	1184 GTTGCGCTCTAGACTCGAGACTCAATGACGTGGACTTAGACTGGGGCTCGGCTCGCT 1243
Db	1302 GTTGCGCTCTAGACTCGAGACTCAATGACGTGGACTTAGACTGGGGCTCGGCTCGCT 1243
OY	1244 CTGAAAAGTGTTAAGAAAAATCTTCCTCACTTCTCTTCGAGAGAGATGGCGCCGGAGACC 1303
Db	1242 CTGAAAAGTGTTAAGAAAAATCTTCCTCACTTCTCTTCGAGAGAGATGGCGCCGGAGACC 1183

Oy	1304	GAGAGACAAAGGGCCCTGCACAAAAGCGGGCGCTGTCGGTGTGTGAATGGCATGTACCG	1363
Db	1182	GAAAGACAAAGGGCGCTGCACAAAAGCGGGCGCTGTCCGTGTGTGAATGGCATGTACCG	1123
Oy	1364	CAGGCGCTTCTGCTGTGGTGGCGCTGCTGCAGCGACAGGCGGCGACACAGCACTGCAGAA	1423
Db	1122	CAGGCGCTTCTGCTGTGGTGGCGCTGCTGCAGCGACAGGCGGCGACACAGCACTGCAGAA	1063
Oy	1424	CACCCCGCGAAACTGCTGCGAGAGACACCCGTTATAGAGAGCGGGTTTATATACCCGACTGAG	1483
Db	1062	CACCCCGCGAAACTGCTGCGAGAGACACCCGTTATAGAGAGCGGGTTTATATACCCGACTGAG	1003
Oy	1484	GTGAAAAACGCTCCGAGAAAGGAGAGGATCATGTACGCCCGGAAATAGAGACTCGT	1543
Db	1002	GTGAAAAACGCTCCGAGAAAGGAGAGGATCATGTACGCCCGGAAATAGAGACTCGT	943
Oy	1544	CCAGTGTGCTTGGCTTGGTGGCGCGACGCCATGATCCTCCGATCTGGTGGGATCCAGCA	1603
Db	942	CCAGTGTGCTTGGTGGTGGTGGCGCGACGCCATGATCCTCCGATCTGGTGGGATCCAGCA	883
Oy	1604	TACGGCCATGTACACACATCAGCC	1629
Db	882	TACGGCCATGTACACACATCAGCC	857
RESULT 19			
ID	ABT03283		
XX	ABT03283	standard; cDNA; 480 BP.	
XX	ABT03283;		
AC	XX		
DT	05-SEP-2002	(first entry)	
XX			
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 213.		
XX			
KW	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;		
KW	cytostatic; gene; ss.		
XX			
OS	Homo sapiens.		
PN	WO200239885-A2.		
PD	23-MAY-2002.		
XX			
PE	13-NOV-2001; 2001MO-US45395.		
XX			
PR	14-NOV-2000; 2000US-0713550.		
PR	03-APR-2001; 2001US-0825294.		
PR	02-OCT-2001; 2001US-0970966.		
PA	(CORI-) CORIXA CORP.		
XX			
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;		
DR	WPI; 2002-500186/53.		
XX			
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for		
PT	detecting the presence of ovarian cancer in a patient, and in		
PT	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer		
PS			
XX	Claim 2; Page 196; 197p; English.		
CC	The present invention provides human ovarian cancer associated proteins		
CC	and coding sequences. The sequences can be used in the diagnosis and		
CC	treatment of ovarian cancers. The present sequence is a coding sequence		
CC	of the invention.		
XX			
SO	Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other;		
Query Match	22.4%;	Score 425;	DB 24; Length 480;
Best Local Similarity	99.8%;	Pred. No. 3.3e-161;	

Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAACTCCGAGGCTCTGTGCTCGCCCGGAGCGGAGCGAGAGAGACCCG 60  
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 GCCAACTCCGAGGCTCTGTGCTCGCCCGGAGCGGAGCGAGAGAGACCCG 60  
 QY 61 CACCCGGAGAGCCGAGCGGGGAGATGACAGGCTCCCGAGCGGACCTCGGCTCTTA 120  
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 CACCCGGAGAGCCGAGCGGGGAGATGACAGGCTCCCGAGCGGACCTCGGCTCTTA 120  
 QY 121 AGTTAGACAGCTGTCTCCGCGGAGAGCGGGGCGGAGAGCTCCGAGCGGACAGC 180  
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 AGTTAGACAGCTGTCTCCGCGGAGAGCGGGGCGGAGAGCTCCGAGCGGACAGC 180  
 QY 181 CGCTGACGCGGGGAGCGCTCGCTGCTGCGCTCTGATGCGCTTGGCTCTCCG 240  
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 CGCTGACGCGGGGAGCGCTCGCTGCTGCGCTCTGATGCGCTTGGCTCTCCG 240  
 QY 241 GCCCGGGAGCTCCGGAGAGATGAGGCTCTAGGAGTCCGCGACCTTTTGGGATGTT 300  
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 GCCCGGGAGCTCCGGAGAGATGAGGCTCTAGGAGTCCGCGACCTTTTGGGATGTT 300  
 QY 301 CTGTCTCCAGGCTTTCGCTGCAATCCAGTCTACAGTGTGAAGATTCAGCTGAA 360  
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 CTGTCTCCAGGCTTTCGCTGCAATCCAGTCTACAGTGTGAAGATTCAGCTGAA 360  
 QY 361 CAACGACTGCTCTCCCGGAGTTCAATTGTAATGACAGGTGAACGTTCAAGACATGTG 420  
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 CAACGACTGCTCTCCCGGAGTTCAATTGTAATGACAGGTGAACGTTCAAGACATGTG 420  
 QY 421 TCAGAAAGAGTGTGAGCAAGTCCGGGATCATGTACCCGACGTCTGTGAT 476  
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 TCAGAAAGAGTGTGAGCAAGTCCGGGATCATGTACCCGACGTCTGTGAT 476

RESULT 20  
 ID ABL40351  
 ID ABL40351 standard; cDNA; 480 BP.

XX ABL40351:  
 AC 28-JUN-2002 (first entry)  
 DT  
 XX  
 DE Ovarian carcinoma BE336607 nucleotide sequence.  
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KM ss.  
 OS Homo sapiens.  
 XX  
 PN US2002004491-A1.  
 PD 10-JAN-2002.  
 XX  
 PD 03-APR-2001; 2001US-0825294.  
 PF 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PA (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 DR WPI; 2002-171027/22.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 PT prevention and/or treatment of cancer, especially ovarian cancer.

XX  
 PS Claim 1a; Page 127; 131p; English.  
 XX  
 CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma BE336607 nucleotide sequence.  
 CC  
 XX  
 SQ Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other;

Query Match 22.4%; Score 425; DB 24; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 3.3e-161;  
 Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAACTCCGAGGCTCTGTGCTCGCCCGGAGCGGAGCGGAGAGAGACCCG 60  
 Db 1 GCCAACTCCGAGGCTCTGTGCTCGCCCGGAGCGGAGCGGAGAGAGACCCG 60  
 QY 61 CACCCGGAGAGCCGAGCGGGGAGATGACAGGCTCCCGAGCGGACCTCGGCTCTTA 120  
 Db 61 CACCCGGAGAGCCGAGCGGGGAGATGACAGGCTCCCGAGCGGACCTCGGCTCTTA 120  
 QY 121 AGTTAGACAGCTGTCTCCGCGGAGAGCGGGGCGGAGAGCTCCGAGCGGACAGC 180  
 Db 121 AGTTAGACAGCTGTCTCCGCGGAGAGCGGGGCGGAGAGCTCCGAGCGGACAGC 180  
 QY 181 CGCTGACGCGGGGAGCGCTCGCTGCTGCGCTCTGATGCGCTTGGCTCTCCG 240  
 Db 181 CGCTGACGCGGGGAGCGCTCGCTGCTGCGCTCTGATGCGCTTGGCTCTCCG 240  
 QY 241 GCCCGGGAGCTCCGGAGAGATGAGGCTCTAGGAGTCCGCGACCTTTTGGGATGTT 300  
 Db 241 GCCCGGGAGCTCCGGAGAGATGAGGCTCTAGGAGTCCGCGACCTTTTGGGATGTT 300  
 QY 301 CTGTCTCCAGGCTTTCGCTGCAATCCAGTCTACAGTGTGAAGATTCAGCTGAA 360  
 Db 301 CTGTCTCCAGGCTTTCGCTGCAATCCAGTCTACAGTGTGAAGATTCAGCTGAA 360  
 QY 361 CAACGACTGCTCTCCCGGAGTTCAATTGTAATGACAGGTGAACGTTCAAGACATGTG 420  
 Db 361 CAACGACTGCTCTCCCGGAGTTCAATTGTAATGACAGGTGAACGTTCAAGACATGTG 420  
 QY 421 TCAGAAAGAGTGTGAGCAAGTCCGGGATCATGTACCCGACGTCTGTGAT 476  
 Db 421 TCAGAAAGAGTGTGAGCAAGTCCGGGATCATGTACCCGACGTCTGTGAT 476

RESULT 21  
 ID AAF94186/c  
 ID AAF94186 standard; DNA; 587 BP.  
 XX  
 AC AAF94186;  
 XX  
 DT 23-MAY-2001 (first entry)  
 DE  
 XX  
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 620.  
 XX  
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; PCR primer; ss.  
 XX  
 OS Synthetic.

```

XX  EP1067182-A2.
XX
XX  10-JAN-2001.
XX
XX  07-JUL-2000; 2000EP-0114090.
XX
XX  08-JUL-1999; 99JP-0194179.
XX  11-JAN-2000; 2000JP-0118775.
XX  02-MAY-2000; 2000JP-0183766.
XX
XX  (HELI-) HELIX RES INST.
XX
PI  Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
DR  WPI; 2001-093989/11.
XX
XX  Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX  gene therapy or as candidate target molecules in drug development -
XX
XX  Claim 5; SEQ ID 620; 609pp + CD ROM; English.
XX
XX  This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX  which encode human secretory or membrane proteins represented by
XX  AAB88317 - AAB88419. Included in the invention are primers
XX  AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
XX  cDNA sequences of the invention. The invention also includes methods for
XX  the production of antibodies directed against the proteins, and cDNA
XX  sequences, which can be used in vaccines. The polynucleotide sequences
XX  can be used in gene therapy. The polynucleotide sequences and the
XX  proteins they encode may be used in the prevention, treatment and
XX  diagnosis of diseases associated with inappropriate secretory
XX  protein/membrane protein expression. The nucleic acids and complementary
XX  sequences may also be used as DNA probes in diagnostic assays
XX  (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
XX  presence of similar nucleic acid sequences in samples. They may also be
XX  used to study the expression and function of secretory proteins/membrane
XX  polypeptides and their role in metabolism. The polypeptides may be used
XX  as antigens in the production of antibodies against them and in assays to
XX  identify modulators (agonists and antagonists) of expression and
XX  activity. The antibodies and antagonists may also be used as therapeutic
XX  agents to down regulate expression and activity. The antibodies may also
XX  be used as diagnostic agents for detecting the presence of the
XX  polypeptides in samples (e.g. by enzyme linked immunosorbent assay
XX  (ELISA). Examples of diseases which may be treated include rheumatoid
XX  arthritis and diabetes.
XX
SQ  Sequence 587 BP; 117 A; 162 C; 140 G; 162 T; 6 other;
Query Match 19.3%; Score 366; DB 22; Length 587;
Best Local Similarity 99.8%; Pred. No. 1.7e-137;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY  1761 TTTCAGTGTGGAGCTTGACAGCTTCCTTTGCGACAGAGAGAGAAATTTAACACTGTTT 1820
DB  117 TTTCAGTGTGGAGCTTGACAGCTTCCTTTGCGACAGAGAGAGAAATTTAACACTGTTT 58
QY  1821 CAACCCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAGACAGTGT 1877
DB  57 CAACCCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAGACAGTGT 1
RESULT 22
AAH50766/c
ID  AAH50766 standard; cDNA; 444 BP.
XX
AC  AAH50766;
XX
XX  23-AUG-2001 (first entry)
XX
DE  Human tumour associated cDNA #95.
XX
XX  Human; cancer specific gene expression; gene therapy;
XX  age related differential expression; ss.
XX
XX  Homo sapiens.
XX
XX  WO200136685-A2.
XX
PD  25-MAY-2001.
XX
PF  17-NOV-2000; 2000WO-US31809.
XX
XX  17-NOV-1999; 99US-0166056.
XX  17-NOV-1999; 99US-0166106.
XX
XX  (NYXT-) NYXIS NEURO THERAPIES INC.
XX
PI  Kroes RA, Moskal JR, Yamamoto H;
XX
DR  WPI; 2001-355647/37.
XX
XX  Novel nucleic acid molecules differentially expressed in brain cancers,
XX  useful for ascertaining propensity of cell for malignant phenotype or
XX  ascertaining suitability of anti-neoplastic drug candidate -
XX
XX  Claim 28; Page 50; 82pp; English.
XX
XX  The present invention provides the sequences of 184 cDNA fragments which
XX  are differentially expressed in cancer cell depending on the age of the
XX  patient. They can be used to diagnose and identify treatments for
XX  cancers, particularly brain cancers such as haemangioblastoma, teratoma,
XX  haemangioma, glioblastoma, schwannoma, osteoma and pinealoma. The
XX  present sequence is a cancer-associated cDNA of the invention.
XX
SQ  Sequence 444 BP; 95 A; 113 C; 94 G; 142 T; 0 other;
Query Match 19.2%; Score 364; DB 22; Length 444;
Best Local Similarity 99.8%; Pred. No. 1.1e-136;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1714 TTATGCCCTCTGTTCTGTTACTGCGCAGGAATGTTACCAATTTTTCAGTGTGA 1773  
 |||||||  
 Db 191 TTATGCCCTCTGTTCTGTTACTGCGCAGGAATGTTACCAATTTTTCAGTGTGA 132  
 |||||||  
 QY 1774 CTTGACAGCTTCTTTTCCACAGAGAGATAATTTTCAACCTGTTTCAACCCGGGGA 1833  
 |||||||  
 Db 131 CTTGACAGCTTCTTTTCCACAGAGAGATAATTTTCAACCTGTTTCAACCCGGGGA 72  
 |||||||  
 QY 1834 GTTGGCTGTATAAGAAAGACATTAATGCTTTGACAGTGTAAAAA 1888  
 |||||||  
 Db 71 GTTGGCTGTATAAGAAAGACATTAATGCTTTGACAGTGTAAAAA 17

## RESULT 23

AA94818  
 ID AAF94818 standard; cDNA: 396 BP.

AC AAF94818;

DT 23-MAY-2001 (first entry)

DE Human ovarian cancer associated coding sequence SEQ ID NO: 9.

KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

OS Homo sapiens.

PN WO200118046-A2.

PD 15-MAR-2001.

PF 08-SEP-2000; 2000WO-US24827.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA;

DR WPI: 2001-211395/21.

XX Isolated polypeptides associated with ovarian carcinomas, and the

XX nucleic acids that encode them, useful for the prevention diagnosis and

XX treatment of ovarian cancers.

XX Claim 5; Page 119; 189pp; English.

XX The present invention provides a number of coding sequences and proteins,

XX the over-expression of which is associated with ovarian carcinoma/cancer.

XX These can be used in the diagnosis, treatment and prevention of ovarian

XX cancer, optionally by gene therapy or in the form of a vaccine. The

XX present sequence is an example of one of these sequences.

XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

QY Query Match 16.7%; Score 316; DB 22; Length 396;

Db Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 CATCGCGCAACTTTTGGGATGTTGCTTCCAGGCTTTGGGCTGCAAAATCCAGTG 333  
 |||||||  
 Db 5 CATCGCGCAACTTTTGGGATGTTGCTTCCAGGCTTTGGGCTGCAAAATCCAGTG 64  
 |||||||  
 QY 334 CTACCAAGTGTGAAGATTCCAGCTGAACAGACTGCTCTCCCGAGTTCAATTGTGAA 393  
 |||||||  
 Db 65 CTACCAAGTGTGAAGATTCCAGCTGAACAGACTGCTCTCCCGAGTTCAATTGTGAA 124  
 |||||||  
 QY 394 TTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAGATGAGCAAGTCCGGGAT 453  
 |||||||

Db 125 TTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAGACTGATGACGAAGTCCCGGAT 184  
 |||||||  
 QY 454 CATGTAACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTTGGCGGTACCA 513  
 |||||||  
 Db 185 CATGTAACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTTGGCGGTACCA 244  
 |||||||  
 QY 514 GTCCCTTGTGCTCCCGAGGAACGTAACACTGATTGATCATGCTGTCGACACACCTCT 573  
 |||||||  
 Db 245 GTCCCTTGTGCTCCCGAGGAACGTAACACTGATTGATCATGCTGTCGACACACCTCT 304  
 |||||||  
 QY 574 TTGTAACGGGCCCAAGG 589  
 |||||||  
 Db 305 TTGTAACGGGCCCAAGG 320

## RESULT 24

ABT03085  
 ID ABT03085 standard; cDNA: 396 BP.

AC ABT03085;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 9.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR WPI: 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for

XX detecting the presence of ovarian cancer in a patient, and in

XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

XX Example 1; Page 116; 197pp; English.

XX The present invention provides human ovarian cancer associated proteins

XX and coding sequences. The sequences can be used in the diagnosis and

XX treatment of ovarian cancers. The present sequence is a coding sequence

XX of the invention.

XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

QY Query Match 16.7%; Score 316; DB 24; Length 396;

Db Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 CATCGCGCAACTTTTGGGATGTTGCTTCCAGGCTTTGGGCTGCAAAATCCAGTG 333  
 |||||||  
 Db 5 CATCGCGCAACTTTTGGGATGTTGCTTCCAGGCTTTGGGCTGCAAAATCCAGTG 64  
 |||||||  
 QY 334 CTACCAAGTGTGAAGATTCCAGCTGAACAGACTGCTCTCCCGAGTTCAATTGTGAA 393  
 |||||||  
 Db 65 CTACCAAGTGTGAAGATTCCAGCTGAACAGACTGCTCTCCCGAGTTCAATTGTGAA 124  
 |||||||  
 QY 394 TTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAGATGAGCAAGTCCGGGAT 453  
 |||||||

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|||||
Db 125 TTGCACGGTGAACGTTCAAGACATGTGCAGAAAGATGAGCAAAAGTCCGGGAT 184
Oy 454 CATGTACCGCAAGTCTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGTACCA 513
Db 185 CATGTACCGCAAGTCTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGTACCA 244
Oy 514 GTCTTCTGCTCCCGAGGAACGTGACATGTTGCATCAGCTGCTGCAACACCCCTCT 573
Db 245 GTCTTCTGCTCCCGAGGAACGTGACATGTTGCATCAGCTGCTGCAACACCCCTCT 304
Oy 574 TTGTACGGGCCCAAG 589
Db 305 TTGTACGGGCCCAAG 320

RESULT 25
ABLA8768
ID ABLA8768 standard; cDNA; 396 BP.
AC ABLA8768;
XX 18-JUN-2002 (first entry)
DE Ovarian carcinoma sequence isolate 21920.
XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX ss.
XX Homo sapiens.
XX US2002004491-A1.
XX 10-JAN-2002.
XX 03-APR-2001; 2001US-0825294.
XX 10-SEP-1999; 99US-0394374.
XX 01-MAY-2000; 2000US-0561778.
XX 15-AUG-2000; 2000US-0640173.
XX 07-SEP-2000; 2000US-0656668.
XX 14-NOV-2000; 2000US-0713550.
XX (XUJ/J) XU J.
XX (STOL/) STOLK J A.
XX (ALCA/) ALGATE P A.
XX (FLIN/) FLING S P.
XX Xu J, Stolk JA, Algate PA, Fling SP;
XX WPI; 2002-171027/22.
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer.
XX Claim 1a; Page 41-42; 131pp; English.
XX The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or
XX gene therapy. Polypeptides and polynucleotides of the invention are
XX useful for detecting a cancer in a patient, for stimulating and/or
XX expanding T-cells specific for a tumour protein, and for inhibiting the
XX development of a cancer in a patient. They are also useful for
XX stimulating an immune response in a patient, and for treating a cancer in
XX a patient and for determining the presence of a cancer in a patient.
XX The isolated polynucleotides of the invention are useful for their
XX ability to selectively form duplex molecules with complementary stretches
XX of the entire desired gene or gene fragments, and for designing and
XX preparing ribozyme molecules for inhibiting expression of tumour
XX polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX invention are also useful in recombinant DNA molecules to direct
XX expression of a polypeptide in appropriate host cells. The sequences
XX given in records ABLA8760-ABLA8956 represent polynucleotides encoding

```

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CC ovarian carcinoma proteins.
XX
SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;
Query Match 16.7%; Score 316; DB 24; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 274 CATGCGGGCAACTTTTGGCGATTGTTCTGTCCAGGCTTGGCGCAAAATCCAGTG 333
Db 5 CATGCGGGCAACTTTTGGCGATTGTTCTGTCCAGGCTTGGCGCAAAATCCAGTG 64
Oy 334 CTACCACTGTGAAGAAATTCAGCTGAACAAGACTGCTCTCCCGAGTTCAATTGAA 393
Db 65 CTACCACTGTGAAGAAATTCAGCTGAACAAGACTGCTCTCCCGAGTTCAATTGAA 124
Oy 394 TTGCACGGTGAAGCTTGAACAATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGAT 453
Db 125 TTGCACGGTGAAGCTTGAACAATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGGAT 184
Oy 454 CATGTACCGCAAGTCTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGTACCA 513
Db 185 CATGTACCGCAAGTCTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGTACCA 244
Oy 514 GTCTTCTGCTCCCGAGGAACGTGACATGTTGCATCAGCTGCTGCAACACCCCTCT 573
Db 245 GTCTTCTGCTCCCGAGGAACGTGACATGTTGCATCAGCTGCTGCAACACCCCTCT 304
Oy 574 TTGTACGGGCCCAAG 589
Db 305 TTGTACGGGCCCAAG 320

RESULT 26
AAF95007
ID AAF95007 standard; DNA; 369 BP.
XX
XX AAF95007;
XX 23-MAY-2001 (first entry)
DE Human ovarian cancer associated coding sequence SEQ ID NO: 199.
XX Human, ovarian cancer; vaccine; gene therapy; carcinoma; ds.
XX Homo sapiens.
XX NO200118046-A2.
XX 15-MAR-2001.
XX 08-SEP-2000; 2000WO-US24827.
XX 10-SEP-1999; 99US-0394374.
XX 01-MAY-2000; 2000US-0561778.
XX 15-AUG-2000; 2000US-0640173.
XX 07-SEP-2000; 2000US-0656668.
XX (CORI-) CORIXA CORP.
XX Xu J, Stolk JA;
XX WPI; 2001-211395/21.
XX Isolated polypeptides associated with ovarian carcinomas, and the
XX nucleic acids that encode them, useful for the prevention diagnosis and
XX treatment of ovarian cancers.
XX Claim 18; Page 189; 189pp; English.
XX The present invention provides a number of coding sequences and proteins,
XX the over-expression of which is associated with ovarian carcinoma/cancer.
XX These can be used in the diagnosis, treatment and prevention of ovarian

```



CC cancer, optionally by gene therapy or in the form of a vaccine. The  
CC present sequence is an example of one of these sequences.  
XX  
XX  
SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 16.6%; Score 315; DB 22; Length 369;  
Best Local Similarity 100.0%; Pred. No. 5,7e-117;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 309 CAGGCTTTCGCGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACACGACT 368
DB 30 CAGGCTTTCGCGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACACGACT 89
OY 369 GCTCCTCCCCGAGTTTCATGTGAATGACAGGTGAACCTCAAGATGTGTGCAAG 428
DB 90 GCTCCTCCCCGAGTTTCATGTGAATGACAGGTGAACCTCAAGATGTGTGCAAG 149
OY 429 AAGTGTGAGCAAGAGTCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 488
DB 150 AAGTGTGAGCAAGAGTCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
OY 489 GTCTCATCGCCTTGCGCGGATACAGTCTCTGCTCCCGAGGAACTGAATCAGTTT 548
DB 210 GTCTCATCGCCTTGCGCGGATACAGTCTCTGCTCCCGAGGAACTGAATCAGTTT 269
OY 549 GCATCAGCTGTGCAACACCCCTTTTGTAAAGGCGCAAGGCCCAAGAAAGGGAAGTT 608
DB 270 GCATCAGCTGTGCAACACCCCTTTTGTAAAGGCGCGCAAGGCCCAAGAAAGGGAAGTT 329
OY 609 CTGCCTCGGCGCTCA 623
DB 330 CTGCCTCGGCGCTCA 344
```

## RESULT 27

ABT03274

ID ABT03274 standard; cDNA; 369 BP.

XX ABT03274;

XX 05-SEP-2002 (first entry)

XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 199.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

XX cytoskeletal; gene; ss.

XX Homo sapiens.

XX MO200239885-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US45395.

XX 14-NOV-2000; 2000US-0713550.

XX 03-APR-2001; 2001US-0825294.

XX 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

XX WPI; 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for

XX detecting the presence of ovarian cancer in a patient, and in

XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

XX Example 1; Page 187; 197pp; English.

CC and coding sequences. The sequences can be used in the diagnosis and  
CC treatment of ovarian cancers. The present sequence is a coding sequence  
XX of the invention.

SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 16.6%; Score 315; DB 24; Length 369;  
Best Local Similarity 100.0%; Pred. No. 5,7e-117;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 309 CAGGCTTTCGCGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACACGACT 368
DB 30 CAGGCTTTCGCGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACACGACT 89
OY 369 GCTCCTCCCCGAGTTTCATGTGAATGACAGGTGAACCTCAAGATGTGTGCAAG 428
DB 90 GCTCCTCCCCGAGTTTCATGTGAATGACAGGTGAACCTCAAGATGTGTGCAAG 149
OY 429 AAGTGTGAGCAAGAGTCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 488
DB 150 AAGTGTGAGCAAGAGTCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
OY 489 GTCTCATCGCCTTGCGCGGATACAGTCTCTGCTCCCGAGGAACTGAATCAGTTT 548
DB 210 GTCTCATCGCCTTGCGCGGATACAGTCTCTGCTCCCGAGGAACTGAATCAGTTT 269
OY 549 GCATCAGCTGTGCAACACCCCTTTTGTAAAGGCGCGCAAGGCCCAAGAAAGGGAAGTT 608
DB 270 GCATCAGCTGTGCAACACCCCTTTTGTAAAGGCGCGCGCAAGGCCCAAGAAAGGGAAGTT 329
OY 609 CTGCCTCGGCGCTCA 623
DB 330 CTGCCTCGGCGCTCA 344
```

## RESULT 28

ABL48956

ID ABL48956 standard; cDNA; 369 BP.

XX ABL48956;

XX 18-JUN-2002 (first entry)

XX Ovarian carcinoma sequence isolate 57887.

XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

XX ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

XX 01-MAY-2000; 2000US-0561778.

XX 15-AUG-2000; 2000US-0640173.

XX 07-SEP-2000; 2000US-0656668.

XX 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J,

XX (STOL/) STOLK J A.

XX (ALGA/) ALGATE P A.

XX (FLIN/) FLING S P.

XX Xu J, Stolk JA, Algate PA, Fling SP;

XX WPI; 2002-171027/22.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

XX prevention and/or treatment of cancer, especially ovarian cancer

XX PS Claim 1a; Page 116; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides

CC that may be utilised in cancer therapy, for example in a vaccine or

CC gene therapy. Polypeptides and polynucleotides of the invention are

CC useful for detecting a cancer in a patient, for stimulating and/or

CC expanding T-cells specific for a tumour protein, and for inhibiting the

CC development of a cancer in a patient. They are also useful for

CC stimulating an immune response in a patient, and for treating a cancer in

CC a patient and for determining the presence of a cancer in a patient.

CC The isolated polynucleotides of the invention are useful for their

CC ability to selectively form duplex molecules with complementary stretches

CC of the entire desired gene or gene fragments, and for designing and

CC preparing ribozyme molecules for inhibiting expression of tumour

CC polypeptides in tumour cells. Polypeptides and polynucleotides of the

CC invention are also useful in recombinant DNA molecules to direct

CC expression of a polypeptide in appropriate host cells. The sequences

CC given in records ABL48760-ABL48956 represent polynucleotides encoding

CC ovarian carcinoma proteins.

XX SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other:

Query Match 16.6%; Score 315; DB 24; Length 369;

Best Local Similarity 100.0%; Pred. No. 5.7e-117;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAGGCTTGGCTGCAATCCAGTCTACAGTGAAGAATTCAGCTGAACAACGACT 368

DB 30 CAGGCTTGGCTGCAATCCAGTCTACAGTGAAGAATTCAGCTGAACAACGACT 89

QY 369 GCTCTCCGCCAGTTCATTGTGATTCACAGGTAACAGTTCATGTCAGAAAG 428

DB 90 GCTCTCCGCCAGTTCATTGTGATTCACAGGTAACAGTTCATGTCAGAAAG 149

QY 429 AAGTATGAGCAAGAGTCCGGGATCATGTACCCAGTCTCTGTCATCATCAGCGCT 488

DB 150 AAGTATGAGCAAGAGTCCGGGATCATGTACCCAGTCTCTGTCATCATCAGCGCT 209

QY 489 GTCCTATGCGCTTCGCGGGTACAGTCTCTGTCCTCCCGAGGAAACTGAAGTCT 548

DB 210 GTCCTATGCGCTTCGCGGGTACAGTCTCTGTCCTCCCGAGGAAACTGAAGTCT 269

QY 549 GCATCAGCTGTGTCAACACCCCTTTTGAACGGGCAAGGCCCAAGAAAGGGGAAGTT 608

DB 270 GCATCAGCTGTGTCAACACCCCTTTTGAACGGGCAAGGCCCAAGAAAGGGGAAGTT 329

QY 609 CTGCTCGGCGCTCA 623

DB 330 CTGCTCGGCGCTCA 344

RESULT 29

ABL78538/c

ID ABL78538 standard; cDNA; 373 BP.

XX ABL78538;

DT 17-MAY-2002 (first entry)

XX Human ovarian cancer related CDNA clone SEQ ID NO:1516.

XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

XX WO200192581-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US17756.

XX 26-MAY-2000; 2000US-207484P.

XX PA (CORI-) CORIXA CORP.

XX PI Algate PA, Harlocker SL, Jones R;

XX WI; 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide

XX Claim 1; SEQ ID 1516; 489pp; English.

CC The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of a ovarian tumour

CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence

CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to

CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell

CC population of (II), or antigen presenting cells that express (II).

CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to

CC (S1) can be used for detecting ovarian cancer in a patient's biological

CC sample preferably serum or ovarian tissue. The method comprises

CC contacting a biological sample from a patient with (IV), detecting the

CC amount of polynucleotide hybridising to (IV) and comparing the amount to

CC a predetermined cutoff value and thereby detecting ovarian cancer in the

CC patient, where the amount of polynucleotide hybridising to (IV) is

CC detected preferably by polymerase chain reaction (PCR). (I) comprising

CC (III) and/or (II) is useful for stimulating and/or expanding T cells

CC specific for an ovarian tumour protein comprising contacting T cells

CC with (III) or (II). (III) is useful in design and preparation of

CC ribozyme molecules for inhibiting expression of the tumour polypeptides

CC and proteins in tumour cells; and to isolate a full length gene from a

CC suitable library e.g., a tumour cDNA library using well known

CC techniques.

XX SQ Sequence 373 BP; 83 A; 96 C; 80 G; 114 T; 0 other:

Query Match 16.6%; Score 315; DB 24; Length 373;

Best Local Similarity 100.0%; Pred. No. 5.7e-117;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1563 GCCGACCATGATCTCGAATCTGTTGGCATCCAGTACGGCCATGTCAACA 1622

DB 315 GCCGACCATGATCTCGAATCTGTTGGCATCCAGTACGGCCATGTCAACA 256

QY 1623 ATCAGCCCTGGGACAGACAGAGGAGAGACAGACAGAAAAACACAGCATGA 1682

DB 255 ATCAGCCCTGGGACAGACAGAGGAGAGACAGACAGAAAAACACAGCATGA 196

QY 1683 GAACACAGTAATGAATGAACATTAATATTTAGCCCTCTGTTCTGCTTACTGGC 1742

DB 195 GAACACAGTAATGAATGAACATTAATATTTAGCCCTCTGTTCTGCTTACTGGC 136

QY 1743 CAGGAATGGTACCAATTTTCACTGTGACCTTCTTTTCCACAGCAAGA 1802

DB 135 CAGGAATGGTACCAATTTTCACTGTGACCTTCTTTTCCACAGCAAGA 76

QY 1803 GAGAAATTAACATGTTCAACCCGGGAGTGGCTGTTAAAGAAAGACATTAA 1862

DB 75 GAGAAATTAACATGTTCAACCCGGGAGTGGCTGTTAAAGAAAGACATTAA 16

QY 1863 TGCTTTAGACAGTGT 1877

DB 15 TGCTTTAGACAGTGT 1

RESULT 30

ABL79431/c

ID ABL79431 standard; cDNA; 349 BP.

XX ABL79431;

DT 17-MAY-2002 (first entry)  
XX Human ovarian cancer related cDNA clone SEQ ID NO:2409.  
DE Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
XX Homo sapiens.  
OS WO200192581-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 29-MAY-2001; 2001WO-US17756.  
XX  
XX 26-MAY-2000; 2000US-207484P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Algate PA, Harlocker SL, Jones R;  
XX WPI: 2002-122075/16.  
XX  
XX Composition for therapy and diagnosis of ovarian cancer comprising  
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
PT polypeptide, antibody specific to polypeptide or T cell expressing  
PT polypeptide  
XX  
XX Claim 1: SEQ ID 2409; 489pp; English.  
XX  
XX The present invention describes a composition (I) comprising: carriers  
CC and immunostimulants; and a polypeptide (II) of a ovarian tumor  
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
CC (SI) from the 10912 nucleotide sequences as given in ABL77023 to  
CC ABL87934, (II) encoding (II) having a sequence (S2), a T cell  
CC population of (II), or antigen presenting cells that express (II).  
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridizes to  
CC (SI) can be used for detecting ovarian cancer in a patient's biological  
CC sample preferably serum or ovarian tissue. The method comprises  
CC contacting a biological sample from a patient with (IV), detecting the  
CC amount of polynucleotide hybridizing to (IV) and comparing the amount to  
CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
CC patient, where the amount of polynucleotide hybridizing to (IV) is  
CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
CC specific for an ovarian tumor protein comprising contacting T cells  
CC with (III) or (II). (III) is useful in design and preparation of  
CC ribozyme molecules for inhibiting expression of the tumor polypeptides  
CC and proteins in tumor cells; and to isolate a full length gene from a  
CC suitable library e.g., a tumor cDNA library using well known  
CC techniques.  
XX  
XX Sequence 349 BP; 79 A; 84 C; 78 G; 108 T; 0 other;  
SQ  
Query Match 16.2%; Score 307; DB 24; Length 349;  
Best Local Similarity 100.0%; Pred. No. 9.5e-114;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1810 TAACAGTGTTCACAAACCGGGGAGTGGCTGTGTTAAGAAACCATTAATGCTTTA 1869  
DB 70 TAACAGTGTTCACAAACCGGGGAGTGGCTGTGTTAAGAAACCATTAATGCTTTA 11  
QY 1870 GACAGCTG 1876  
DB 10 GACAGCTG 4  
RESULT 31  
ABT03282  
ID ABT03282 standard; cDNA; 1010 BP.  
XX  
AC ABT03282;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 212.  
XX  
XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
XX cytostatic; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200239885-A2.  
XX  
XX 23-MAY-2002.  
XX  
XX 13-NOV-2001; 2001WO-US45395.  
XX  
XX 14-NOV-2000; 2000US-0713550.  
XX  
XX 03-APR-2001; 2001US-0825294.  
XX  
XX 02-OCT-2001; 2001US-0970966.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;  
XX WPI: 2002-500186/53.  
XX  
XX Novel ovarian cancer polypeptide and polynucleotide, useful for  
XX detecting the presence of ovarian cancer in a patient, and in  
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
XX  
XX Claim 2: Page 195; 197pp; English.  
XX  
XX The present invention provides human ovarian cancer associated proteins  
XX and coding sequences. The sequences can be used in the diagnosis and  
XX treatment of ovarian cancers. The present sequence is a coding sequence  
XX of the invention.  
XX  
XX Sequence 1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;  
SQ  
Query Match 14.3%; Score 271; DB 24; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 2.5e-99;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



CC suitable library e.g., a tumour cDNA library using well known  
CC techniques.  
XX

Sequence 409 BP; 89 A; 106 C; 87 G; 127 T; 0 other;

Query Match 13.9%; Score 264; DB 24; Length 409;  
Best Local Similarity 99.7%; Pred. No. 1.8e-96;  
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1563 GCCGACGATGATCTCCGAAATCTGTTGGGATCCAGCATACGGCCAAATGACACACA 1622  
|||||  
315 GCCGACGATGATCTCCGAAATCTGTTGGGATCCAGCATACGGCCAAATGACACACA 256  
1623 ATCAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1682  
|||||  
255 ATCAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196  
1683 GAACACAGTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1742  
|||||  
195 GAACACAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 136  
1743 CAGGAATGATGATCAATTTTTCAGTGTGAGCTTGCAGCTTCTTTTGCACAGACAGA 1802  
|||||  
135 CAGGAATGATGATCAATTTTTCAGTGTGAGCTTGCAGCTTCTTTTGCACAGACAGA 76  
1803 GAGCAATTTAACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTA 1862  
|||||  
75 GAGCAATTTAACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTA 16  
1863 TGCTTAGACAGTGT 1877  
|||||  
15 TGCTTAGACAGTGT 1

RESULT 34  
ABL75916/c  
ID ABL75916 standard; cDNA; 201 BP.

17-MAY-2002 (first entry)

Human ovarian cancer related cDNA clone SEQ ID NO:8894.

Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

Homo sapiens.

WO200192581-A2.

06-DEC-2001.

29-MAY-2001; 2001WO-US17756.

26-MAY-2000; 2000US-207484P.

(CORI-) CORIXA CORP.

Algate PA, Harlocker SL, Jones R;

WPI; 2002-122075/16.

Composition for therapy and diagnosis of ovarian cancer comprising  
polypeptide of a ovarian tumor polyepptide, polynucleotide encoding  
polypeptide, antibody specific to polyepptide or T cell expressing  
polypeptide

Claim 1; SEQ ID 8894; 489pp; English.

The present invention describes a composition (I) comprising: carriers  
and immunostimulants; and a polyepptide (II) of a ovarian tumour  
cDNA polyepptide encoded by a polynucleotide (III) having a cDNA sequence  
(SI) from the 10912 nucleotide sequences as given in ABL77023 to

CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
CC population of (II), or antigen presenting cells that express (II).  
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
CC (SI) can be used for detecting ovarian cancer in a patient's biological  
CC sample preferably serum or ovarian tissue. The method comprises  
CC contacting a biological sample from a patient with (IV), detecting the  
CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
CC patient, where the amount of polynucleotide hybridising to (IV) is  
CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
CC specific for an ovarian tumour protein comprising contacting T cells  
CC with (III) or (II). (III) is useful in design and preparation of  
CC ribozyme molecules for inhibiting expression of the tumour polyepptides  
CC and proteins in tumour cells; and to isolate a full length gene from a  
CC suitable library e.g., a tumour cDNA library using well known  
CC techniques.

Sequence 201 BP; 28 A; 61 C; 46 G; 66 T; 0 other;

Query Match 8.8%; Score 166; DB 24; Length 201;  
Best Local Similarity 100.0%; Pred. No. 5e-57;  
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1501 AGAAGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
|||||  
181 AGAAGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 122  
1561 TGCGCCGACGATGATCTCCGAAATCTGTTGGGATCCAGCATACGGCCAAATGTCACA 1620  
|||||  
121 TGCGCCGACGATGATCTCCGAAATCTGTTGGGATCCAGCATACGGCCAAATGTCACA 62  
1621 CAATCAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1666  
|||||  
61 CAATCAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 16

RESULT 35  
ABL78554  
ID ABL78554 standard; cDNA; 390 BP.

17-MAY-2002 (first entry)

Human ovarian cancer related cDNA clone SEQ ID NO:1532.

Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

Homo sapiens.

WO200192581-A2.

06-DEC-2001.

29-MAY-2001; 2001WO-US17756.

26-MAY-2000; 2000US-207484P.

(CORI-) CORIXA CORP.

Algate PA, Harlocker SL, Jones R;

WPI; 2002-122075/16.

Composition for therapy and diagnosis of ovarian cancer comprising  
polypeptide of a ovarian tumor polyepptide, polynucleotide encoding  
polypeptide, antibody specific to polyepptide or T cell expressing  
polypeptide

Claim 1; SEQ ID 1532; 489pp; English.

The present invention describes a composition (I) comprising: carriers



PT polypeptide, antibody specific to polypeptide or T cell expressing  
PT polypeptide -  
PS Claim 1; SEQ ID 4251; 489pp; English.  
XX  
XX  
The present invention describes a composition (I) comprising: carriers  
CC and immunostimulants; and a polypeptide (II) of an ovarian tumour  
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
CC population of (II), or antigen presenting cells that express (II).  
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
CC (S1) can be used for detecting ovarian cancer in a patient's biological  
CC sample preferably serum or ovarian tissue. The method comprises  
CC contacting a biological sample from a patient with (IV), detecting the  
CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
CC patient, where the amount of polynucleotide hybridising to (IV) is  
CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
CC specific for an ovarian tumour protein comprising contacting T cells  
CC with (III) or (II). (II) is useful in design and preparation of  
CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
CC and proteins in tumour cells; and to isolate a full length gene from a  
CC suitable library e.g., a tumour cDNA library using well known  
CC techniques.  
XX  
SQ Sequence 430 BP; 92 A; 121 C; 108 G; 109 T; 0 other;  
XX  
Query Match 6.3%; Score 120; DB 24; Length 430;  
Best Local Similarity 100.0%; Pred. No. 1.4e-38;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 710 CTGATGTTGTTCTTCACGACCCGCCCCCAACCCACCTCCCTGAGTGTCTTCTG 769  
DB 182 CTGATGTTGTTCTTCACGACCCGCCCCCAACCCACCTCCCTGAGTGTCTTCTG 241  
OY 770 GGTGTCCTTTTATTCCTGGGTAGGAGCGGAGTCCGTCTCTTTTGTCTTGCAAA 829  
DB 242 GGTGTCCTTTTATTCCTGGGTAGGAGCGGAGTCCGTCTCTTTTGTCTTGCAAA 301  
RESULT 38  
ABL79397  
ID ABL79397 standard; cDNA; 558 BP.  
XX  
XX ABL79397;  
AC  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human ovarian cancer related cDNA clone SEQ ID NO:2375.  
XX  
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192581-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 29-MAY-2001; 2001WO-US17756.  
XX  
XX 26-MAY-2000; 2000US-207484P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Algate PA, Harlocker SL, Jones R;  
XX  
XX WPI: 2002-122075/16.  
XX  
XX Composition for therapy and diagnosis of ovarian cancer comprising  
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide -  
XX  
XX  
PS Claim 1; SEQ ID 2375; 489pp; English.  
XX  
XX  
The present invention describes a composition (I) comprising: carriers  
CC and immunostimulants; and a polypeptide (II) of an ovarian tumour  
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
CC population of (II), or antigen presenting cells that express (II).  
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
CC (S1) can be used for detecting ovarian cancer in a patient's biological  
CC sample preferably serum or ovarian tissue. The method comprises  
CC contacting a biological sample from a patient with (IV), detecting the  
CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
CC patient, where the amount of polynucleotide hybridising to (IV) is  
CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
CC specific for an ovarian tumour protein comprising contacting T cells  
CC with (III) or (II). (III) is useful in design and preparation of  
CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
CC and proteins in tumour cells; and to isolate a full length gene from a  
CC suitable library e.g., a tumour cDNA library using well known  
CC techniques.  
XX  
SQ Sequence 558 BP; 147 A; 133 C; 166 G; 106 T; 6 other;  
XX  
Query Match 6.3%; Score 120; DB 24; Length 558;  
Best Local Similarity 100.0%; Pred. No. 1.4e-38;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1408 ACAGACCTGACGACAAACCCGCGGAAACCTGCTCGAGACACCGTGTACAGAGCGGGT 1467  
DB 134 ACAGACCTGACGACAAACCCGCGGAAACCTGCTCGAGACACCGTGTACAGAGCGGGT 193  
OY 1468 TGATGACCGAGCTGAGTAGAAGAAACGCTCTCGAAGAGGAGGAGATCATGTACGCC 1527  
DB 194 TGATGACCGAGCTGAGTAGAAGAAACGCTCTCGAAGAGGAGGAGATCATGTACGCC 253  
RESULT 39  
ABN41977/c  
ID ABN41977 standard; DNA; 60 BP.  
XX  
XX  
XX ABN41977;  
AC  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:14725.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
XX  
XX splice variant; transcriptome; oligonucleotide library; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200210449-A2.  
XX  
XX 07-FEB-2002.  
XX  
XX 20-JUL-2001; 2001WO-IB01903.  
XX  
XX 28-JUL-2000; 2000US-221607P.  
XX  
XX 02-MAY-2001; 2001US-287724P.  
XX  
XX (COMP-) COMPUGEN INC.  
XX  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
XX WPI: 2002-257383/30.  
XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of

PT a genome, useful for detecting tissue-, pathology-, and  
 PT developmental-specific genes -

XX Example 1; SEQ ID 14725; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridizing selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.  
 CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition; to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN27253 to ABN29589 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 60 BP; 17 A; 17 C; 15 G; 11 T; 0 other;

Query Match 3.2%; Score 60; DB 24; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-14;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1143 AACCATCTCTGCACAGAAATGCTGCTTCGCGCCCTGAGTGGCTCTAGTACTCG 1202  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 60 AACCATCTCTGCACAGAAATGCTGCTTCGCGCCCTGAGTGGCTCTAGTACTCG 1

RESULT 40  
 AAS60824

ID AAS60824 standard; cDNA; 1368 BP.

XX AAS60824;

XX 29-JAN-2002 (first entry)

XX Human cancer agent-sensitive marker #326.

XX Human cancer cell marker; TAXOL; cyrostatic; tumour; carcinoma;

XX squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;

XX lymphocytic leukaemia; lymphoma; plasmocytoma; reticulium cell sarcoma;

XX Hodgkin's disease; glioma; ss.

XX Homo sapiens.

XX WO200179556-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US12132.

XX 14-APR-2000; 2000US-197538P.

XX (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lillie J, Brown JL, Bolt A, Van Huffel C;

XX WPI: 2001-602933/68.

XX Novel nucleic acid, used as a marker to determine the effectiveness of

PT using TAXOL to treat cancer cell growth in individuals -

XX Claim 1; Page 339-340; 527pp; English.

XX The invention relates to 1046 novel nucleic acids which are used as  
 CC markers for determining the sensitivity of a cancer cell to the  
 CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when  
 CC they are shown to express one of the 242 sensitivity markers or the  
 CC cells are shown not to express one of the 804 resistance markers.  
 CC The methods can be used to determine the effectiveness of TAXOL  
 CC in the treatment of cancer cell growth in an individual. The markers  
 CC can be used as targets in developing anti-cancer agents such as  
 CC chemotherapeutic compounds. The markers can also be used as targets in  
 CC displaying treatments for cancer, particularly those cancers which  
 CC display resistance to agents and exhibit expression of the markers. The  
 CC anticancer agents developed by the novel method can be used to treat  
 CC cancer. Probes based on the markers can be used to detect transcripts or  
 CC genomic sequences corresponding to the markers. In the identification of  
 CC cells or tissues which mis-express the protein. Cancers which may  
 CC be targeted include carcinoma (e.g. squamous cell carcinoma),  
 CC sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia),  
 CC lymphoma, plasmocytoma, reticulium cell sarcoma, Hodgkin's disease and  
 CC tumours (e.g. glioma). The present sequence is one of the 1046  
 CC novel cancer cell markers.

XX Sequence 1368 BP; 517 A; 312 C; 321 G; 213 T; 5 other;

Query Match 1.4%; Score 27; DB 22; Length 1368;  
 Best Local Similarity 100.0%; Pred. No. 0.3;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 AACTGTAAATAAAAAAAAAAAAAAAAAA 1897  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 459 AACTGTAAATAAAAAAAAAAAAAAAAAA 485

RESULT 41  
 AAL33984/C

ID AAL33984 standard; DNA; 50 BP.

XX AAL33984;

XX 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #7192.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cyrostatic;

XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;

XX amyloid protein; angiotensin; apoptosis related protein; cadherin;

XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

XX complement related protein; cytochrome; kinase; cytokine; interferon;

XX interleukin; G-protein coupled receptor; thioesterase; inflammation;

XX multifactorial disease; autoimmune disease; infection;

XX nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,



PT Oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
XX Claim 1, Page 3450; 4143pp; English.  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 50 BP; 11 A; 16 C; 10 G; 13 T; 0 other;  
Query Match 1.4%; Score 26; DB 22; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1212 GACTGGAGCTAGACTGGGCTCGGC 1237  
DB 50 GACTGGAGCTAGACTGGGCTCGGC 25  
RESULT 42  
ID AAL33985/C  
XX AAL33985 standard; DNA; 50 BP.  
AC AAL33985;  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #7193.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinase; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US35498.  
XX  
PR 28-DEC-1999; 99US-0173419.  
XX 27-DEC-2000; 2000US-0173419.  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI; 2001-465210/50.  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
XX Claim 1, Page 3451; 4143pp; English.

PS Claim 1, Page 3451; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 50 BP; 14 A; 13 C; 17 G; 6 T; 0 other;  
Query Match 1.4%; Score 26; DB 22; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1563 GCCCGAGCCATGATCCCTCGAATCG 1588  
DB 26 GCCCGAGCCATGATCCCTCGAATCG 1  
RESULT 43  
ID AAL33986/C  
XX AAL33986 standard; DNA; 50 BP.  
AC AAL33986;  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #7194.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinase; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US35498.  
XX  
PR 28-DEC-1999; 99US-0173419.  
XX 27-DEC-2000; 2000US-0173419.  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI; 2001-465210/50.  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
XX Claim 1, Page 3451; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic

CC variants of proteins related to amylases, amyloid proteins, angiotensin, CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, CC histones, kinases, colony stimulating factors, complement related CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, CC G-protein coupled receptors and thioesterases. The present sequence is CC one such oligonucleotide. The oligonucleotides and the peptides encoded CC by them may be used in the prevention, diagnosis and treatment of CC diseases associated with inappropriate expression of the proteins listed CC above. Disorders that may be prevented, diagnosed and/or treated include CC multifactorial diseases with a genetic component, such as autoimmune CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, CC systemic lupus erythematosus and Grave's disease), inflammation, cancer CC (e.g. cancers of the bladder, brain, breast, colon and kidney, CC leukemias), diseases of the nervous system and an infection of pathogenic CC organisms.

XX Sequence 50 BP; 14 A; 12 C; 17 G; 7 T; 0 other;

Query Match 1.4%; Score 26; DB 22; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1537 ACCTGCTCAGTCTGCTGGGTTTG 1562  
DB 50 ACCTGCTCAGTCTGCTGGGTTTG 25  
|||||

RESULT 44  
AAC84571  
ID AAC84571 standard; cDNA: 2481 BP.  
XX AAC84571:  
XX 02-APR-2001 (first entry)  
XX Soybean magnesium chelatase subunit cDNA (clone sd4c.pk022.h18[RTS]).  
XX Magnesium chelatase; transgenic; herbicide; gene marker; plant breeding;  
XX soybean; ss.  
XX Glycine max.  
XX OS  
XX FH Key Location/Qualifiers  
XX FT CDS 9..2261  
XX FT /\*tag= a  
XX FN WO200075340-A2.  
XX PD 14-DEC-2000.  
XX PF 02-JUN-2000; 2000WO-US15351.  
XX PR 04-JUN-1999; 99US-0137461.  
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX PI Butler KH, Famodu OO, Gutteridge S, Maxwell CA;  
XX DR WPI: 2001-091215/10.  
XX DR P-PSDB: AAB48252.  
XX PT Isolated nucleic acid fragments encoding magnesium chelatase subunits,  
XX useful as probes for genetic and physical mapping of genes, as markers  
XX for traits linked to these genes, and in plant breeding -  
XX Claim 2; Page 59-60; 103pp; English.

XX The invention relates to nucleic acid fragments encoding magnesium  
XX chelatase subunits. The nucleic acid fragments may be used to create  
XX transgenic plants in which the new polypeptides are present at higher or  
XX lower levels than normal or in cell types or developmental stages in  
XX which they are not normally found, and for overexpression in bacterial  
XX or yeast hosts to efficiently produce large amounts of the encoded

CC polypeptides which could then be used for screening different compounds  
CC for potential herbicidal activity. The polynucleotides may also be used  
CC as probes for genetic and physical mapping the genes that they are part  
CC of, and as markers for traits linked to these genes. Such information  
CC is useful in plant breeding. The polypeptides are used for preparing  
CC antibodies, which are useful for detecting the polypeptides in situ or  
CC in vitro, and as a target to facilitate design and/or identification of  
CC inhibitors of enzymes that may be used as herbicides. Host cells may also  
CC be used directly for screening different compounds for potential  
CC herbicidal activity. The present sequence represents the soybean  
CC magnesium chelatase subunit encoding cDNA.

XX Sequence 2481 BP; 783 A; 489 C; 589 G; 620 T; 0 other;

Query Match 1.4%; Score 26; DB 22; Length 2481;  
Best Local Similarity 100.0%; Pred. No. 0.7;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1872 CAGTGTAAAAA 1897  
DB 2424 CAGTGTAAAAA 2449  
|||||

RESULT 45  
AAL27277/C  
ID AAL27277 standard; DNA: 51 BP.  
XX AAL27277:  
XX 24-JAN-2002 (first entry)  
XX Human SNP oligonucleotide #485.  
XX DE  
XX XX  
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX complement related protein; cytochrome; kinesin; cytokine; interferon;  
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX multifactorial disease; autoimmune disease; infection;  
XX nervous system disease; ss.  
XX KW  
XX OS Homo sapiens.  
XX FH WO200147944-A2.  
XX FT 05-JUL-2001.  
XX PD 28-DEC-2000; 2000WO-US35498.  
XX PF 28-DEC-1999; 99US-0173419.  
XX PR 27-DEC-2000; 2000US-0173419.  
XX PA (CURA-) CURAGEN CORP.  
XX PI Shimkets RA, Leach M;  
XX DR WPI: 2001-465210/50.  
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -  
XX Claim 1; Page 1529; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
XX variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
XX histones, kinases, colony stimulating factors, complement related  
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
XX G-protein coupled receptors and thioesterases. The present sequence is  
XX one such oligonucleotide. The oligonucleotides and the peptides encoded  
XX by them may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.

XX  
 SQ Sequence 51 BP; 9 A; 5 C; 10 G; 27 T; 0 other;

Query Match 1.3%; Score 25; DB 22; Length 51;  
 Best Local Similarity 100.0%; Pred No. 2.9;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1671 AACACAGCATGAGAACACAGTAAT 1695  
 |||||||||||||||||||||

DB 51 AACACAGCATGAGAACACAGTAAT 27

Search completed: November 7, 2002, 18:16:25  
 Job time : 399.511 secs

430

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:00:33 ; Search time 71.0849 Seconds  
(without alignments)  
8184.096 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897

Sequence: 1 gccaaactccgagagctctg.....aaaaaaaaaaaaaaaa 1897

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size: 10

Total number of hits satisfying chosen parameters: 162838

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Issued Patents.NA:  
1: /cgn2\_6/ptodata/1/lna/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PCRTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	1.3	967 3	US-09-248-335-59
2	24	1.3	1046 4	US-09-068-140A-5
3	24	1.3	1522 4	US-09-413-574-1
4	24	1.3	2671 6	5168051-9
5	24	1.3	3073 1	US-07-688-352C-31
6	24	1.3	3073 2	US-08-474-379C-31
7	24	1.3	3073 3	US-09-146-249A-31
8	24	1.3	3073 4	US-08-206-188B-31
9	24	1.3	3073 5	PCT-US91-02714-30
10	24	1.3	3375 4	US-09-511-625B-67
11	24	1.3	4184 2	US-08-785-310A-4
12	24	1.3	176373 3	US-09-128-155-17
13	23	1.2	40 4	US-09-306-290-16
14	23	1.2	40 4	US-08-171-385-22
15	23	1.2	321 1	US-08-361-441B-22
16	23	1.2	340 1	US-08-171-385-27
17	23	1.2	340 1	US-08-361-441B-27
18	23	1.2	340 1	US-08-171-385-20
19	23	1.2	345 3	US-08-361-441B-20
20	23	1.2	347 1	US-08-104-072B-2
21	23	1.2	350 1	US-08-171-385-14
22	23	1.2	350 3	US-08-361-441B-14
23	23	1.2	393 4	US-09-605-785-357
24	23	1.2	393 4	US-09-439-313-357
25	23	1.2	393 4	US-09-352-616A-357
26	23	1.2	413 2	US-09-014-969-5
27	23	1.2	413 2	US-09-014-969-5

c 28	23	1.2	436 4	US-09-605-785-353	Sequence 353, App
c 29	23	1.2	436 4	US-09-439-313-353	Sequence 353, App
c 30	23	1.2	436 4	US-09-352-616A-353	Sequence 353, App
c 31	23	1.2	442 4	US-09-372-422A-75	Sequence 29, App
c 32	23	1.2	502 4	US-08-842-445-29	Sequence 29, App
c 33	23	1.2	502 4	US-08-842-445-29	Sequence 29, App
c 34	23	1.2	502 4	US-08-842-445-29	Sequence 29, App
c 35	23	1.2	530 1	US-08-462-894-5	Sequence 5, App
c 36	23	1.2	530 1	US-08-206-185-5	Sequence 5, App
c 37	23	1.2	588 4	US-09-433-248A-7	Sequence 7, App
c 38	23	1.2	593 4	US-09-385-982-262	Sequence 7, App
c 39	23	1.2	752 6	5212073-1	Sequence 262, App
c 40	23	1.2	772 4	US-09-575-602-1	Sequence 1, App
c 41	23	1.2	933 1	US-08-032-393-5	Sequence 1, App
c 42	23	1.2	1008 1	US-08-252-966B-15	Sequence 5, App
c 43	23	1.2	1162 4	US-09-173-300-21	Sequence 15, App
c 44	23	1.2	1174 1	US-07-869-933-10	Sequence 21, App
c 45	23	1.2	1174 4	US-09-103-663-10	Sequence 10, App

## ALIGNMENTS

RESULT 1  
US-09-248-335-59  
Sequence 59, Application US/09248335  
Patent No. 6096504  
GENERAL INFORMATION:  
APPLICANT: MCGONIGLE, BRIAN  
APPLICANT: O'KEEF, DANIEL  
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
FILE REFERENCE: CL-1128-A  
CURRENT APPLICATION NUMBER: US/09/248, 335  
CURRENT FILING DATE: 1999-02-10  
EARLIER APPLICATION NUMBER: 08/924, 759  
EARLIER FILING DATE: 1997-September-05  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: Microsoft Word Version 7.0A  
SEQ ID NO 59  
LENGTH: 967  
TYPE: DNA  
ORGANISM: maize  
US-09-248-335-59

Query Match 1.3%; Score 24; DB 3; Length 967;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897  
Db 943 GTGTAAAAAAAAAAAAAAAAAAAA 966

RESULT 2  
US-09-068-140A-5  
Sequence 5, Application US/09068140A  
Patent No. 6281409  
GENERAL INFORMATION:  
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor  
APPLICANT: and Rex Michael Brennan  
TITLE OF INVENTION: Blackcurrant Promoters and Genes  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/068,140A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCP/EP96/04807  
FILING DATE: NO.6281409ember 4, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Diner, Dara L.  
REGISTRATION NUMBER: 33,680  
REFERENCE/DOCKET NUMBER: C70237  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5017  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1046 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Ribes nigrum  
STRAIN: Ben Alder  
US-09-068-140A-5  
Query Match 1.3%; Score 24; DB 4; Length 1046;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1874 GTGTAAGAAAAAAGAAAAA 1897  
|||||  
Db 1015 GTGTAAGAAAAAAGAAAAA 1038  
RESULT 3  
US-09-413-574-1  
Sequence 1, Application US/09413574  
Patent No. 6235972  
GENERAL INFORMATION:  
APPLICANT: Mahajan, Pramod B.  
TITLE OF INVENTION: Maize Rad23 Genes and Uses Thereof  
FILE REFERENCE: 0964  
CURRENT APPLICATION NUMBER: US/09/413,574  
CURRENT FILING DATE: 1999-10-06  
EARLIER APPLICATION NUMBER: 60/109,728  
EARLIER FILING DATE: 1998-11-23  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 1522  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (58)...(1272)  
US-09-413-574-1  
Query Match 1.3%; Score 24; DB 4; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1874 GTGTAAGAAAAAAGAAAAA 1897  
|||||  
Db 1456 GTGTAAGAAAAAAGAAAAA 1479  
RESULT 4

5168051-9  
Patent No. 5168051  
APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/389,929  
FILING DATE: 04-AUG-1989  
SEQ ID NO:9  
LENGTH: 2671  
5168051-9  
Query Match 1.3%; Score 24; DB 6; Length 2671;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1874 GTGTAAGAAAAAAGAAAAA 1897  
|||||  
Db 2577 GTGTAAGAAAAAAGAAAAA 2600  
RESULT 5  
US-07-688-352C-31  
Sequence 31, Application US/07688352C  
Patent No. 5527896  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/688,352C  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25447  
REFERENCE/DOCKET NUMBER: 27805/30197  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3073 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1111  
US-07-688-352C-31  
Query Match 1.3%; Score 24; DB 1; Length 3073;

Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897  
DB 1520 GTGTAACAAAAA 1543

## RESULT 6

US-08-474-379C-31  
; Sequence 31, Application US/08474379C  
; Patent No. 5977305  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED  
; TITLE OF INVENTION: PROCESSES  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,379C  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/206,188  
; FILING DATE: 01-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,352  
; FILING DATE: 19-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 27866/32771  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3073 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1109  
; US-08-474-379C-31

Query Match 1.3%; Score 24; DB 2; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897  
DB 1520 GTGTAACAAAAA 1543

## RESULT 7

US-09-146-249A-31

; Sequence 31, Application US/09146249A  
; Patent No. 6069240  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: Cloning by Complementation and Related  
; TITLE OF INVENTION: Processes  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/146,249A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,715  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3073 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1111  
; US-09-146-249A-31

Query Match 1.3%; Score 24; DB 3; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897  
DB 1520 GTGTAACAAAAA 1543

## RESULT 8

US-08-206-188B-31  
; Sequence 31, Application US/08206188B  
; Patent No. 6100025  
; GENERAL INFORMATION:  
; APPLICANT: Wigler, Michael H.  
; APPLICANT: Colicelli, John J.  
; TITLE OF INVENTION: Cloning by Complementation and Related  
; TITLE OF INVENTION: Processes  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:

Query Match 1.3%; Score 24; DB 3; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/206.1888  
FILING DATE: 01-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3073 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1111  
US-08-206-188B-31

Query Match 1.3%; Score 24; DB 3; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1874 GTGTAATAAAAAAAAAAAAAA 1897  
|||||  
DB 1520 GTGTAATAAAAAAAAAAAAAA 1543

RESULT 9  
PCT-US91-02714-30  
Sequence 30, Application PC/TUS9102714  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning By Complementation and Related  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
STREET: Two First National Plaza, 20 South Clark  
Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02714  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25447  
REFERENCE/DOCKET NUMBER: 27805/30197

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3073 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1111  
PCT-US91-02714-30

Query Match 1.3%; Score 24; DB 5; Length 3073;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1874 GTGTAATAAAAAAAAAAAAAA 1897  
|||||  
DB 1520 GTGTAATAAAAAAAAAAAAAA 1543

RESULT 10  
US-09-511-625B-67  
Sequence 67, Application US/09511625B  
Patent No. 6368828  
GENERAL INFORMATION:  
APPLICANT: Larocheille, William J.  
APPLICANT: Patel, Bhavin  
APPLICANT: Pierce, Jacalyn H.  
TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVEVARIANT  
TITLE OF INVENTION: CDNAS OF STAT6: STAT6b AND STAT6c  
FILE REFERENCE: 14014.0300u1  
CURRENT APPLICATION NUMBER: US/09/511,625B  
CURRENT FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: PCT/US98/17821  
PRIOR FILING DATE: 1998-08-27  
PRIOR APPLICATION NUMBER: 60/070,397  
PRIOR FILING DATE: 1998-01-05  
PRIOR APPLICATION NUMBER: 60/056,075  
PRIOR FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 67  
LENGTH: 3375  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial Sequence: /No. 6368828e -  
OTHER INFORMATION: synthetic construct  
NAME/KEY: CDS  
LOCATION: (115)...(2655)  
US-09-511-625B-67

Query Match 1.3%; Score 24; DB 4; Length 3375;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1874 GTGTAATAAAAAAAAAAAAAA 1897  
|||||  
DB 3321 GTGTAATAAAAAAAAAAAAAA 3344

RESULT 11  
US-08-785-310A-4  
Sequence 4, Application US/08785310A  
Patent No. 5840532  
GENERAL INFORMATION:  
APPLICANT: McKnight, Steven L.  
APPLICANT: Russell, David W.



```

; TITLE OF INVENTION: Neuronal PAS Domain Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,310A
; FILING DATE: 21-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UTSD:1226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4184 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-785-310A-4

Query Match
Best Local Similarity 1.3%; Score 24; DB 2; Length 4184;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897
Db 4138 GTGTAACAAAAA 4161

RESULT 12
US-09-128-155-17/c
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
; US-09-128-155-17

Query Match
Best Local Similarity 1.3%; Score 24; DB 3; Length 176373;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1874 GTGTAACAAAAA 1897
Db 68491 GTGTAACAAAAA 68468

RESULT 13
US-09-306-290-11/c
; Sequence 11, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
; APPLICANT: Rovera, Giovanni
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/306,290
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer RCP
; US-09-306-290-11

Query Match
Best Local Similarity 1.2%; Score 23; DB 4; Length 40;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
Db 23 TGTAAAAA 1

RESULT 14
US-09-306-290-16/c
; Sequence 16, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
; APPLICANT: Rovera, Giovanni
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/306,290
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PrimerRCP
; US-09-306-290-16

Query Match
Best Local Similarity 1.2%; Score 23; DB 4; Length 40;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1875 TGTAAAAA 1897
Db 23 TGTAAAAA 1

RESULT 15
US-08-171-385-22/c
; Sequence 22, Application US/08171385
```

Patent No. 5527884  
GENERAL INFORMATION:  
APPLICANT: Mary E. Russell  
TITLE OF INVENTION: Mediators of Chronic Allograft  
TITLE OF INVENTION: Rejection  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171,385  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/006001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-171-385-22  
Query Match 1.2%; Score 23; DB 1; Length 321;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
DB 24 TGTAAAAAAAAAAAAAAAAAAAA 2  
RESULT 16  
US-08-361-441B-22/C  
Sequence 22, Application US/08361441B  
GENERAL INFORMATION:  
PATENT No. 6077948  
APPLICANT: Russell, Mary E.  
APPLICANT: Utans, Ulrike  
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/361,441B  
FILING DATE: 21-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/171,385  
FILING DATE: 21-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-361-441B-22  
Query Match 1.2%; Score 23; DB 3; Length 321;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
DB 24 TGTAAAAAAAAAAAAAAAAAAAA 2  
RESULT 17  
US-08-171-385-27/C  
Sequence 27, Application US/08171385  
PATENT No. 5527884  
GENERAL INFORMATION:  
APPLICANT: Mary E. Russell  
APPLICANT: Ulrike Utans  
TITLE OF INVENTION: Mediators of Chronic Allograft  
TITLE OF INVENTION: Rejection  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171,385  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/006001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 340  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

US-08-171-385-27

Query Match 1.2%; Score 23; DB 1; Length 340;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAA  
DB 40 TGTAAAAA 18

RESULT 18

US-08-361-441B-27/C  
Sequence 27, Application US/08361441B  
Patent No. 6077948  
GENERAL INFORMATION:  
APPLICANT: Russell, Mary E.  
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,441B  
FILING DATE: 21-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/171,385  
FILING DATE: 21-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 340 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

US-08-361-441B-27

Query Match 1.2%; Score 23; DB 3; Length 340;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAA  
DB 40 TGTAAAAA 18

RESULT 19

US-08-171-385-20/C  
Sequence 20, Application US/08171385  
Patent No. 5527884  
GENERAL INFORMATION:  
APPLICANT: Mary E. Russell  
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT  
FILING DATE: 21-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171,385  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/006001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

US-08-171-385-20

Query Match 1.2%; Score 23; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAA  
DB 23 TGTAAAAA 1

RESULT 20

US-08-361-441B-20/C  
Sequence 20, Application US/08361441B  
Patent No. 6077948  
GENERAL INFORMATION:  
APPLICANT: Russell, Mary E.  
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,441B  
FILING DATE: 21-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/171,385  
FILING DATE: 21-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-361-441B-20

Query Match  
Best Local Similarity 100.0%; Score 23; DB 3; Length 345;  
Pred. No. 0.91;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897  
DB 23 TGTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 21  
US-08-104-072B-2  
Sequence 2, Application US/08104072B  
Patent No. 5639948  
GENERAL INFORMATION:  
APPLICANT: Michiels, Frank  
APPLICANT: Morloka, Sinjl  
APPLICANT: Schellinck, Trees  
APPLICANT: Komari, Toshiko  
TITLE OF INVENTION: Stramen-specific Promoters from Rice  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 No. 5639948west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/104,072B  
FILING DATE: 05-AUG-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 9200272  
FILING DATE: 06-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 91403352.7  
FILING DATE: 10-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 91402590.3  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 91400318.1  
FILING DATE: 08-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kowalchuk, Katherine M.  
REGISTRATION NUMBER: 36,848  
REFERENCE/DOCKET NUMBER: 8076,93USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-9081  
TELEFAX: 612-332-5300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 347 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: rice  
TISSUE TYPE: anther  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 1..322  
OTHER INFORMATION: /product= "cDNA T23"  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 333..347  
OTHER INFORMATION: /product= "cloning adaptor"  
US-08-104-072B-2

Query Match  
Best Local Similarity 100.0%; Score 23; DB 1; Length 347;  
Pred. No. 0.91;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897  
DB 284 TGTAAAAAAAAAAAAAAAAAAAAA 306

RESULT 22  
US-08-171-385-14/C  
Sequence 14, Application US/08171385  
Patent No. 5527884  
GENERAL INFORMATION:  
APPLICANT: Mary E. Russell  
APPLICANT: Ulrike Utans  
TITLE OF INVENTION: Mediators of Chronic Allograft  
TITLE OF INVENTION: Rejection  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171,385  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/006001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-171-385-14

Query Match  
Best Local Similarity 100.0%; Score 23; DB 1; Length 350;  
Pred. No. 0.91;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
 |||  
 Db 43 TGTAAAAAAAAAAAAAAAAA 21

RESULT 23  
 US-08-361-441B-14/C  
 ; Sequence 14, Application US/08361441B  
 ; Patent No. 6077948  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Russell, Mary E.  
 ; APPLICANT: Utans, Ulrike  
 ; TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/361,441B  
 ; FILING DATE: 21-DEC-1994  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/171,385  
 ; FILING DATE: 21-DEC-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fraser, Jais K.  
 ; REGISTRATION NUMBER: 34,819  
 ; REFERENCE/DOCKET NUMBER: 05433/014001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617/542-5070  
 ; TELEFAX: 617/542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 350 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; US-08-361-441B-14

Query Match 1.2%; Score 23; DB 3; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0.91;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
 |||  
 Db 43 TGTAAAAAAAAAAAAAAAAA 21

RESULT 24  
 US-09-605-785-357/C  
 ; Sequence 357, Application US/09605785  
 ; Patent No. 6321716  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, David C.  
 ; APPLICANT: Mitchell, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vegivick, Thomas S.  
 ; APPLICANT: Carter, Darlick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.427C16  
 ; CURRENT APPLICATION NUMBER: US/09/605,785  
 ; CURRENT FILING DATE: 2000-06-27  
 ; NUMBER OF SEQ ID NOS: 835  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 357  
 ; LENGTH: 393  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-09-605-785-357

Query Match 1.2%; Score 23; DB 4; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
 |||  
 Db 34 TGTAAAAAAAAAAAAAAAAA 12

RESULT 25  
 US-09-439-313-357/C  
 ; Sequence 357, Application US/09439313  
 ; Patent No. 6329505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, David C.  
 ; APPLICANT: Mitchell, Jennifer L.  
 ; APPLICANT: Harlocker, Susan Louise  
 ; APPLICANT: Jiang Yugu  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Kalos, Michael  
 ; APPLICANT: Fanger, Gary  
 ; APPLICANT: Retter, Mark  
 ; APPLICANT: Solk, John  
 ; APPLICANT: Day, Craig  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
 ; FILE REFERENCE: 210121.427C9  
 ; CURRENT APPLICATION NUMBER: US/09/439,313  
 ; CURRENT FILING DATE: 1999-11-12  
 ; NUMBER OF SEQ ID NOS: 575  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 357  
 ; LENGTH: 393  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-09-439-313-357

Query Match 1.2%; Score 23; DB 4; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
 |||  
 Db 34 TGTAAAAAAAAAAAAAAAAA 12

RESULT 26  
 US-09-352-616A-357/C  
 ; Sequence 357, Application US/09352616A  
 ; Patent No. 6395278  
 ; GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang, Yuqi  
APPLICANT: Xu, Jiangchun  
APPLICANT: Mitcham, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.427C8  
CURRENT APPLICATION NUMBER: US/09/352.616A  
CURRENT FILING DATE: 1999-07-13  
NUMBER OF SEQ ID NOS: 472  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 357  
LENGTH: 393  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-352-616A-357

Query Match 1.2%; Score 23; DB 4; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.9;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 34 TGTAAAAAAAAAAAAAAAAAAAA 12

RESULT 27  
US-09-014-969-5  
Sequence 5, Application US/09014969  
Patent No. 5965397

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: Lavallee, Edward R.  
APPLICANT: Racle, Lisa A.  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Spaulding, Vikki  
APPLICANT: Agostino, Michael J.  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014.969  
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne A.  
REGISTRATION NUMBER: 41,323  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 413 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-014-969-5

Query Match 1.2%; Score 23; DB 2; Length 413;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 387 TGTAAAAAAAAAAAAAAAAAAAA 409

RESULT 28  
US-09-605-785-353/C  
Sequence 353, Application US/09605785  
Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C16  
CURRENT APPLICATION NUMBER: US/09/605,785  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 835  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 353  
LENGTH: 436  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-605-785-353

Query Match 1.2%; Score 23; DB 4; Length 436;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 29 TGTAAAAAAAAAAAAAAAAAAAA 7

RESULT 29  
US-09-439-313-353/C  
Sequence 353, Application US/09439313  
Patent No. 6329505

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang Yuqi  
APPLICANT: Reed, Steven G.  
APPLICANT: Kalos, Michael  
APPLICANT: Fanger, Gary  
APPLICANT: Retter, Mark  
APPLICANT: Solk, John  
APPLICANT: Day, Craig  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C9

CURRENT APPLICATION NUMBER: US/09/439,313  
CURRENT FILING DATE: 1999-11-12  
NUMBER OF SEQ ID NOS: 575  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 353  
LENGTH: 436  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-439-313-353

Query Match 1.2%; Score 23; DB 4; Length 436;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897  
DB 29 TGTAAAAAAAAAAAAAAAAAAAAA 7

RESULT 30  
US-09-352-616A-353/C  
Sequence 353, Application US/09352616A  
Patent No. 6395278  
GENERAL INFORMATION:  
APPLICANT: Dillon, Davin C.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang, Yugu  
APPLICANT: Xu, Jianshun  
APPLICANT: Mitcham, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
FILE REFERENCE: 210121.427C8  
CURRENT APPLICATION NUMBER: US/09/352,616A  
CURRENT FILING DATE: 1999-07-13  
NUMBER OF SEQ ID NOS: 472  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 353  
LENGTH: 436  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-352-616A-353

Query Match 1.2%; Score 23; DB 4; Length 436;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897  
DB 29 TGTAAAAAAAAAAAAAAAAAAAAA 7

RESULT 31  
US-09-372-422A-35  
Sequence 35, Application US/09372422A  
Patent No. 6313375  
GENERAL INFORMATION:  
APPLICANT: Rudolf Jung  
APPLICANT: Francois Barrieu  
TITLE OF INVENTION: Matre Aquaporins and Uses Thereof  
FILE REFERENCE: 0919  
CURRENT APPLICATION NUMBER: US/09/372,422A  
CURRENT FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: US 60/098,692  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 35  
LENGTH: 442  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)...(257)

US-09-372-422A-35

Query Match 1.2%; Score 23; DB 4; Length 442;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897  
DB 406 TGTAAAAAAAAAAAAAAAAAAAAA 428

RESULT 32  
US-09-186-276B-29/C  
Sequence 29, Application US/09186276B  
Patent No. 6388173  
GENERAL INFORMATION:  
APPLICANT: Benfey, Philip  
APPLICANT: Dilaurenzio, Laura  
APPLICANT: Wysocka-Diller, Joanna  
APPLICANT: Malamy, Jocelyn E.  
APPLICANT: Pysh, Leonard  
APPLICANT: Helariutta, Yrjo  
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof  
FILE REFERENCE: 5914-075-999  
CURRENT APPLICATION NUMBER: US/09/186,276B  
CURRENT FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: 08/842,445  
PRIOR FILING DATE: 1997-04-24  
PRIOR APPLICATION NUMBER: 08/638,617  
PRIOR FILING DATE: 1996-04-26  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 29  
LENGTH: 502  
TYPE: DNA  
ORGANISM: Oryza sp.  
US-09-186-276B-29

Query Match 1.2%; Score 23; DB 4; Length 502;  
Best Local Similarity 100.0%; Pred. No. 0.88;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897  
DB 34 TGTAAAAAAAAAAAAAAAAAAAAA 12

RESULT 33  
US-08-842-445-29/C  
Sequence 29, Application US/08842445A  
Patent No. 6441270  
GENERAL INFORMATION:  
APPLICANT: Benfey et al.  
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses  
FILE REFERENCE: 5914-056-999  
CURRENT APPLICATION NUMBER: US/08/842,445A  
CURRENT FILING DATE: 1997-04-24  
EARLIER APPLICATION NUMBER: 08/638,617  
EARLIER FILING DATE: 1996-04-26  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 29  
LENGTH: 502  
TYPE: DNA  
ORGANISM: Plant  
US-08-842-445-29

Query Match 1.2%; Score 23; DB 4; Length 502;  
Best Local Similarity 100.0%; Pred. No. 0.88;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897

Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

## RESULT 34

US-09-186-188B-29/c  
Sequence 29, Application US/09186188B  
Patent No. 6455672  
GENERAL INFORMATION:  
APPLICANT: Benfey et al.  
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses  
FILE REFERENCE: 5914-074-999  
CURRENT APPLICATION NUMBER: US/09/186,188B  
CURRENT FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: 08/842,445  
PRIOR FILING DATE: 1997-04-24  
PRIOR APPLICATION NUMBER: 08/638,617  
PRIOR FILING DATE: 1996-04-26  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 29  
LENGTH: 502  
TYPE: DNA  
ORGANISM: Plant  
US-09-186-188B-29

Query Match 1.2%; Score 23; DB 4; Length 502;  
Best Local Similarity 100.0%; Pred. No. 0.88;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
Db 34 TGTAAAAAAAAAAAAAAAAAAAA 12

## RESULT 35

US-08-462-894-5  
Sequence 5, Application US/08462894  
Patent No. 5723312  
GENERAL INFORMATION:  
APPLICANT: NOESKE-JUNGBLUT, CHRISTIANE  
APPLICANT: HAENDLER, BERNHARD  
APPLICANT: KRAETZSCHMAR, JOERN  
APPLICANT: SCHLEUNING, WOLF-DIETER  
APPLICANT: ALAGON, ALEJANDRO  
APPLICANT: POSSANI, LOURIVAL  
APPLICANT: CUEVAS-AGUIRRE, DELIA  
TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD., SUITE 1400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,894  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/206,185  
FILING DATE: 07-MAR-1994  
APPLICATION NUMBER: US 08/116,889  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP92/02052  
FILING DATE: 04-SEP-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/914,383

FILING DATE: 17-JUL-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/814,884

FILING DATE: 31-DEC-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/756,211

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: SCH 1359

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 530 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

US-08-462-894-5

Query Match 1.2%; Score 23; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 0.88;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
Db 508 TGTAAAAAAAAAAAAAAAAAAAA 530

## RESULT 36

US-08-206-185-5  
Sequence 5, Application US/08206185  
Patent No. 5756454  
GENERAL INFORMATION:  
APPLICANT: NOESKE-JUNGBLUT, CHRISTIANE  
APPLICANT: HAENDLER, BERNHARD  
APPLICANT: KRAETZSCHMAR, JOERN  
APPLICANT: SCHLEUNING, WOLF-DIETER  
APPLICANT: ALAGON, ALEJANDRO  
APPLICANT: POSSANI, LOURIVAL  
APPLICANT: CUEVAS-AGUIRRE, DELIA  
TITLE OF INVENTION: COLLAGEN-INDUCED PLATELET AGGREGATION  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD., SUITE 1400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/206,185  
FILING DATE: 07-MAR-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,889  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP92/02052  
FILING DATE: 04-SEP-1992



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/914,383  
FILING DATE: 17-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/814,884  
FILING DATE: 31-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/756,211  
FILING DATE: 05-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: SCH 1359  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 530 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-206-185-5

Query Match 1.2%; Score 23; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 0.88;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAA 1897  
Db 508 TGTAAAAA 530

RESULT 37  
US-09-433-248A-7  
Sequence 7, Application US/09433248A  
Patent No. 6355462  
GENERAL INFORMATION:  
APPLICANT: Falco, S. Carl  
APPLICANT: Farnodu, Omolayo O.  
APPLICANT: Han, Feng  
APPLICANT: Rafalski, J. Antoni  
TITLE OF INVENTION: Disease Resistance Factors  
FILE REFERENCE: B1252 US NA  
CURRENT APPLICATION NUMBER: US/09/433,248A  
CURRENT FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107,242  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 7  
LENGTH: 588  
TYPE: DNA  
ORGANISM: Trilicium aestivum  
US-09-433-248A-7

Query Match 1.2%; Score 23; DB 4; Length 588;  
Best Local Similarity 100.0%; Pred. No. 0.87;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAA 1897  
Db 563 TGTAAAAA 585

RESULT 38  
US-09-385-982-262/C  
Sequence 262, Application US/09385982  
Patent No. 6262334  
GENERAL INFORMATION:  
APPLICANT: ENDEGE, WILSON O., ET AL.  
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II  
FILE REFERENCE: CCDNA-260XX  
CURRENT APPLICATION NUMBER: US/09/385,982  
CURRENT FILING DATE: 1999-08-30  
EARLIER APPLICATION NUMBER: 09/328,111  
EARLIER FILING DATE: 1999-06-08  
EARLIER APPLICATION NUMBER: 60/117,393  
EARLIER FILING DATE: 1999-01-27  
EARLIER APPLICATION NUMBER: 60/098,639  
EARLIER FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 544  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 262  
LENGTH: 593  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(593)  
OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-262

Query Match 1.2%; Score 23; DB 4; Length 593;  
Best Local Similarity 100.0%; Pred. No. 0.87;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAA 1897  
Db 75 TGTAAAAA 53

RESULT 39  
5212073-1  
Patent No. 5212073  
APPLICANT: ROLLINS, BARRETT,STILES, CHARLES;MONG, GORDON G.  
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE  
NUMBER OF SEQUENCES: 1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/351,008  
FILING DATE:12-MAY-1989  
SEQ ID NO:1;  
LENGTH: 752  
5212073-1

Query Match 1.2%; Score 23; DB 6; Length 752;  
Best Local Similarity 100.0%; Pred. No. 0.85;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAA 1897  
Db 730 TGTAAAAA 752

RESULT 40  
US-09-575-602-1  
Sequence 1, Application US/09575602  
Patent No. 6392123  
GENERAL INFORMATION:  
APPLICANT: Crosland, Lyle D  
APPLICANT: Harper, Stacy M  
TITLE OF INVENTION: Method of Hybrid Seed Production Using  
TITLE OF INVENTION: Conditional Female Sterility  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6392123artis Corporation - Patent & Trademark  
ADDRESSER: Dept.  
STREET: P.O. Box 12257  
CITY: Research Triangle Park  
STATE: NCNY  
COUNTRY: USA  
ZIP: 22057  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/575,602  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/032,086  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40,403  
REFERENCE/DOCKET NUMBER: CGC 1915/Reg  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8582  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 772 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "cDNA sequence for  
DESCRIPTION: female-preferential transcript designated B20014-2"  
HYPOTHETICAL: NO  
US-09-575-602-1

Query Match 1.2%; Score 23; DB 4; Length 772;  
Best Local Similarity 100.0%; Pred. No. 0.85;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 747 TGTAAAAAAAAAAAAAAAAA 769

RESULT 41  
US-08-032-393-5  
Sequence 5, Application US/08032393  
Patent No. 5332660  
GENERAL INFORMATION:  
APPLICANT: Osamu TAKEDA et al.  
TITLE OF INVENTION: Gene of Candida Yeast  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/032,393  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/729,414  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Check, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 933 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Candida albicans  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-032-393-5

Query Match 1.2%; Score 23; DB 1; Length 933;  
Best Local Similarity 100.0%; Pred. No. 0.83;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 911 TGTAAAAAAAAAAAAAAAAA 933

RESULT 42  
US-08-252-966B-15  
Sequence 15, Application US/08252966B  
Patent No. 5624818  
GENERAL INFORMATION:  
APPLICANT: Eisenman, Robert N.  
APPLICANT: Hurlin, Peter J.  
TITLE OF INVENTION: Regulatory Proteins that Dimerize with  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Christensen, O'Connor, Johnson, and KindnessP/LC  
STREET: 1420 Fifth Ave., Suite 2800  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101-2347

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,966B
FILING DATE: 01-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: FHCRI7694
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: clone 19; see Figure 26
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus

US-08-252-966B-15

Query Match
Best Local Similarity 1.2%; Score 23; DB 1; Length 1008;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1875 TGTAAAAA 1897
Db 975 TGTAAAAA 997

RESULT 43
US-09-173-300-21
Sequence 21, Application US/09173300
Patent No. 6451581
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Hiltz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/09/173,300
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 60/063,423
EARLIER FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 21
LENGTH: 1162
TYPE: DNA
ORGANISM: Glycine max
US-09-173-300-21

Query Match
Best Local Similarity 1.2%; Score 23; DB 4; Length 1162;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1875 TGTAAAAA 1897
Db 1132 TGTAAAAA 1154

RESULT 44
US-07-869-933-10
```

```
Sequence 10, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: Kinet, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..880
US-07-869-933-10

Query Match
Best Local Similarity 1.2%; Score 23; DB 1; Length 1174;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1875 TGTAAAAA 1897
Db 1150 TGTAAAAA 1172

RESULT 45
US-09-103-663-10
Sequence 10, Application US/09103663D
Patent No. 6171803
GENERAL INFORMATION:
APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: subunit of the high affinity receptor for
FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 1174
TYPE: DNA
ORGANISM: Homo sapiens
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FEATURE:  
NAME/KEY: CDS  
LOCATION: (107)..(880)  
US-09-103-663-10

867

Query Match 1.2%; Score 23; DB 4; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 1150 TGTAAAAAAAAAAAAAAAAAAAA 1172

Search completed: November 7, 2002, 23:21:20  
Job time : 366.085 secs



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OY 181 GGTGAGCGGGGAGGAGCTCCGCTGTCGCTCTCTGATGGCTTGGCTCCCG 240
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Db 181 GCTGAGCGGGGAGGAGCTCCGCTGTCGCTCTCTGATGGCTTGGCTCCCG 240
OY 241 GCGCGGAGCTCGGGAGATGTGGTCTTAAGCATCGCGCACTTTTGGATTTGT 300
    |||
Db 241 GCGCGGAGCTCGGGAGATGTGGTCTTAAGCATCGCGCACTTTTGGATTTGT 300
OY 301 CTTCGCTCAAGCTTTGGCTGCAATCAGTGTACCAAGTGTGAAGATTCAGCTAA 360
    |||
Db 301 CTTCGCTCAAGCTTTGGCTGCAATCAGTGTACCAAGTGTGAAGATTCAGCTAA 360
OY 361 CAAGCACTGCTCTCCCGAGTTCATTGTGAATTCAGCGGTGAAGCTTCAAGCATGTG 420
    |||
Db 361 CAAGCACTGCTCTCCCGAGTTCATTGTGAATTCAGCGGTGAAGCTTCAAGCATGTG 420
OY 421 TCAGAAAGAGTATGAGCAAAAGTCCGGGATCATGATCCGCAAGCTCTGTGATATC 480
    |||
Db 421 TCAGAAAGAGTATGAGCAAAAGTCCGGGATCATGATCCGCAAGCTCTGTGATATC 480
OY 481 AGCGGCTGTCTCATGCGCTTCGCGGGTACAGATCTTCTGCTCCCAAGGAAACTGAA 540
    |||
Db 481 AGCGGCTGTCTCATGCGCTTCGCGGGTACAGATCTTCTGCTCCCAAGGAAACTGAA 540
OY 541 CTCAGTTTCATCAGCTGCTGCAACACCCCTTTGTAAAGGAGGAGGAGGAGGAGGAG 600
    |||
Db 541 CTCAGTTTCATCAGCTGCTGCAACACCCCTTTGTAAAGGAGGAGGAGGAGGAGGAG 600
OY 601 GGGAGTTTCGCTCGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
    |||
Db 601 GGGAGTTTCGCTCGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
OY 661 AGCCCTCTCTGAGCACTGCTGAAGTGAAGAGATGCCACCCCTCTGCTGATGTC 720
    |||
Db 661 AGCCCTCTCTGAGCACTGCTGAAGTGAAGAGATGCCACCCCTCTGCTGATGTC 720
OY 721 TTCAGACCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
    |||
Db 721 TTCAGACCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
OY 781 ATTCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
    |||
Db 781 ATTCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
OY 841 CTCGGTGAAGCAATTCGAATTAATTCAGCTGAATTCAGTGAATTCAGTGAATTCAG 900
    |||
Db 841 CTCGGTGAAGCAATTCGAATTAATTCAGCTGAATTCAGTGAATTCAGTGAATTCAG 900
OY 901 AGGAGGTGAGTGAAGTTCACCCCATCTGTGTAAACCGGAGTCAAGGAGGAGGAGGAG 960
    |||
Db 901 AGGAGGTGAGTGAAGTTCACCCCATCTGTGTAAACCGGAGTCAAGGAGGAGGAGGAG 960
OY 961 AGAGTGTGCTTGAAGTCACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1020
    |||
Db 961 AGAGTGTGCTTGAAGTCACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1020
OY 1021 CATTCATCCCTGATGGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1080
    |||
Db 1021 CATTCATCCCTGATGGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1080
OY 1081 GGCTGAGGAGGAGTTCACCACTCAAGGCTCCCTGCTTACATTCATTCATTCATTCAT 1140
    |||
Db 1081 GGCTGAGGAGGAGTTCACCACTCAAGGCTCCCTGCTTACATTCATTCATTCATTCAT 1140
OY 1141 GAAACCAATTCCTGAGAGCAAGATTTGGCTTTCGCGCTGAGTGTGAGTGTGAGTGT 1200
    |||
Db 1141 GAAACCAATTCCTGAGAGCAAGATTTGGCTTTCGCGCTGAGTGTGAGTGTGAGTGT 1200
OY 1201 CGAGCATCAATGAGTGGAGCTTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1260
    |||
Db 1201 CGAGCATCAATGAGTGGAGCTTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1260
OY 1261 AATCTTCTCAGTTCTCTTGAAGAGTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
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Db 1261 AATCTTCTCAGTTCTCTTGAAGAGTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAG 1320
    |||
OY 1321 GCACAAAGCGGCGCTGTCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1380
    |||
Db 1321 GCACAAAGCGGCGCTGTCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1380
OY 1381 TGCGGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
    |||
Db 1381 TGCGGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
OY 1441 GCGAGACACCGCTGTACAGAGGCGGTTGATGACCGAGTGAAGTGAAGAAAGTCTCG 1500
    |||
Db 1441 GCGAGACACCGCTGTACAGAGGCGGTTGATGACCGAGTGAAGTGAAGAAAGTCTCG 1500
OY 1501 AGAAGGAGGAGGAGGAGTATGATGAGCGCGGAGTGAAGTGTGAGTGTGAGTGTGAG 1560
    |||
Db 1501 AGAAGGAGGAGGAGGAGTATGATGAGCGCGGAGTGAAGTGTGAGTGTGAGTGTGAG 1560
OY 1561 TGCGCGAGCGCATGATCTCGGAATCTGTTGGGATCCAGATACGCGCAATGTACAA 1620
    |||
Db 1561 TGCGCGAGCGCATGATCTCGGAATCTGTTGGGATCCAGATACGCGCAATGTACAA 1620
OY 1621 CAATCAGCCCTGGGAGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
    |||
Db 1621 CAATCAGCCCTGGGAGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
OY 1681 GAGAACACAGTAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
    |||
Db 1681 GAGAACACAGTAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
OY 1741 GCGAGAAATGATGATCAATTTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1800
    |||
Db 1741 GCGAGAAATGATGATCAATTTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1800
OY 1801 GAGAGAAATTAACACTGTTTCAAAACCGGAGGAGTGTGAGTGTGAGTGTGAGTGT 1860
    |||
Db 1801 GAGAGAAATTAACACTGTTTCAAAACCGGAGGAGTGTGAGTGTGAGTGTGAGTGT 1860
OY 1861 AATGCTTTAGCAGTGTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
    |||
Db 1861 AATGCTTTAGCAGTGTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920

RESULT 2
US-09-825-294-205
: Sequence 205, Application US/09825294
: Patent No. US2002004491A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolx, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: CURRENT APPLICATION NUMBER: US/09/825,294
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 205
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-825-294-205

Query Match 73.6%; Score 1396; DB 10; Length 1619;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 280 GCGAATTTTGGGAGATTTGTTGCTTCCACAGCTTGGCGCTGCAATTCAGTGTACCA 339
    |||
Db 1 GCGAATTTTGGGAGATTTGTTGCTTCCACAGCTTGGCGCTGCAATTCAGTGTACCA 60
    |||

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Db 181 CCGCAGTCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGTACCACTCTT 240
QY 520 CTGCTCCCAAGGAAAGTGAAGTCTGATGATGCTGCTGCAACACCCCTTTGTAA 579
    |||||
Db 241 CTGCTCCCAAGGAAAGTGAAGTCTGATGATGCTGCTGCAACACCCCTTTGTAA 300
QY 580 CCGGCGCAAGGCGCAAGAAAGGGAATTTGCTGCTGCGGCTCAGGCGCAAGGCTCCGCGAC 639
    |||||
Db 301 CCGGCGCAAGGCGCAAGAAAGGGAATTTGCTGCTGCGGCTCAGGCGCAAGGCTCCGCGAC 360
QY 640 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTCGGCACACTGCTGAAGCTGAAGAGATG 699
    |||||
Db 361 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTCGGCACACTGCTGAAGCTGAAGAGATG 420
QY 700 CCACCCCTCTCTGATGTTCTTCTCAAGCCCTGCGCCCAACCCCGCACTCTCTGATGA 759
    |||||
Db 421 CCACCCCTCTCTGATGTTCTTCTCAAGCCCTGCGCCCAACCCCGCACTCTCTGATGA 480
QY 760 GTTCTCTGCTGCTGCTCTTCTTATCTGCTGAGGAGGCGGAGTCCGATGTTCTTTGTT 819
    |||||
Db 481 GTTCTCTGCTGCTGCTCTTCTTATCTGCTGAGGAGGCGGAGTCCGATGTTCTTTGTT 540
QY 820 CCTGTCAAAATATGAAAGAGCTCGTAAAGCATTTGAAATTAATGAGCTGATGAT 879
    |||||
Db 541 CCTGTCAAAATATGAAAGAGCTCGTAAAGCATTTGAAATTAATGAGCTGATGAT 600
QY 880 TTTTCACTATGTAAGTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 939
    |||||
Db 601 TTTTCACTATGTAAGTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 660
QY 940 CCGAGTCAAGGCGCAGGCTGCGAGAGTCTGCTTGAAGTCACTGAGTGGGCTCTGCTGCC 999
    |||||
Db 661 CCGAGTCAAGGCGCAGGCTGCGAGAGTCTGCTTGAAGTCACTGAGTGGGCTCTGCTGCC 720
QY 1000 TTTTGTAAAGCTCTCAAGTCTCAATCCCTGATGCGGCGATATGTTGAGACTGCAGA 1059
    |||||
Db 721 TTTTGTAAAGCTCTCAAGTCTCAATCCCTGATGCGGCGATATGTTGAGACTGCAGA 780
QY 1060 GTGAGAGTACGCTTTCTTGAAGGCGTGAAGGCGCACTCCCACTCAAGGCTCCCTGCTG 1119
    |||||
Db 781 GTGAGAGTACGCTTTCTTGAAGGCGTGAAGGCGCACTCCCACTCAAGGCTCCCTGCTG 840
QY 1120 ACATTTCAAACTTCATGCTCTCTGAAAACCATTTCTGACAGAGAAATTTGGCTTTGCGGC 1179
    |||||
Db 841 ACATTTCAAACTTCATGCTCTCTGAAAACCATTTCTGACAGAGAAATTTGGCTTTGCGGC 900
QY 1180 CTGAGTGGGCTCTGATGACTGCAACATCTAATGACTGGGACTTAACACTGGGCTCTGCGCT 1239
    |||||
Db 901 CTGAGTGGGCTCTGATGACTGCAACATCTAATGACTGGGACTTAACACTGGGCTCTGCGCT 960
QY 1240 CCGTCTGAAAAGTGGCTTAAGAAATCTTCTCAGTTCTCTCTGCAAGAGACTGGCGCGG 1299
    |||||
Db 961 CCGTCTGAAAAGTGGCTTAAGAAATCTTCTCAGTTCTCTCTGCAAGAGACTGGCGCGG 1020
QY 1300 ACGCGAAGAGCAAGCGGCGCTGCAAGAGCGGCGCTGTGCTGCTGAGTGGCGCATGTA 1359
    |||||
Db 1021 ACGCGAAGAGCAAGCGGCGCTGCAAGAGCGGCGCTGTGCTGAGTGGCGCATGTA 1080
QY 1360 CCGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
    |||||
Db 1081 CCGCGAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1419 ACGAACAACCGCGGAAAGTCTGCGAGAGACACCTGTAAGAGAGCGGTTGATGACCGAG 1478
    |||||
Db 1141 ACGAACAACCGCGGAAAGTCTGCGAGAGACACCTGTAAGAGAGCGGTTGATGACCGAG 1200
QY 1479 CTGAGGTAGAAAACGTTCTCGAGAGAGGAGAGAGATCATGTACGCCGGAAGTAGAGAC 1538
    |||||
Db 1201 CTGAGGTAGAAAACGTTCTCGAGAGAGGAGAGAGATCATGTACGCCGGAAGTAGAGAC 1260
QY 1539 CTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1598
    |||||
Db 1261 CTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

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QY 1599 CAGCATAGCGCCATGATGTCAACAACATTAATGATGATGATGATGATGATGATGATGAT 1658
    |||||
Db 1321 CAGCATAGCGCCATGATGTCAACAACATTAATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1659 AGAAGAAAGAAAGAAAGCAAGCATGAGAAACAGTAATTAATTAATTAATTAATTAATTAAT 1718
    |||||
Db 1381 AGAAGAAAGAAAGAAAGCAAGCATGAGAAACAGTAATTAATTAATTAATTAATTAATTAAT 1440
QY 1719 CCGCTCTGTTCTGCTTACTGCTGCGGCAAGAAATGTAACCAATTTTCAAGTGTGAGCTGA 1778
    |||||
Db 1441 CCGCTCTGTTCTGCTTACTGCTGCGGCAAGAAATGTAACCAATTTTCAAGTGTGAGCTGA 1500
QY 1779 CAGCTCTTTTGGCAACAAGAGAGAAATTAACACTGTTTCAAAACCGGGGAGATTGG 1838
    |||||
Db 1501 CAGCTCTTTTGGCAACAAGAGAGAAATTAACACTGTTTCAAAACCGGGGAGATTGG 1560
QY 1839 CTGTGTAAAGAAAGCAATTAATGCTTTAGACAGTGTAAAGAAAGAAAGAAAGAAAG 1897
    |||||
Db 1561 CTGTGTAAAGAAAGCAATTAATGCTTTAGACAGTGTAAAGAAAGAAAGAAAGAAAG 1619

```

```

RESULT 4
US-09-825-294-210
; Sequence 210, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Aligale, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(625)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210

```

```

Query Match          31.9%; Score 606; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 8.6e-241;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1271 AGTTCCTCTTGCAGAGACTGGCGCCGCGAGCGGAAGAGCAAGCGGCGCTGCAAAAGCG 1330
    |||||
Db 1 AGTTCCTCTTGCAGAGACTGGCGCCGCGAGCGGAAGAGCAAGCGGCGCTGCAAAAGCG 60
QY 1331 GGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1390
    |||||
Db 61 GGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 1391 CAGGACAGAGGCGGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1450
    |||||
Db 121 CAGGACAGAGGCGGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
QY 1451 CGTGTACAGAGCGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1510
    |||||
Db 181 CGTGTACAGAGCGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 1511 GAGATCATGTAGCCCGGGAAGTAGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1570
    |||||
Db 241 GAGATCATGTAGCCCGGGAAGTAGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 1571 CATGATCTCCGAAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1630

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|||||
Db 301 CATGATCCTCCGATCTGGTGGGCATCCAGCATACGGCCAAATGTCACAAATCAGCCC 360
Oy 1631 TGGGACACACGAGCAGGAGGAGAGACAGAAAAGAAAACACAGCATGAGAACACAG 1690
Db 361 TGGGACACACGAGCAGGAGGAGAGACAGAAAAGAAAACACAGCATGAGAACACAG 420
Oy 1691 TAAATGAATAAACCATAAATATTTAGCCCCCTGTTGCTGCTTACTGCGCAGGAAT 1750
Db 421 TAAATGAATAAACCATAAATATTTAGCCCCCTGTTGCTGCTTACTGCGCAGGAAT 480
Oy 1751 GGTACCAATTTTCAAGTGTGAGCTTGACAGCTTCTTTGCCAACAAGACAGAAATT 1810
Db 481 GGTACCAATTTTCAAGTGTGAGCTTGACAGCTTCTTTGCCAACAAGACAGAAATT 540
Oy 1811 AACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAACACATTAATGCTTTAG 1870
Db 541 AACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAACACATTAATGCTTTAG 600
Oy 1871 ACAGTG 1876
Db 601 ACAGTG 606

```

## RESULT 5

```

US-09-867-701-10876
/ Sequence 10876, Application US/09867701
/ Patent No. US2002013237A1
/ GENERAL INFORMATION:
/ APPLICANT: Aglate, Paul A.
/ APPLICANT: Jones, Robert
/ APPLICANT: Harlocker, Susan L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.497
/ CURRENT APPLICATION NUMBER: US/09/867,701
/ NUMBER OF SEQ ID NOS: 10912
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10876
/ LENGTH: 625
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 607
/ OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10876

```

```

Query Match          31.9%; Score 606; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 8.6e-241;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1271 AGTTCTCTTCGACAGAGCTGGGGCGGGAGGAGCAACAGGGCGGTGACAAAGG 1330
Db 1 AGTTCTCTTCGACAGAGCTGGGGCGGGAGGAGCAACAGGGCGGTGACAAAGG 60
Oy 1331 GGGCGTGTGCTGTGAGTGGCATGTACGGCGACGGCTTCTGCTGCTGGCTGCTG 1390
Db 61 GGGCGTGTGCTGTGAGTGGCATGTACGGCGACGGCTTCTGCTGCTGGCTGCTG 120
Oy 1391 CAGCGACAGCGGCGACACAGCACTGCGAAGAACCCCGCAAACTGCTGCGAGGACAC 1450
Db 121 CAGCGACAGCGGCGACACAGCACTGCGAAGAACCCCGCAAACTGCTGCGAGGACAC 180
Oy 1451 CGGTACAGAGCGGCGGTGATGACGAGCTGAGTGAAGAAAAGTCTCGAGAAAGGAG 1510
Db 181 CGGTACAGAGCGGCGGTGATGACGAGCTGAGTGAAGAAAAGTCTCGAGAAAGGAG 240
Oy 1511 GAGGATCATGTACCGCGGAGTAGAGCTGTCAGTGTGCTTGGGTTGGCGGACG 1570
Db 241 GAGGATCATGTACCGCGGAGTAGAGCTGTCAGTGTGCTTGGGTTGGCGGACG 300

```

```

Oy 1571 CATGATCCTCCGATCTGGTGGGCATCCAGCATACGGCCAAATGTCACAAATCAGCCC 1630
Db 301 CATGATCCTCCGATCTGGTGGGCATCCAGCATACGGCCAAATGTCACAAATCAGCCC 360
Oy 1631 TGGGACACACGAGCAGGAGGAGAGACAGAAAAGAAAACACAGCATGAGAACACAG 1690
Db 361 TGGGACACACGAGCAGGAGGAGAGACAGAAAAGAAAACACAGCATGAGAACACAG 420
Oy 1691 TAAATGAATAAACCATAAATATTTAGCCCCCTGTTGCTGCTTACTGCGCAGGAAT 1750
Db 421 TAAATGAATAAACCATAAATATTTAGCCCCCTGTTGCTGCTTACTGCGCAGGAAT 480
Oy 1751 GGTACCAATTTTCAAGTGTGAGCTTGACAGCTTCTTTGCCAACAAGACAGAAATT 1810
Db 481 GGTACCAATTTTCAAGTGTGAGCTTGACAGCTTCTTTGCCAACAAGACAGAAATT 540
Oy 1811 AACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAACACATTAATGCTTTAG 1870
Db 541 AACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAACACATTAATGCTTTAG 600
Oy 1871 ACAGTG 1876
Db 601 ACAGTG 606

```

## RESULT 6

```

US-09-825-294-208/C
/ Sequence 208, Application US/09825294
/ Patent No. US2002004491A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Stolk, John A.
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Fling, Steven P.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ FILE REFERENCE: 210121.4845
/ CURRENT APPLICATION NUMBER: US/09/825,294
/ NUMBER OF SEQ ID NOS: 215
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 208
/ LENGTH: 1362
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-825-294-208

```

```

Query Match          26.7%; Score 506; DB 10; Length 1362;
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1124 TCAACTTCATGCTCTCTAATAACCATTTCTGTCAGACAGAAATGGCTGGCTGTA 1183
Db 1362 TCAACTTCATGCTCTCTAATAACCATTTCTGTCAGACAGAAATGGCTGGCTGTA 1303
Oy 1184 GTTGGCTCTAGTGAATGAGATCAATGACTGGGACTTAAGTGGGCTGGCTGGCT 1243
Db 1302 GTTGGCTCTAGTGAATGAGATCAATGACTGGGACTTAAGTGGGCTGGCTGGCT 1243
Oy 1244 CTGAAGAGTCTTAAGAAATCTTCTAGTTCCTTTCAGAGAGACTGGCCCGGAGCG 1303
Db 1242 CTGAAGAGTCTTAAGAAATCTTCTAGTTCCTTTCAGAGAGACTGGCCCGGAGCG 1183
Oy 1304 GAAAGCAAGCGGCGCTGTCACAAAGCGGGCGCTGCGTGTGAGATGCCATACCGG 1363
Db 1182 GAAAGCAAGCGGCGCTGTCACAAAGCGGGCGCTGCGTGTGAGATGCCATACCGG 1123
Oy 1364 CAGGCGCTTCTGCTGTGAGCGCTGTCAGCGAGCAGCGGCGGACAGACACTGACGAA 1423
Db 1122 CAGGCGCTTCTGCTGTGAGCGCTGTCAGCGAGCAGCGGCGGACAGACACTGACGAA 1063
Oy 1424 CAGGCGCGAAAGTCTGCGAGGACACCGTGTACAGAGCGGGCTTGTGACGAGCTGAG 1483

```

Db 1062 CACCGCGCGAAGTCTGTCGAGACACCGTGTACAGAGCGGGTGTGATGACCGAGCTGAG 1003  
Qy 1484 GTAGAAAAACCTCTCCGAGAGGGGAGAGATCATGTACCCCGGAGAAATGAGACCTCGT 1543  
Db 1002 GTAGAAAAACCTCTCCGAGAGGGGAGAGATCATGTACCCCGGAGAAATGAGACCTCGT 943  
Qy 1544 CCAGTCGCTGTTGGGTTGGCGCGAGCATGATCTCCGAAATGTTGGGATCCAGCA 1603  
Db 942 CCAGTCGCTGTTGGGTTGGCGCGAGCATGATCTCCGAAATGTTGGGATCCAGCA 883  
Qy 1604 TACGGCCAATGTCAACACATCAGCC 1629  
Db 882 TACGGCCAATGTCAACACATCAGCC 857

## RESULT 7

US-09-825-294-213  
; Sequence 213, Application US/09825294  
; Patent No. US20020004491A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolck, John A.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C5  
; CURRENT APPLICATION NUMBER: US/09/825,294  
; CURRENT FILING DATE: 2001-04-03  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 213  
; LENGTH: 480  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-825-294-213

Query Match 22.4%; Score 425; DB 10; Length 480;  
Best Local Similarity 99.8%; Pred. No. 3,7e-166;

Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCAACTCCGAGGCTGTGTGCTCGGCCCGGAGCGCGAGCGGAGGAGCAGACACCG 60  
Db 1 GCCAACTCCGAGGCTGTGTGCTCGGCCCGGAGCGCGAGCGGAGGAGCAGACACCG 60  
Qy 61 CAGCGCGGAGCGCGAGCGCGGCGATGAGGCTCCGCGAGCGGCGACCTGCGGCTCTTA 120  
Db 61 CAGCGCGGAGCGCGAGCGCGGCGATGAGGCTCCGCGAGCGGCGACCTGCGGCTCTTA 120  
Qy 121 AGCTAGACCGTCTGCTCGCGGAGCAGCGCGGCGCCAGCAGCCTCGGAGCCAGC 180  
Db 121 AGCTAGACCGTCTGCTCGCGGAGCAGCGCGGCGCCAGCAGCCTCGGAGCCAGC 180  
Qy 181 CGCTGACGCGGCGGAGCGCTCCGCTGCTGTGCTCTGTGATGGCTTGGCTTCCG 240  
Db 181 CGCTGACGCGGCGGAGCGCTCCGCTGCTGTGCTCTGTGATGGCTTGGCTTCCG 240  
Qy 241 GCCCGGAGCGCGGAGAAATGTGGTCTAGCATCGCGGCACTTTTGGGAGTTGT 300  
Db 241 GCCCGGAGCGCGGAGAAATGTGGTCTAGCATCGCGGCACTTTTGGGAGTTGT 300  
Qy 301 CTGTGCTTCAGGCTTGGCTGCAAAATCAGTGTACAGTGTGAAGAAATTCACAGTGA 360  
Db 301 CTGTGCTTCAGGCTTGGCTGCAAAATCAGTGTACAGTGTGAAGAAATTCACAGTGA 360  
Qy 361 CAACGACCTCTCTCCCGAGTGTGTAATGACGCGGAGCGTTCACAGAAATTTG 420  
Db 361 CAACGACCTCTCTCCCGAGTGTGTAATGACGCGGAGCGTTCACAGAAATTTG 420  
Qy 421 TGAGAAAGAAATGTGAGCAAGTGCAGATCATGTACCGCAAGTCTGTGCAAT 476  
Db 421 TGAGAAAGAAATGTGAGCAAGTGCAGATCATGTACCGCAAGTCTGTGCAAT 476

## RESULT 8

US-09-825-294-9  
; Sequence 9, Application US/09825294  
; Patent No. US20020004491A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolck, John A.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C5  
; CURRENT APPLICATION NUMBER: US/09/825,294  
; CURRENT FILING DATE: 2001-04-03  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 396  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(396)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-825-294-9

Query Match 16.7%; Score 316; DB 10; Length 396;  
Best Local Similarity 100.0%; Pred. No. 3.2e-121;

Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 CATCGCGCAACTTTTTCGATGTTGCTTCAGCGCTTTCGCTCAATTCAGTG 333  
Db 5 CATCGCGCAACTTTTTCGATGTTGCTTCAGCGCTTTCGCTCAATTCAGTG 64  
Qy 334 CTACCAATGTGAAGATTCAGCTGAACAGCACTCTCTCCCGGAGTTCAATTTGAA 393  
Db 65 CTACCAATGTGAAGATTCAGCTGAACAGCACTCTCTCCCGGAGTTCAATTTGAA 124  
Qy 394 TTGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 453  
Db 125 TTGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 184  
Qy 454 CATGACCGAAGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 513  
Db 185 CATGACCGAAGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 244  
Qy 514 GTCTTGTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 573  
Db 245 GTCTTGTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 304  
Qy 574 TTGTAAGGCGCAAG 589  
Db 305 TTGTAAGGCGCAAG 320

## RESULT 9

US-09-825-294-199  
; Sequence 199, Application US/09825294  
; Patent No. US20020004491A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolck, John A.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C5  
; CURRENT APPLICATION NUMBER: US/09/825,294  
; CURRENT FILING DATE: 2001-04-03  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 199

```

; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

```

```

Query Match
Best Local Similarity 100.0%; Score 315; DB 10; Length 369;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 309 CAGGCTTGGCGTCAATCCAGTGTACCAAGTGAAGATTCCAGTGAACAGACT 368
DB 30 CAGGCTTGGCGTCAATCCAGTGTACCAAGTGAAGATTCCAGTGAACAGACT 89
QY 369 GCTCTCCCCGAGTTCATTTGTAATTCGACGGTGAACGTTCAAGCATGTGCAGAAAG 428
DB 90 GCTCTCCCCGAGTTCATTTGTAATTCGACGGTGAACGTTCAAGCATGTGCAGAAAG 149
QY 429 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 488
DB 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
QY 489 GTCTCATCCCTTGCCTGCGGATACCACTCTTCTGCTCCCGAGGAACTGAATCAGTTT 548
DB 210 GTCTCATCCCTTGCCTGCGGATACCACTCTTCTGCTCCCGAGGAACTGAATCAGTTT 269
QY 549 GCATCAGCTGCTCAACACCCCTTTGTAAGCGGGCCAGGCCCCAGAAAGGGAAGTT 608
DB 270 GCATCAGCTGCTCAACACCCCTTTGTAAGCGGGCCAGGCCCCAGAAAGGGAAGTT 329
QY 609 CTGCTCTGCGGCTCA 623
DB 330 CTGCTCTGCGGCTCA 344

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RESULT 10
US-09-867-701-1516/c
; Sequence 1516, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:

```

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; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1516
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-1516

```

```

Query Match
Best Local Similarity 100.0%; Score 315; DB 10; Length 373;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1563 GCCGAGCCATGATCTCTCGAATCTGTTGGCATCCAGCATACGGCCAATGTCAACA 1622
DB 315 GCCGAGCCATGATCTCTCGAATCTGTTGGCATCCAGCATACGGCCAATGTCAACA 256
QY 1623 ATCAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1682
DB 255 ATCAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
QY 1683 GAACACAGTAATGAATAAACCATTAATATTTAGCCCTCTGTTGTTCTGTTCTG 1742

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DB 195 GAACACAGTAATGAATAAACCATTAATATTTAGCCCTCTGTTGTTCTGTTCTG 136
QY 1743 CAGGAATGTGTCCAAATTTTTCAGTGTGAGTGTACAGCTTCTTTGCCACAGACA 1802
DB 135 CAGGAATGTGTCCAAATTTTTCAGTGTGAGTGTACAGCTTCTTTGCCACAGACA 76
QY 1803 GAGAAATTTACACTGTTTCAACCCCGGGAGTGTGCTGTGTTAAGAAAGCATTTAA 1862
DB 75 GAGAAATTTACACTGTTTCAACCCCGGGAGTGTGCTGTGTTAAGAAAGCATTTAA 16
QY 1863 TCGTTTACAGACTGT 1877
DB 15 TCGTTTACAGACTGT 1

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```

RESULT 11
US-09-867-701-2409/c
; Sequence 2409, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2409
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-2409

```

```

Query Match
Best Local Similarity 100.0%; Score 307; DB 10; Length 349;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1570 CCATATCTCTCGAATCTGTTGGCATCCAGCATACGGCCAATGTCAACAATCAGCC 1629
DB 310 CCATATCTCTCGAATCTGTTGGCATCCAGCATACGGCCAATGTCAACAATCAGCC 251
QY 1630 CTGGGACAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1689
DB 250 CTGGGACAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
QY 1690 GTAAATGAATAAAACCATTAATATTTAGCCCTCTGTTGTTCTGTTCTGTTCTG 1749
DB 190 GTAAATGAATAAAACCATTAATATTTAGCCCTCTGTTGTTCTGTTCTGTTCTG 131
QY 1750 TGGTACCAATTTTTCAGTGTGAGTGTACAGCTTCTTTGCCACAGAGAGAAAT 1809
DB 130 TGGTACCAATTTTTCAGTGTGAGTGTACAGCTTCTTTGCCACAGAGAGAAAT 71
QY 1810 TAACACTGTTTCAACCCCGGGAGTGTGCTGTGTTAAGAAAGCATTTAAATGCTTTA 1869
DB 70 TAACACTGTTTCAACCCCGGGAGTGTGCTGTGTTAAGAAAGCATTTAAATGCTTTA 11
QY 1870 GACAGTG 1876
DB 10 GACAGTG 4

```

```

RESULT 12
US-09-825-294-212
; Sequence 212, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.

```

APPLICANT: Filing, Steven P.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
FILE REFERENCE: 210121.4845  
CURRENT APPLICATION NUMBER: US/09/825,294  
CURRENT FILING DATE: 2001-04-03  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 212  
LENGTH: 1010  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-825-294-212

Query Match 14.3%; Score 271; DB 10; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 1.1e-102;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 AGGCTTGGCTGCAAAATCCAGTGTACAGTGAAGAAATCCAGTGAACAGACTG 369  
DB 258 AGGCTTGGCTGCAAAATCCAGTGTACAGTGAAGAAATCCAGTGAACAGACTG 317  
QY 370 CTCCTCCCGGAGTTGATTTGATGCAAGGTGAACGTTCAAGCATGTGTGAGAAAGA 429  
DB 318 CTCCTCCCGGAGTTGATTTGATGCAAGGTGAACGTTCAAGCATGTGTGAGAAAGA 377  
QY 430 ACTGATGAGCAAAATCCAGTGTACAGTGAAGAAATCCAGTGAACAGACTG 489  
DB 378 ACTGATGAGCAAAATCCAGTGTACAGTGAAGAAATCCAGTGAACAGACTG 437  
QY 490 TCTCATCGCCTTGGCGGGTACAGTGTCTGCTCCCGAGGAATGAACTAGTTTG 549  
DB 438 TCTCATCGCCTTGGCGGGTACAGTGTCTGCTCCCGAGGAATGAACTAGTTTG 497  
QY 550 CATCAGCTGCTGCAACACCCCTTTTGTAC 580  
DB 498 CATCAGCTGCTGCAACACCCCTTTTGTAC 528

RESULT 13

US-09-867-701-4240/c  
Sequence 4240, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4240  
LENGTH: 409  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-867-701-4240

Query Match 13.9%; Score 264; DB 10; Length 409;  
Best Local Similarity 99.7%; Pred. No. 8.7e-100;  
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1563 GCCGCGCCATGATCTCTCGAATCTGTTGGCATTCAGATACGCGCCATGTCAACA 1622  
DB 315 GCCGCGCCATGATCTCTCGAATCTGTTGGCATTCAGATACGCGCCATGTCAACA 256  
QY 1623 ATCAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1682  
DB 255 ATCAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196  
QY 1683 GAACACGTAATGATTAAGCATTAATATTAGCCCTCTGTTGCTTACTGGC 1742

DB 195 GAACACGTAATGATTAAGCATTAATATTAGCCCTCTGTTGCTTACTGGC 136  
QY 1743 CAGGAATGTGACCAATTTTTCAGTGTGACCTTGACAGCTTTTTCACAGAGAA 1802  
DB 135 CAGGAATGTGACCAATTTTTCAGTGTGACCTTGACAGCTTTTTCACAGAGAA 76  
QY 1803 GAGATTTTACACTGTTTCAAAACCGGGAGAGTTGGCTGTGTTAAAGAAAGCATTA 1862  
DB 75 GAGATTTTACACTGTTTCAAAACCGGGAGAGTTGGCTGTGTTAAAGAAAGCATTA 16  
QY 1863 TGCCTTAGACAGTGT 1877  
DB 15 TGCCTTAGACAGTGT 1

RESULT 14

US-09-867-701-8894/c  
Sequence 8894, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8894  
LENGTH: 201  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-867-701-8894

Query Match 8.8%; Score 166; DB 10; Length 201;  
Best Local Similarity 100.0%; Pred. No. 2.3e-59;  
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 AGAAGGGAGAGATATGATGACCCCGGAAGTAGACCTGTCAGTGTGCGTT 1560  
DB 181 AGAAGGGAGAGATATGATGACCCCGGAAGTAGACCTGTCAGTGTGCGTT 122  
QY 1561 TGGCCGAGCCATATCTCTCGAATCTGTTGGCATTCAGATACGCGCCATGTCA 1620  
DB 121 TGGCCGAGCCATATCTCTCGAATCTGTTGGCATTCAGATACGCGCCATGTCA 62  
QY 1621 CAATCAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1666  
DB 61 CAATCAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 16

RESULT 15

US-09-867-701-1532  
Sequence 1532, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1532  
LENGTH: 390  
TYPE: DNA  
ORGANISM: Homo sapiens



```
;
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 825
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1368)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-825

Query Match
Best Local Similarity 1.4%; Score 27; DB 10; Length 1368;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1871 ACAGTGTAAAAAAAAAAAAAAAAA 1897
Db 459 ACAGTGTAAAAAAAAAAAAAAAAA 485

RESULT 20
US-09-960-352-9079/c
; Sequence 9079, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9079
; LENGTH: 152
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB3058-009-Q1-K1-B12
US-09-960-352-9079

Query Match
Best Local Similarity 1.3%; Score 25; DB 10; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1873 AGTGTAAAAAAAAAAAAAAAAA 1897
Db 52 AGTGTAAAAAAAAAAAAAAAAA 28

RESULT 21
US-09-867-701-4911/c
; Sequence 4911, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4911
; LENGTH: 363
```

```
;
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4911

Query Match
Best Local Similarity 1.3%; Score 25; DB 10; Length 363;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1873 AGTGTAAAAAAAAAAAAAAAAA 1897
Db 27 AGTGTAAAAAAAAAAAAAAAAA 3

RESULT 22
US-09-867-701-5174/c
; Sequence 5174, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5174
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-5174

Query Match
Best Local Similarity 1.3%; Score 25; DB 10; Length 395;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1873 AGTGTAAAAAAAAAAAAAAAAA 1897
Db 27 AGTGTAAAAAAAAAAAAAAAAA 3

RESULT 23
US-09-919-580-143/c
; Sequence 143, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 62, 74, 231, 357, 405, 499, 510, 532, 564
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-143

Query Match
Best Local Similarity 1.3%; Score 25; DB 10; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1873 AGTGTAAAAAAAAAAAAAAAAA 1897
```

Db 35 AGTGTAAAAA 11

## RESULT 24

US-09-925-301-584

Sequence 584, Application US/09925301

Patent No. US20020052308A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 584

LENGTH: 2968

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc-feature

LOCATION: (454)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc-feature

LOCATION: (1437)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc-feature

LOCATION: (2961)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc-feature

LOCATION: (2964)

OTHER INFORMATION: n equals a,t,g, or c

US-09-925-301-584

Query Match 1.3%; Score 25; DB 10; Length 2968;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1873 AGTGTAAAAA 1897

|||||

Db 2886 AGTGTAAAAA 2910

## RESULT 25

US-09-770-696-104

Sequence 104, Application US/09770696

Patent No. US20010044940A1

GENERAL INFORMATION:

APPLICANT: Goriach, Jörn

APPLICANT: An, Yong-Qiang

APPLICANT: Hamilton, Carol M.

APPLICANT: Price, Jennifer L.

APPLICANT: Raines, Tracy M.

APPLICANT: Yu, Yang

APPLICANT: Rameaka, Joshua G.

APPLICANT: Page, Amy

APPLICANT: Matthew, Abraham V.

APPLICANT: Ledford, Brooke L.

APPLICANT: Woessner, Jeffrey P.

APPLICANT: Haas, William David

APPLICANT: Garcia, Carlos A.

APPLICANT: Kricker, Maaja

APPLICANT: Slader, Ted

APPLICANT: Davis, Keith R.

APPLICANT: Allen, Keith

APPLICANT: Hoffman, Neil

APPLICANT: Hurdan, Patrick

TITLE OF INVENTION: Expressed Sequences of Arabidopsis

TITLE OF INVENTION: thaliana

FILE REFERENCE: 2031US (PARA-020PRV)

CURRENT APPLICATION NUMBER: US/09/770,696

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/178,278

PRIOR FILING DATE: 2000-01-27

NUMBER OF SEQ ID NOS: 911

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 104

LENGTH: 208

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-770-696-104

Query Match 1.3%; Score 24; DB 10; Length 208;  
Best Local Similarity 100.0%; Pred. No. 0.8;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897

|||||

Db 169 GTGTAAAAA 192

## RESULT 26

US-09-920-300A-58

Sequence 58, Application US/09920300A

Patent No. US20020136728A1

GENERAL INFORMATION:

APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeline Joy

APPLICANT: Xu, Jianshun

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.547

CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 58

LENGTH: 258

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc-feature

LOCATION: 258

OTHER INFORMATION: n = A,T,C or G

US-09-920-300A-58

Query Match 1.3%; Score 24; DB 10; Length 258;

Best Local Similarity 100.0%; Pred. No. 0.79;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAA 1897

|||||

Db 228 GTGTAAAAA 251

## RESULT 27

US-10-033-528-58

Sequence 58, Application US/10033528

Patent No. US20020131971A1

GENERAL INFORMATION:

APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeline Joy

APPLICANT: Xu, Jianshun

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.547C1

CURRENT APPLICATION NUMBER: US/10/033,528

CURRENT FILING DATE: 2001-12-26

NUMBER OF SEQ ID NOS: 1896

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 258
; OTHER INFORMATION: n = A,T,C or G
; US-10-033-528-58
```

```
Query Match          1.3%; Score 24; DB 12; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1874 GTGTAATAAAAAAAAAAAAAAAAAA 1897
DB 228 GTGTAATAAAAAAAAAAAAAAAAAA 251
```

```
RESULT 28
US-09-770-791-315/C
```

```
; Sequence 315, Application US/09770791
; Patent No. US2002062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Ramwaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hufman, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-770-791-315
```

```
Query Match          1.3%; Score 24; DB 10; Length 373;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1874 GTGTAATAAAAAAAAAAAAAAAAAA 1897
DB 24 GTGTAATAAAAAAAAAAAAAAAAAA 1
```

```
RESULT 29
US-09-924-035A-439/C
; Sequence 439, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gorlach, Jörn
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 439
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-924-035A-439
```

```
Query Match          1.3%; Score 24; DB 10; Length 419;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1874 GTGTAATAAAAAAAAAAAAAAAAAA 1897
DB 45 GTGTAATAAAAAAAAAAAAAAAAAA 22
```

```
RESULT 30
US-10-062-254-125
; Sequence 125, Application US/10062254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yixen
; APPLICANT: Hanke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 125
; LENGTH: 766
```



```
; TYPE: DNA
; ORGANISM: Picramnia pentandra
; US-10-062-254-125

Query Match
Best Local Similarity 1.3%; Score 24; DB 12; Length 766;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
DB 734 GTGTAAAAAAAAAAAAAAAAAAAA 757

RESULT 31
US-09-925-300-627
; Sequence 627, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 627
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (863)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-300-627

Query Match
Best Local Similarity 1.3%; Score 24; DB 10; Length 871;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
DB 836 GTGTAAAAAAAAAAAAAAAAAAAA 859

RESULT 32
US-10-078-929-89
; Sequence 89, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
```

```
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 89
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-078-929-89

Query Match
Best Local Similarity 1.3%; Score 24; DB 12; Length 939;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
DB 886 GTGTAAAAAAAAAAAAAAAAAAAA 909

RESULT 33
US-09-925-300-384
; Sequence 384, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 384
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1014)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1015)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1026)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-300-384

Query Match
Best Local Similarity 1.3%; Score 24; DB 10; Length 1029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897
DB 978 GTGTAAAAAAAAAAAAAAAAAAAA 1001
```

RESULT 34  
US-09-800-528-5  
; Sequence 5, Application US/09800528  
; Patent No. US20010016955A1  
; GENERAL INFORMATION:  
; APPLICANT: Woodhead, Mary Rose  
; APPLICANT: Taylor, Mark Andrew  
; APPLICANT: Brennan, Rex Michael  
; TITLE OF INVENTION: BLACKCURRANT PROMOTERS AND GENES  
; FILE REFERENCE: C70237D1  
; CURRENT APPLICATION NUMBER: US/09/800,528  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: 09/068,140  
; PRIOR FILING DATE: 1998-11-02  
; PRIOR APPLICATION NUMBER: PCT/EP/9604807  
; PRIOR FILING DATE: 1996-11-04  
; PRIOR APPLICATION NUMBER: GB9522558.7  
; PRIOR FILING DATE: 1995-11-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1046  
; TYPE: DNA  
; ORGANISM: Ribes nigrum  
US-09-800-528-5

Query Match 1.3%; Score 24; DB 10; Length 1046;  
Best Local Similarity 100.0%; Pred. No. 0.73;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAATAAAAAAAAAAAAAA 1897  
|||||  
DB 1015 GTGTAATAAAAAAAAAAAAAA 1038

RESULT 35  
US-09-764-870-15  
; Sequence 15, Application US/09764870  
; Patent No. US20020042386A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P214  
; CURRENT APPLICATION NUMBER: US/09/764,870  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 646  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 1066  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-870-15

Query Match 1.3%; Score 24; DB 10; Length 1066;  
Best Local Similarity 100.0%; Pred. No. 0.73;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAATAAAAAAAAAAAAAA 1897  
|||||  
DB 1043 GTGTAATAAAAAAAAAAAAAA 1066

RESULT 36  
US-09-410-194-14  
; Sequence 14, Application US/09410194  
; Patent No. US20020095030A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jurg  
; APPLICANT: Thome, Margot  
; APPLICANT: Burns, Kimberly

; APPLICANT: Irmier, Marten  
; APPLICANT: Hahne, Michael  
; APPLICANT: Schroeter, Michael  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Bodmer, Jean-Luc  
; APPLICANT: Steiner, Veronique  
; APPLICANT: Rimoldi, Donata  
; APPLICANT: Hofmann, Kay  
; APPLICANT: French, E. Lars  
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
; FILE REFERENCE: 11141-002001  
; CURRENT APPLICATION NUMBER: US/09/410,194  
; CURRENT FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: PCT/EP98/01857  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 1190  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (394)...(1056)  
US-09-410-194-14

Query Match 1.3%; Score 24; DB 10; Length 1190;  
Best Local Similarity 100.0%; Pred. No. 0.73;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAATAAAAAAAAAAAAAA 1897  
|||||  
DB 1121 GTGTAATAAAAAAAAAAAAAA 1144

RESULT 37  
US-09-992-598-286  
; Sequence 286, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paonli, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16



PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092162  
PRIOR FILING DATE: 1998-07-09

## Query Match

Best Local Similarity 1.3%; Score 24; DB 9; Length 1337;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1874 GTGTAAAAA 1897  
Db 1298 GTGTAAAAA 1321

## RESULT 38

US-09-989-722-286

Sequence 286, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
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PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
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PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
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PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
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PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17

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 PRIOR FILING DATE: 1998-06-17  
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 PRIOR FILING DATE: 1998-06-18  
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 PRIOR FILING DATE: 1998-06-18  
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 PRIOR FILING DATE: 1998-06-22  
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 PRIOR FILING DATE: 1998-06-24  
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 PRIOR FILING DATE: 1998-06-24  
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 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090557  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090676  
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 PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544

PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 24; DB 10; Length 1337;  
 Best Local Similarity 100.0%; Pred. No. 0.72;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAAGAAAAA 1897  
 DB 1298 GTGTAAGAAAAA 1321

RESULT 39  
 US-09-989-723-286  
 Sequence 286, Application US/09989723  
 Patent No. US2002072092A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gunney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P27301P62  
 CURRENT APPLICATION NUMBER: US/09/989,723  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28



;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
Query Match 1.38; Score 24; DB 10; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1874 GTGTAAAAA 1897  
Db 1298 GTGTAAAAA 1321  
RESULT 40  
US-09-989-279-286  
; Sequence 286, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltzen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC56  
; CURRENT APPLICATION NUMBER: US/09/989,279  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087609

;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088021  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088025  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088030  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088326  
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;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
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PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
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PRIOR FILING DATE: 1998-06-19  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 24; DB 10; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1874 GTGTAAAAAAAAAAAAAAAAAAAA 1897  
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Db 1298 GTGTAAAAAAAAAAAAAAAAAAAA 1321

RESULT 41  
US-09-989-727-286  
; Sequence 286, Application US/0989727  
; Patent No. US20020072497A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerder, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C65  
; CURRENT APPLICATION NUMBER: US/09/989,727  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Query Match

Best Local Similarity 100.0%; Score 24; DB 10; Length 1337;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1298 GTGTAAAAAAAAAAAAAAAA 1321

RESULT 42  
US-09-989-731-286  
Sequence 286, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
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CURRENT FILING DATE: 2001-11-20  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
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Query Match 1.3%; Score 24; DB 10; Length 1337;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;;  
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Db 1298 GTGTAAAAAAAAAAAAAAAA 1321  
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RESULT 43  
US-09-989-732-286  
; Sequence 286, Application US/09989732  
; Patent No. US20020123463A1  
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
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;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC57  
;; CURRENT APPLICATION NUMBER: US/09/989,732  
;; CURRENT FILING DATE: 2001-11-19  
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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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APPLICANT: Wood, William I.
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29: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
30: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
31: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
32: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
33: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
34: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
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36: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
37: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
38: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
39: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
40: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
41: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
42: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*
43: /cgn2_6/ptoddata/1/pna/US0958_COMB.seq:*

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Result No.	Score	Query Match	Length	ID	Description
1	1897	100.0	1897	1 PCT-US01-45395-214	Sequence 214, App
2	1897	100.0	1897	1 US-09-825-294-214	Sequence 214, App
3	1897	100.0	1897	36 US-09-970-966-214	Sequence 214, App
4	1897	100.0	1897	42 US-10-212-677-214	Sequence 214, App
5	1718	90.6	1967	1 PCT-US02-29964-16	Sequence 16, Appl
6	1714	90.4	1918	17 US-09-597-022-4454	Sequence 4454, App
7	1707	90.0	1925	31 US-09-808-383-4454	Sequence 4454, App
8	1707	90.0	1925	25 US-09-652-121-7293	Sequence 7293, App
9	1707	90.0	1925	25 US-09-652-128-9375	Sequence 9375, App
10	1707	90.0	1925	25 US-09-652-917-3346	Sequence 3346, App
11	1707	90.0	1925	27 US-09-652-917-3346	Sequence 3346, App
12	1707	90.0	1925	28 US-09-652-917-3346	Sequence 3346, App
13	1707	90.0	1925	28 US-09-652-917-3346	Sequence 3346, App
14	1587	83.7	1917	25 US-09-652-121-6191	Sequence 6191, App
15	1587	83.7	1917	25 US-09-652-128-7518	Sequence 7518, App
16	1587	83.7	1917	25 US-09-652-355-9112	Sequence 9112, App
17	1587	83.7	1917	25 US-09-652-914-8473	Sequence 8473, App
18	1587	83.7	1917	25 US-09-652-917-2477	Sequence 2477, App
19	1587	83.7	1917	25 US-09-652-917-2477	Sequence 2477, App
20	1587	83.7	1917	25 US-09-652-917-2477	Sequence 2477, App
21	1587	83.7	1917	25 US-09-652-917-2477	Sequence 2477, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES



Db	1321	GCACAAAGCGGGCGCTGTGCTGTGTGGAGTGGCCATGTACGGGCAAGGGCGCTTCTGTGTGT	1380
OY	1381	TGGCGTGTGCAAGCGACAGCGCGGACACAGCACTGTGACAGAACCCGGCGAAATCTCT	1440
Db	1381	TGGCGTGTCTGAGCGACAGCGCGGACAGCAAGCACTGTGACAGAACCCGGCGAAATCTCT	1440
OY	1441	GGGAGACACCGCTGTACAGGAGGGGGGTGATGACCGAGCTGAGGTAGAAAAACGTCTCCG	1500
Db	1441	GGGAGGACACCGCTGTACAGGAGGGGGGTGATGACCGAGCTGAGGTAGAAAAACGTCTCCG	1500
OY	1501	AGAGGGGAGAGAGCATATTTACGCCCGGAGTAGAGCACTCTCCAGTGTGCTGGGTT	1560
Db	1501	AGAGGGGAGAGAGCATATTTACGCCCGGAGTAGAGCACTCTCTCCAGTGTGCTGGGTT	1560
OY	1561	TGGCCGAGCCATGATCTCTCGAATCTGTTGGGCACTCCAGCATAGGCAATGTACAA	1620
Db	1561	TGGCCGAGCCATGATCTCTCGAATCTGTTGGGCACTCCAGCATAGGCAATGTACAA	1620
OY	1621	CAATCAGCCCTGGGCAACACAGCAGAGGAGGAGAGACAGAAAAAGAAAAACACAGCAT	1680
Db	1621	CAATCAGCCCTGGGCAACACAGCAGAGGAGGAGAGACAGAAAAAGAAAAACACAGCAT	1680
OY	1681	GAGAACACAGTAATGAAATAAACCCATTAATAATTTTAGCCCCCTGTGTGTGTGTACTG	1740
Db	1681	GAGAACACAGTAATGAAATAAACCCATTAATAATTTTAGCCCCCTGTGTGTGTGTACTG	1740
OY	1741	GGCAGAGAAATGTTACCAATTTTTCAGTGTGTGACTGACAGCTTCTTTTGGCACAGCAA	1800
Db	1741	GGCAGAGAAATGTTACCAATTTTTCAGTGTGTGACTGACAGCTTCTTTTGGCACAGCAA	1800
OY	1801	GAGAGAAATTTACACTGTCTTCAAAACCCGGGGGAGTGGCTGTGTTAAAGAAAGACATTA	1860
Db	1801	GAGAGAAATTTACACTGTCTTCAAAACCCGGGGGAGTGGCTGTGTTAAAGAAAGACATTA	1860
OY	1861	AATGCTTTAGCAGGTGTAAAAAAGAAAAAAGAAAAA 1897	
Db	1861	AATGCTTTAGCAGGTGTAAAAAAGAAAAAAGAAAAA 1897	

```
US-09-825-294-214
RESULT 2
US-09-825-294-214
Sequence: 214, Application US/09825294
GENERAL INFORMATION:
APPLICANT: Xu, JIangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484c5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 214
LENGTH: 1697
TYPE: DNA
ORGANISM: Homo sap lens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1697)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214
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Query Match	100.0%	Score 1897	DB 31	Length 1897
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1897, Conservative	0	Mismatches	0	Indels 0
				Gaps 0

0y 1 GCCAACTCCGSAAGGCTCTGGTGTCTGGCCCGGAGACCGGAGACAGACAGACCCG 60  
|||||  
|||  
Db 1 GCCAACTCCGSAAGGCTCTGGTGTCTGGCCCGGAGACCGGAGACAGACAGACCCG 60  
|||||  
0y 61 CAGCCGSGAGCCGCGAGCGCGGCGCATGCAAGGCTCCGGGAGCGGCACTGCGGGCTCTCTTA 120

Db	61	CAGCCGGGAGGCCAGAGGGCGGGCGATTCAGAGCTCCGCGAGCGGACACTCGGCTCTCTCA	120
Qy	121	AGCTACGACGCTGCTTCACGGGAGAGAGGGGGGCCACAGAGCTCGGGACGCCACAGC	180
Db	121	AGCTACGACGCTCTCTTCGCGGGAGAGAGGGGGGCCACAGAGCTCGGGACGCCACAGC	180
Qy	181	CGCTGCACCCGGGGCAGCGTCGCGTGCCTGCTGCGCTCTGTGATGCGCTTGGCCCTGCCG	240
Db	181	CGCTGCACCCGGGGCAGCGTCGCGTGCCTGCTGCGCTCTGTGATGCGCTTGGCCCTGCCG	240
Qy	241	GCCCCGGGACCTCCGGAGAAATGTAAGTCTTAGCATTCGCGGCACTTTTTCGGATTTGTT	300
Db	241	GCCCCGGGACCTCCGGAGAAATGTAAGTCTTAGCATTCGCGGCACTTTTTCGGATTTGTT	300
Qy	301	CTTGCTTCAGAGCTTTTCGCGTGCATAATCCAGTCTACAGTGTGAAGAAATTCACACTGA	360
Db	301	CTTGCTTCAGAGCTTTTCGCGTGCATAATCCAGTCTACAGTGTGAAGAAATTCACACTGA	360
Qy	361	CACGACCTGCTCTCCGCCAGATTCAATTTGAATTCACGGGTGAACGTTCAAGACATGTG	420
Db	361	CACGACCTGCTCTCCGCCAGATTCAATTTGAATTCACGGGTGAACGTTCAAGACATGTG	420
Qy	421	TCAGAAACAAATGTATGAGGAGAAATGCGCGGATCAATGTACCCGAACTCTGTGCATCATC	480
Db	421	TCAGAAACAAATGTATGAGGAGAAATGCGCGGATCAATGTACCCGAACTCTGTGCATCATC	480
Qy	481	AGCGGCTGTCTCATCGCTCTGCGGGGTACAGTCTCTTGCTGCCAGGGAACATGAA	540
Db	481	AGCGGCTGTCTCATCGCTCTGCGGGGTACAGTCTCTTGCTGCCAGGGAACATGAA	540
Qy	541	CTCAGTTTGATCATAGCTGTGCAACACCCCTCTTTGTAAAGGGCCAAAGCCCAAGAAAG	600
Db	541	CTCAGTTTGATCATAGCTGTGCAACACCCCTCTTTGTAAAGGGCCAAAGCCCAAGAAAG	600
Qy	601	GGGAGTTCTCCCTCGGCGCTCAGGGCAGGGCTCCGACACACATCTTTCCTCAAAAT	660
Db	601	GGGAGTTCTCCCTCGGCGCTCAGGGCAGGGCTCCGACACACATCTTTCCTCAAAAT	660
Qy	661	AGCCCTCTTCTCGGCACACAGTGTGAAGATGCAACCCCTCTCTCCTCAATTTTC	720
Db	661	AGCCCTCTTCTCGGCACACAGTGTGAAGATGCAACCCCTCTCTCCTCAATTTTC	720
Qy	721	TTCCAGCCCTGGCCCCAACCCCACTCTCGAGTGAATTTCTCTGGGCTGCTCTTTT	780
Db	721	TTCCAGCCCTGGCCCCAACCCCACTCTCGAGTGAATTTCTCTGGGCTGCTCTTTT	780
Qy	781	ATTCTGGGTAGGAGGGGAGTCGTTCTCTTTGTTCTCTGTGCATAATTAATGAAG	840
Db	781	ATTCTGGGTAGGAGGGGAGTCGTTCTCTTTGTTCTCTGTGCATAATTAATGAAG	840
Qy	841	CTCGGTAAAGCATTCGTAATTAATTAACGTGTGACTCAATTTTCAGATGTACTTAAGA	900
Db	841	CTCGGTAAAGCATTCGTAATTAATTAACGTGTGACTCAATTTTCAGATGTACTTAAGA	900
Qy	901	AGGAGGTGAGTGAATTTACCCCACTGTCTGTGAACCGGAGTCAAGGCCAGGCTGGC	960
Db	901	AGGAGGTGAGTGAATTTACCCCACTGTCTGTGAACCGGAGTCAAGGCCAGGCTGGC	960
Qy	961	AGAGTCWGTCTTTGAAGTACATGAGTGGGCACTTGCTTTTGTAAAGCTCCAGTGC	1020
Db	961	AGAGTCWGTCTTTGAAGTACATGAGTGGGCACTTGCTTTTGTAAAGCTCCAGTGC	1020
Qy	1021	CATTTCATCCCTGTATGGGGCATAGTTTGATGTGAGAGTGAAGTGAAGTTCCTTTT	1080
Db	1021	CATTTCATCCCTGTATGGGGCATAGTTTGATGTGAGAGTGAAGTGAAGTTCCTTTT	1080
Qy	1081	GCGTGAAGGCCACTTCCCACTCAAGGCTCCCTGCTTGACATTCAAACTTCATCTCTCT	1140
Db	1081	GCGTGAAGGCCACTTCCCACTCAAGGCTCCCTGCTTGACATTCAAACTTCATCTCTCT	1140
Qy	1141	GAAGAACATTCCTGCGAGGAATTTGGCTGTTCGCGCTAGTTGGGCTCTACTACT	1200
Db	1141	GAAGAACATTCCTGCGAGGAATTTGGCTGTTCGCGCTAGTTGGGCTCTACTACT	1200





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Db 901 AGAGGTGAGTGAAGTTCCACCCCATGTCTGTGTAACGGAGTCAAGGCCAGCTGGC 960
Qy 961 AGAGTCTGCTTGAAGTCACTAGAGTGGGACATCTGCTTTTGAAGCCTCCAGTGC 1020
Db 961 AGAGTCTGCTTGAAGTCACTAGAGTGGGACATCTGCTTTTGAAGCCTCCAGTGC 1020
Qy 1021 CATTTCATCCCTGATGGGGGATAGTTGAGACTGACAGAGTGAAGTACGCTTTCTAG 1080
Db 1021 CATTTCATCCCTGATGGGGGATAGTTGAGACTGACAGAGTGAAGTACGCTTTCTAG 1080
Qy 1081 GCGTGGAGGGGACGTTCCCACTCAAGGCTCCCTGCTTGAACATTCATGCTCCT 1140
Db 1081 GCGTGGAGGGGACGTTCCCACTCAAGGCTCCCTGCTTGAACATTCATGCTCCT 1140
Qy 1141 GAAACCATCTCTGACAGCAAAATGGCTGCTTGGCGCTGAGTGGGCTCTAGTACT 1200
Db 1141 GAAACCATCTCTGACAGCAAAATGGCTGCTTGGCGCTGAGTGGGCTCTAGTACT 1200
Qy 1201 CGAGACTCAATGACTGGGACTTAACTGGGCTGGCTCTGCTTGAAGTGGTTAAGA 1260
Db 1201 CGAGACTCAATGACTGGGACTTAACTGGGCTGGCTCTGCTTGAAGTGGTTAAGA 1260
Qy 1261 AAATCTTCTCAATCTCTGACAGCACTGGCGCCGGGAGCGCAAGAGCAAGCGGCT 1320
Db 1261 AAATCTTCTCAATCTCTGACAGCACTGGCGCCGGGAGCGCAAGAGCAAGCGGCT 1320
Qy 1321 GCACAAAGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1321 GCACAAAGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Qy 1381 TGGCGTGTGACAGGAGCGGGGGGAGCAGACAGCTGACAGCAACCGCGGAAAGCT 1440
Db 1381 TGGCGTGTGACAGGAGCGGGGGGAGCAGACAGCTGACAGCAACCGCGGAAAGCT 1440
Qy 1441 GCGAGGACACCGTGTACAGAGCGGGGTTGATGACCGAGCTGAGTGAAGAAACGCTCCG 1500
Db 1441 GCGAGGACACCGTGTACAGAGCGGGGTTGATGACCGAGCTGAGTGAAGAAACGCTCCG 1500
Qy 1501 AGAAGGGGAGGAGTCAATGACAGCGCGGAAAGTGGAGCTGCTGCTGCTGCTGCTGCT 1560
Db 1501 AGAAGGGGAGGAGTCAATGACAGCGCGGAAAGTGGAGCTGCTGCTGCTGCTGCTGCT 1560
Qy 1561 TGGCGGACCGATGATCCCGAATCTGTTGGGATCCAGCATACGGCAATGTCACAA 1620
Db 1561 TGGCGGACCGATGATCCCGAATCTGTTGGGATCCAGCATACGGCAATGTCACAA 1620
Qy 1621 CAATGAGCCCTGGGAGACAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1680
Db 1621 CAATGAGCCCTGGGAGACAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1680
Qy 1681 GAGAACACAGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
Db 1681 GAGAACACAGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
Qy 1741 GCCAGGAATGTTACCAATTTTTCAGTGTGAGCTTGAACAGCTTTTGGCACAAAGCA 1800
Db 1741 GCCAGGAATGTTACCAATTTTTCAGTGTGAGCTTGAACAGCTTTTGGCACAAAGCA 1800
Qy 1801 GAGAGAAATTTAACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGCATTA 1860
Db 1801 GAGAGAAATTTAACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGCATTA 1860
Qy 1861 AATGCTTTAGACAGTGTAAAAA 1897
Db 1861 AATGCTTTAGACAGTGTAAAAA 1897

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RESULT 5
PCT-US02-29964-16
: Sequence 16, Application PC/TUS0229964
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom

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: APPLICANT: Ren, Feiyan
: APPLICANT: Zhang, Jie
: APPLICANT: Zhao, Qing A.
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Xue, Aiding J.
: APPLICANT: Wang, Dunrui
: APPLICANT: Ghosh, Malabika
: APPLICANT: Asundi, Vinod
: APPLICANT: Wehrman, Tom
: APPLICANT: Zhou, Ping
: APPLICANT: Goodrich, Ryle W.
: APPLICANT: Weng, Gezhi
: APPLICANT: Haley-Vicente, Dana
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: Novel Nucleic Acids and
: FILE REFERENCE: 809ACIP PCT
: CURRENT APPLICATION NUMBER: PCT/US02/29964
: CURRENT FILING DATE: 2002-09-19
: PRIOR FILING DATE: US 60/323,739
: PRIOR FILING DATE: 2001-09-19
: PRIOR APPLICATION NUMBER: US 09/488,725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: PCT/US01/02623
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: US 09/491,404
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: PCT/US00/35017
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: PCT/US01/03800
: PRIOR FILING DATE: 2001-02-05
: PRIOR APPLICATION NUMBER: US 09/515,126
: PRIOR FILING DATE: 2000-02-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: SOFTWARE: PCT-FL-Genes Version 6.0
: SEQ ID NO 16
: LENGTH: 1967
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (338)..(763)
: PCT-US02-29964-16

Query Match 90.6%; Score 1718; DB 1; Length 1967;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1866; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GGTGCTGCGCCGGAGCGGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 78
Db 97 GTGCTGCGCCGGAGCGGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 156
Qy 79 CGGGGATGAGAGCTCCGAGAGGGGACCTGGCGCTCTTAAGCTAAGCAAGCTGTCTC 138
Db 157 CGGGGATGAGAGCTCCGAGAGGGGACCTGGCGCTCTTAAGCTAAGCAAGCTGTCTC 216
Qy 139 CGGGGAGAGAGCGGGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 198
Db 217 CGGGGAGAGAGCGGGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 276
Qy 199 CTCGGTGTGTGCTGCTCTGTATGAGGCTTGGCTCTCTCCGGGCGCGGAGCTCGGGAG 258
Db 277 CTCGGTGTGTGCTGCTCTGTATGAGGCTTGGCTCTCTCCGGGCGCGGAGCTCGGGAG 336
Qy 259 AATGTGGTCTTAGAGCATCGCGGCACTTTTGGGATTTCTTCTTCCAGAGCTTTGC 318

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Db 337 AATGTGGCTCTAGCAGTCGGGCAACTTTTGGGATTTCTTGTCTCCAGGCTTTGC 396
Qy 319 GCTGCAAAATCCAGTGTCTACAGTGTGAAGAAATTCAGTGAACAACGAGTCTCTCC 378
Db 397 GCTGCAAAATCCAGTGTCTACAGTGTGAAGAAATTCAGTGAACAACGAGTCTCTCC 456
Qy 379 CGAGTTCATTTGTGAATTTGCACGAGTGAACGTTCAAGACATGTGTGAGAAGAGTATGA 438
Db 457 CGAGTTCATTTGTGAATTTGCACGAGTGAACGTTCAAGACATGTGTGAGAAGAGTATGA 516
Qy 439 GCAAAAGTCCCGGATCATGTATCCGCAAGTCTCTGTGATCATCAGGCGCTGTCTATGC 498
Db 517 GCAAAAGTCCCGGATCATGTATCCGCAAGTCTCTGTGATCATCAGGCGCTGTCTATGC 576
Qy 499 CTGTGCGGGGTACCAAGTCTCTGTCTCCCGGAGGAACTGAACATGTTGATCATCAGCTG 558
Db 577 CTGTGCGGGGTACCAAGTCTCTGTCTCCCGGAGGAACTGAACATGTTGATCATCAGCTG 636
Qy 559 CTGCAACACCCCTCTTTGTAAACGGGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGG 618
Db 637 CTGCAACACCCCTCTTTGTAAACGGGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGG 696
Qy 619 CCTGAGGCGAGGCTCCGCAACCATCTGTCTCTCAAAATATAGCCCTCTCTCGGCA 678
Db 697 CCTGAGGCGAGGCTCCGCAACCATCTGTCTCTCAAAATATAGCCCTCTCTCGGCA 756
Qy 679 CTGCTGAAGCTGAAGAGATGCCACCCCTCTGTGATTTCTTCCAGCCCTCGGCCCA 738
Db 757 CTGCTGAAGCTGAAGAGATGCCACCCCTCTGTGATTTCTTCCAGCCCTCGGCCCA 816
Qy 739 ACCCCCAACCTCTGTGATGTTCTTCTGGGTCCTTTTCTGGGTAGGAGCGG 798
Db 817 ACCCCCAACCTCTGTGATGTTCTTCTGGGTCCTTTTCTGGGTAGGAGCGG 876
Qy 799 GAGTCCGTCTTCTTTTGTCTGTGCAAAATATGAAGAGCTCGTAAACATTTCTGA 858
Db 877 GAGTCCGTCTTCTTTTGTCTGTGCAAAATATGAAGAGCTCGTAAACATTTCTGA 936
Qy 859 ATAAATTCACGTCGATGATTTTCAATATGATCTTGAAGAGAGAGGTGAGTGAAGT 918
Db 937 ATAAATTCACGTCGATGATTTTCAATATGATCTTGAAGAGAGAGGTGAGTGAAGT 996
Qy 919 TCACCCCATGTGTGTAAACCGAGTCAAGCCAGGTGCGAGAGTCTGCTTGAAG 978
Db 997 TCACCCCATGTGTGTAAACCGAGTCAAGCCAGGTGCGAGAGTCTGCTTGAAG 1056
Qy 979 TCACGAGGTGGGATCTGCTTTTAAAGCTCCAGTGTCCATTCATCCCTGATGG 1038
Db 1057 TCACGAGGTGGGATCTGCTTTTAAAGCTCCAGTGTCCATTCATCCCTGATGG 1116
Qy 1039 GGCATAGTTGAGACTGCAAGAGTGAAGAGTCTTTTAAAGGCTGAGAGGCCAGTTCC 1098
Db 1117 GGCATAGTTGAGACTGCAAGAGTGAAGAGTCTTTTAAAGGCTGAGAGGCCAGTTCC 1176
Qy 1099 CACTCAAGGCTCCCTGCTTGAACATTCATGCTCTGAAAGACATTTCTCTGAG 1158
Db 1177 CACTCAAGGCTCCCTGCTTGAACATTCATGCTCTGAAAGACATTTCTCTGAG 1236
Qy 1159 CAGAATTTGCTGTTTGGGCTGAGTTGGGCTAGTACGAGTCAATGATGAGG 1218
Db 1237 CAGAATTTGCTGTTTGGGCTGAGTTGGGCTAGTACGAGTCAATGATGAGG 1296
Qy 1219 ACTTAGACTGGGCTGCGCTGCTGTAAGAGTCTTAAAGAAATCTTCAATCTCC 1278
Db 1297 ACTTAGACTGGGCTGCGCTGCTGTAAGAGTCTTAAAGAAATCTTCAATCTCC 1356
Qy 1279 TTGCAAGAGCAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1338
Db 1357 TTGCAAGAGCAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1416
Qy 1339 CGGTGTGAGTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1398
Db 1417 CGGTGTGAGTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1476

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Qy 1399 GCGGAGACAGACAGACCTGACAGAAACACCCCGCAAACTGCTCGAGACAGCTGTACA 1458
Db 1477 GCGGAGACAGACAGACCTGACAGAAACACCCCGCAAACTGCTCGAGACAGCTGTACA 1536
Qy 1459 GGAGGGGTTGATGACCGAGCTGAGGTGAGAAACGTTCTCCGAGAGAGAGAGATCA 1518
Db 1537 GGAGGGGTTGATGACCGAGCTGAGGTGAGAAACGTTCTCCGAGAGAGAGAGATCA 1596
Qy 1519 TGTACGCCCGGAGTAGAGACCTGCTCCAGTGTGCTTGGGTTGGCGGAGCATATCC 1578
Db 1597 TGTACGCCCGGAGTAGAGACCTGCTCCAGTGTGCTTGGGTTGGCGGAGCATATCC 1656
Qy 1579 TCCGATCTGTTGGGATCCAGCATACGGCAATGTACACAAATCAGCCCTGGGCA 1638
Db 1657 TCCGATCTGTTGGGATCCAGCATACGGCAATGTACACAAATCAGCCCTGGGCA 1716
Qy 1639 CACGAGCAGAGGGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1698
Db 1717 CACGAGCAGAGGGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1776
Qy 1699 TAAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGAAATGTTACCA 1758
Db 1777 TAAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGAAATGTTACCA 1836
Qy 1759 TTTTCAAGTGTGAGTGTGACAGTCTTTTGTCCACAGAGAGAGAGATTTAACACTGT 1818
Db 1837 TTTTCAAGTGTGAGTGTGACAGTCTTTTGTCCACAGAGAGAGAGATTTAACACTGT 1896
Qy 1819 TTCAACCCGAGGAGTGTGCTGTGTTAAAGAGAGAGATTAATGCTTTAGAGGTGA 1878
Db 1897 TTCAACCCGAGGAGTGTGCTGTGTTAAAGAGAGAGATTAATGCTTTAGAGGTGA 1956
Qy 1879 AAAAAAAAAA 1889
Db 1957 AAAAAAAAAA 1967

```

## RESULT 6

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US-09-397-022-4454
: Sequence 4454, Application US/09397022
: GENERAL INFORMATION:
: APPLICANT: Gearing, David P.
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
: FILE REFERENCE: HUMAN FETAL SKIN LIBRARY
: CURRENT APPLICATION NUMBER: US/09/397,022
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: 60/100,465
: PRIOR FILING DATE: 1998-09-15
: PRIOR APPLICATION NUMBER: 60/106,443
: PRIOR FILING DATE: 1998-10-30
: PRIOR APPLICATION NUMBER: 60/107,257
: PRIOR FILING DATE: 1998-11-05
: PRIOR APPLICATION NUMBER: 60/126,906
: PRIOR FILING DATE: 1999-03-30
: PRIOR APPLICATION NUMBER: 60/132,099
: NUMBER OF SEQ ID NOS: 1999-04-30
: SOFTWARE: PASTSEQ for Windows Version 3.0
: SEQ ID NO 4454
: LENGTH: 1918
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-397-022-4454

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Query Match 90.4%, Score 1714, DB 17, Length 1918;
Best Local Similarity 99.8%, Pred. No. 0;
Matches 1864; Conservative 8%; Mismatches 3; Indels 0; Gaps 0;
Qy 19 GGTGTGCGCCCGGAGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 78

```















Db 208 TAAACCATATAATTTAGCCCCCTCTTCTGTCTTACTGCGCCAGCAAAATGTTACCA 149  
Qy 1759 TTTTTCAGTGTGGACTTGACAGCTTCTTTTCCACAAGCAAGAAATTTAACTGT 1818  
Db 148 TTTTTCAGTGTGGACTTGACAGCTTCTTTTCCACAAGCAAGAAATTTAACTGT 89  
Qy 1819 TTTAAACCCGGGGAGTGTGGCTGTGTTAAAGAAAGAACATTAATGCTTTAGACAGTGA 1878  
Db 88 TTTAAACCCGGGGAGTGTGGCTGTGTTAAAGAAAGAACATTAATGCTTTAGACAGTGA 29

## RESULT 11

US-09-970-971-11085/c  
; Sequence 11085, Application US/09699997  
; GENERAL INFORMATION:  
; APPLICANT: Curtiss, Roy A. J.  
; APPLICANT: Siles-Santlago, Immaculada  
; APPLICANT: Distefano, Peter  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.2020-001  
; CURRENT APPLICATION NUMBER: US/09/699,997  
; CURRENT FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: 60/162,359  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 12714  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11085  
; LENGTH: 1925  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-970-971-11085

Query Match 90.0%; Score 1707; DB 27; Length 1925;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1857; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GGTGCTGCGCCCGGAGCGGAGCGGAGAGCAGAGACCCGCGAGCGGAGCGGAGCG 78  
Db 1888 GGTGCTGCGCCCGGAGCGGAGCGGAGAGCAGAGACCCGCGAGCGGAGCGGAGCG 1829  
Qy 79 CGGGCATGAGGCTCGGGAGGCGGAGCGGCTGCTTAAGCTACAGACCGTCTCTC 138  
Db 1828 CGGGCATGAGGCTCGGGAGGCGGAGCGGCTGCTTAAGCTACAGACCGTCTCTC 1769  
Qy 139 CGGGCAGCAGCGCGGGGCCAGCAGCTCGGAGCAGCAGCGGCTGACAGCGGAGCG 198  
Db 1768 CGGGCAGCAGCGCGGGGCCAGCAGCTCGGAGCAGCAGCGGCTGACAGCGGAGCG 1709  
Qy 199 CTCCGCTGCTGCTGCTCTCTCTGATGCGCTTGGCCCTCTCCCGGCGCGGAGTCCGGGAG 258  
Db 1708 CTCCGCTGCTGCTGCTCTCTCTGATGCGCTTGGCCCTCTCCCGGCGCGGAGTCCGGGAG 1649  
Qy 259 AATGTGGTCTTACAGCATGCGGCAACTTTTGGGATTTGTTCTTCTTCCAGGCTTTC 318  
Db 1648 AATGTGGTCTTACAGCATGCGGCAACTTTTGGGATTTGTTCTTCTTCCAGGCTTTC 1589  
Qy 319 GCTGCAATTCAGTGTCTACAGTGTGAAGATTCAGTGTGAACAAGTCTCTCTCC 378  
Db 1588 GCTGCAATTCAGTGTCTACAGTGTGAAGATTCAGTGTGAACAAGTCTCTCTCC 1529  
Qy 379 CGAGTTCATGTGAATTTGACAGGCTGAACCTTTGAAGCATGTGTCAAGAAAGTATGA 438  
Db 1528 CGAGTTCATGTGAATTTGACAGGCTGAACCTTTGAAGCATGTGTCAAGAAAGTATGA 1469  
Qy 439 GCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATGAGGCGCTGTCTATGC 498  
Db 1468 GCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATGAGGCGCTGTCTATGC 1409  
Qy 499 CTCTGCGGGGTACAGTCTCTTGTCTCCCAAGGAAACTGAAGTGTGATCATGCTG 558  
Db 1408 CTCTGCGGGGTACAGTCTCTTGTCTCCCAAGGAAACTGAAGTGTGATCATGCTG 1349

Qy 559 CTGCAACACCCCTCTTGTGTAAGGGGCAAGGCCCAAGAAAGGGAAGTGTGCTCGGC 618  
Db 1348 CTGCAACACCCCTCTTGTGTAAGGGGCAAGGCCCAAGAAAGGGAAGTGTGCTCGGC 1289  
Qy 619 CCTCAGGCGAGGCTCGGAGCAGCAGTCTGTGCTCAATTAAGGCTCTTCTCGGCACA 678  
Db 1288 CCTCAGGCGAGGCTCGGAGCAGCAGTCTGTGCTCAATTAAGGCTCTTCTCGGCACA 1229  
Qy 679 CTGTGAACTGAAGAGATGCAACCCCTCTGATGTTCTTCTCAGCCCTCGGCCCA 738  
Db 1228 CTGTGAACTGAAGAGATGCAACCCCTCTGATGTTCTTCTCAGCCCTCGGCCCA 1169  
Qy 739 ACCCCACCTCCCTGAGAGATTTCTTGGGTCTCTTTATTTCTGGATAGGAGCGG 798  
Db 1168 ACCCCACCTCCCTGAGAGATTTCTTGGGTCTCTTTATTTCTGGATAGGAGCGG 1109  
Qy 799 GAGTCCGTTCTCTTCTTCTGCAAAATGAAGAAAGAGCTGTAAGCATTTCTGA 858  
Db 1108 GAGTCCGTTCTCTTCTTCTGCAAAATGAAGAAAGAGCTGTAAGCATTTCTGA 1049  
Qy 859 ATAAATTCAGCTTGACAGTAATTTAGTATGTTGAGGAAGAGAGTGTGAAGT 918  
Db 1048 ATAAATTCAGCTTGACAGTAATTTAGTATGTTGAGGAAGAGAGTGTGAAGT 989  
Qy 919 TCACCCCATGCTGTGTAACCGGAGTCAAGGCGAGCTGCGAGAGTGTGCTTGAAG 978  
Db 988 TCACCCCATGCTGTGTAACCGGAGTCAAGGCGAGCTGCGAGAGTGTGCTTGAAG 929  
Qy 979 TCAGTAGAGTGGCATCTGCTTTTGTAAAGCTTCAGTGTCCATTCCTCATGATGG 1038  
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Qy 1039 GGCATAGTTTGAGACTGCAAGAGTGAAGTACGTTTCTTAAGGCTGAGGCGCAGTTC 1098  
Db 868 GGCATAGTTTGAGACTGCAAGAGTGAAGTACGTTTCTTAAGGCTGAGGCGCAGTTC 809  
Qy 1099 CACTCAAGGCTCCCTCGCTGCTGATTCATTAACATTCATGCTGTAAGAACATTCCTGAG 1158  
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Qy 1159 CAGAAATGCTGTTTCCGCGCTGAGTGGCTCTAGTACGAGCTCAATGACTGGG 1218  
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Qy 1279 TTGCAGAGACTGGGCGCGGAGCGGAAGAGCAACGGGCGCTGCAAAAGGCGGCGTGT 1338  
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Qy 1339 CGGTGTGAGTGGCATGTACGCGCAGAGCGCTTCTGCTGTGGCTGTGTCAGCGACA 1398  
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Qy 1399 GCGGCGACAGCAGCACTCGGCAAGAAACCCGCGAAGTGTGTGGAGACACCTGTGACA 1458  
Db 508 GCGGCGACAGCAGCACTCGGCAAGAAACCCGCGAAGTGTGTGGAGACACCTGTGACA 449  
Qy 1459 GAGCGGGTGTATGACGAGCTGAGGTGAGAAACGTTCTCCGAGAAAGGAGAGATCA 1518  
Db 448 GAGCGGGTGTATGACGAGCTGAGGTGAGAAACGTTCTCCGAGAAAGGAGAGATCA 389  
Qy 1519 TGTACGCGCGGAAATAGAGACTCTCTCAAGTCTGCTTGGGTTGGCGGAGCATATTC 1578  
Db 388 TGTACGCGCGGAAATAGAGACTCTCTCAAGTCTGCTTGGGTTGGCGGAGCATATTC 329  
Qy 1579 TCCGAATCTGGTTGGGATCCAGCATACGGCAATGTCAACAATAGGCTTGGGAGAGA 1638  
Db 328 TCCGAATCTGGTTGGGATCCAGCATACGGCAATGTCAACAATAGGCTTGGGAGAGA 269  
Qy 1639 CACGAGCAGGAGGAGAGACAGAGAAAGAAACACAGCATGAGAACATGTAATGAA 1698











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QY 1458 AGGACGGGTTGATGATGACCGAGCTGAGTGAAGAAAGCTCTCCGAGAGGGAGGAGATC 1517
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Db 1473 AGGACGGGTTGATGATGACCGAGCTGAGTGAAGAAAGCTCTCCGAGAGGGAGGAGATC 1512
QY 1518 ATGTACGGCCGAGAGTAGAGACCTGCTCCAGTCGTGCTTGGGTTGGCCGAGCCATGATC 1577
|
Db 1533 ATGTACGGCCGAGAGTAGAGACCTGCTCCAGTCGTGCTTGGGTTGGCCGAGCCATGATC 1592
QY 1578 CTCGCAATCTGTTGGGATCGATGACGCAATGTCACAAACATTCAGCCCTGGGAG 1637
|
Db 1593 CTCGCAATCTGTTGGGATCGATGACGCAATGTCACAAACATTCAGCCCTGGGAG 1652
QY 1638 ACACGAGCAGAGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1697
|
Db 1653 ACACGAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1712
QY 1698 ATAAACCATTAATATTTTACCCCTCTGTTCTGTCTACTGCGCCAGAGAAATGTACCA 1757
|
Db 1713 ATAAACCATTAATATTTTACCCCTCTGTTCTGTCTACTGCGCCAGAGAAATGTACCA 1772
QY 1758 ATTTTTCAGTTGTGACTTGACACTTCTTTTGGCAGACAGAGAGAGAAATTTTACACTG 1817
|
Db 1773 ATTTTTCAGTTGTGACTTGACACTTCTTTTGGCAGACAGAGAGAGAAATTTTACACTG 1832
QY 1818 TTTCAGACCCGAGGAGTGTGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1877
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Db 1833 TTTCAGACCCGAGGAGTGTGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1892
QY 1878 A 1878
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Db 1893 A 1893

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RESULT 15
US-09-644-873-9077
; Sequence 9077, Application us/09644873
; GENERAL INFORMATION:
; APPLICANT: Sllios-Santiago, Immaculada
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1169-001
; CURRENT APPLICATION NUMBER: US/09/644, 873
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151, 064
; NUMBER OF SEQ ID NOS: 11286
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9077
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-644-873-9077

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Query Match      83.7%; Score 1587; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 1.2e-298;
Matches 1857; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY 19 GGTGCTGCGCCGCGGAGCGCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 78
|
Db 33 GGTGCTGCGCCGCGGAGCGCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 92
QY 79 CGGCGCATCGAGGCTCCGAGAGCGGACACTGCGGCTCTCTAAGCTAGCAGCCTGTCTC 138
|
Db 93 CGGCGCATCGAGGCTCCGAGAGCGGACACTGCGGCTCTCTAAGCTAGCAGCAGCCTGTCTC 152
QY 139 CGCGGACAGAGCGGCGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
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Db 153 CGCGGACAGAGCGGCGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
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Db 213 CTCGCTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 272
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|
Db 273 AATGTGGTCTCTAGGAGCATTCGCGCAACTTTTGGGATGTTGCTTGTCCAGGCTTTG 332
QY 319 GCTGCAATCCAGTGTACAGAGTGTGAAGAAATTCAGACT-GAACAACAGACTGCTCTCC 377
|
Db 333 GCTGCAATCCAGTGTACAGAGTGTGAAGAAATTCAGACTGAGAACCAACAGACTGCTCTCC 392
QY 378 CCGAGTTCATTTGAATTTGACAGGTGAAGCTTCAAGACATGTCTGAGAGAGAGATG 437
|
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QY 438 AGCAAAATGCGGGAGATCAGTACCGCAAGTCTGTGATCATGACGAGGCTGTCTATG 497
|
Db 453 AGCAAAATGCGGGAGATCAGTACCGCAAGTCTGTGATCATGACGAGGCTGTCTATG 512
QY 498 CCGTGTGCGGGGTACAGTCTCTTGTCTCCGAGGAGAACTGAACTCAGTTCATGACT 557
|
Db 513 CCGTGTGCGGGGTACAGTCTCTTGTCTCCGAGGAGAACTGAACTCAGTTCATGACT 572
QY 558 GCTGCAACACCCCTCTTTGTAACGGGCAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAG 617
|
Db 573 GCTGCAACACCCCTCTTTGTAACGGGCAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAG 632
QY 618 CCTGACGCGGAGGCTCCGACACCATCTGTTCTCAATTAAGCCCTCTCTGCGAC 677
|
Db 633 CCTGACGCGGAGGCTCCGACACCATCTGTTCTCAATTAAGCCCTCTCTGCGAC 692
QY 678 ACTGCTGAAGCTGAAGAGATGCACCCCTCTGATGTTGCTTCCAGCCTGCGCC 737
|
Db 693 ACTGCTGAAGCTGAAGAGATGCACCCCTCTGATGTTGCTTCCAGCCTGCGCC 752
QY 738 AACCCCACTCCCTCAGTGAAGTTCCTGCTGCTCTTATTTAGGAGAGAGAG 797
|
Db 753 AACCCCACTCCCTCAGTGAAGTTCCTGCTGCTCTTATTTAGGAGAGAGAG 812
QY 798 GAGTCCGCTCTCTCTTGTCTCTGCTGCAATTAAGAGAGCTGCTTAAGCATCTG 857
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QY 858 AATAAATTCAGCTACGATGAATTTTCAATATGATCTTGAAGAGAGAGAGAGAGAG 917
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QY 918 TTCACCCCATCTGTGTGAACCGAGTCAAGGCCAGGCTGAGAGTCTCTTAGAA 977
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Db 933 TTCACCCCATCTGTGTGAACCGAGTCAAGGCCAGGCTGAGAGTCTCTTAGAA 992
QY 978 GTCACTGAGGTGGGATGCGCTTTTGAAGCCCTCCAGTCTCATTCATCTCTGATG 1037
|
Db 993 GTCACTGAGGTGGGATGCGCTTTTGAAGCCCTCCAGTCTCATTCATCTCTGATG 1052
QY 1038 GGGCATATTTGAGACTGACAGAGTGAAGTCAAGTCTTCAAGGCTGAGAGGCGAGTTC 1097
|
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QY 1158 GCAGAAATGGCTGTTTGGCGCTGAGTGGGCTGTAGTGAAGTGAAGAGAGAGAGAGAGAG 1217
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Db 1173 GCAGAAATGGCTGTTTGGCGCTGAGTGGGCTGTAGTGAAGTGAAGAGAGAGAGAGAG 1232
QY 1218 GACTTAGACTGGGCTGAGGCTGCTCTGAAAGTGTGAAGAAATCTCTGAGTCTC 1277
|
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Oy 1218 GACTTGAAGTGGGCTGGGCTGCTCTGTAAGAAATGCTTAAAGAAATCTTCTCACTTC 1277
Db 1233 GACTTGAAGTGGGCTGGGCTGCTCTGTAAGAAATGCTTAAAGAAATCTTCTCACTTC 1292
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Db 1353 TCGGTGTGTGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 1412
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Db 1413 AGCGGCGACAGCAGTGTGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1472
Oy 1458 AGGAGCGGCTGTGATGACGAGTGTGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1517
Db 1473 AGGAGCGGCTGTGATGACGAGTGTGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1532
Oy 1518 ATGTACGCGCGGAGTGTGATGACGAGTGTGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1577
Db 1533 ATGTACGCGCGGAGTGTGATGACGAGTGTGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1592
Oy 1578 CTCCCAATCTGTTGGGCTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1637
Db 1593 CTCCCAATCTGTTGGGCTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1652
Oy 1638 ACACGAGCAGAGGAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 1697
Db 1653 ACACGAGCAGAGGAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 1712
Oy 1698 ATAAACCATTAATATTTAGTACCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1757
Db 1713 ATAAACCATTAATATTTAGTACCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1772
Oy 1758 ATTTTCACTGTGTGACTGTGACAGCTCTTTTGCACAAGCAGAGAGATTTTACACTG 1817
Db 1773 ATTTTCACTGTGTGACTGTGACAGCTCTTTTGCACAAGCAGAGAGATTTTACACTG 1832
Oy 1818 TTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGCATTAAATGCTTTAGACAGTGT 1877
Db 1833 TTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGCATTAAATGCTTTAGACAGTGT 1892
Oy 1878 A 1878
Db 1893 A 1893

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-214.rnmp
US-09-970-966-214.rnmp
Query Match 83.7%; Score 1587; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 1.2e-298;
Matches 1857; Conserved 0; Mismatches 3; Indels 1; Gaps 1;

Oy 19 GGTGCTGCGCCCGGAGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 78
Db 33 GGTGCTGCGCCCGGAGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 92
Oy 79 CGGCGATGAGGCTCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 138
Db 93 CGGCGATGAGGCTCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 152
Oy 139 CGGCGAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 198
Db 153 CGGCGAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 212
Oy 199 CTGCGGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 258
Db 213 CTGCGGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 272
Oy 259 AATGTGGTCTTGAAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAG 318
Db 273 AATGTGGTCTTGAAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAG 332
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Db 393 CCGAGTTCATTGTAATGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAGCAGTGTGAG 452
Oy 438 AGCAAAATGCGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
Db 453 AGCAAAATGCGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 512
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Db 513 CTTGCGCGGCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
Oy 558 GCTCAACACCCCTCTTGTGTAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGG 617
Db 573 GCTCAACACCCCTCTTGTGTAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGG 632
Oy 618 CCTCAGGCGAGGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 677
Db 633 CCTCAGGCGAGGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 692
Oy 678 ACTGCTGAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
Db 693 ACTGCTGAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
Oy 738 AACCCCGACCTCCCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
Db 753 AACCCCGACCTCCCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 812
Oy 798 GGAATCGTGTCTCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 857
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QY 1638 ACACGAGCAGAGGAGAGACAGAGAAAGAAACACAGCATGTGAACACAGTAATGA 1697

Db 1653 ACACGAGCAGAGGAGAGAGACAGAGAAAGAAACACAGCATGTGAACACAGTAATGA 1712

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QY 1758 ATTTTTCAGTGTGGATCTGACAGCTCTTCTTCCACAAGAGAGAGAAATTTTACACTG 1817

Db 1773 ATTTTTCAGTGTGGATCTGACAGCTCTTCTTCCACAAGAGAGAGAAATTTTACACTG 1832

QY 1818 TTTTCAACCCGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGT 1877

Db 1833 TTTTCAACCCGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTAGACAGTGT 1892

QY 1878 A 1878

Db 1893 A 1893

RESULT 20  
US-09-652-914-8473

; Sequence 8473, Application US/09652914

; GENERAL INFORMATION:

; APPLICANT: Shyjan, Andrew W.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; FILE REFERENCE: 1600.1193-001

; CURRENT APPLICATION NUMBER: US/09/652,914

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 9677

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8473

; LENGTH: 1917

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-652-914-8473

Query Match 83.7%; Score 1587; DB 25; Length 1917;

Best Local Similarity 99.8%; Pred. No. 1.2e-298;

Matches 1857; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 19 GGTGCTGGCCCGGAGCGGAGCGGAGGAGAGAGACCCGAGCGGAGCGGAGCG 78

Db 33 GGTGCTGGCCCGGAGCGGAGCGGAGGAGAGAGACCCGAGCGGAGCGGAGCG 92

QY 79 CGGGCGATGAGGCTCCGCGAGCGGCACTGGGGCTCTCTAGCTAGACGCTGCTC 138

Db 93 CGGGCGATGAGGCTCCGCGAGCGGCACTGGGGCTCTCTAGCTAGACGCTGCTC 152

QY 139 CGCGGAGCAGAGCGGCGCCAGCAGCTCGCAGGACAGCCGCTGCAAGCGGGGAGC 198

Db 153 CGCGGAGCAGAGCGGCGCCAGCAGCTCGCAGGACAGCCGCTGCAAGCGGGGAGC 212

QY 199 CTCCGCTGCTGTGCTCTCTCTATGAGTGGCTTCCCGGCCCGCGGACTCCGGAG 258

Db 213 CTCCGCTGCTGTGCTCTCTCTATGAGTGGCTTCCCGGCCCGCGGACTCCGGAG 272

QY 259 AATGTGGTCTTATGAGCATATCGGCACTTTTTCGAGATTGTTCTTCTTCAAGCTTTGC 318

Db 273 AATGTGGTCTTATGAGCATATCGGCACTTTTTCGAGATTGTTCTTCTTCAAGCTTTGC 332

QY 319 GCTGCAATCCAGTCTACAGAGTGTGAAGATTCCAGCT- GAACAAAGACTGCTCTCC 377

Db 333 GCTGCAATCCAGTCTACAGAGTGTGAAGATTCCAGCT- GAACAAAGACTGCTCTCC 392

QY 378 CCGAGTCTATGTAATTTGACAGGTGAAGTCAAGCATGTGTCAAGAAAGAGTATG 437

Db 393 CCGAGTCTATGTAATTTGACAGGTGAAGTCAAGCATGTGTCAAGAAAGAGTATG 452

QY 438 AGCAAAATGCGGGATATGTACCGCAAGTCTGTGATCATCAGGGGCTGTCTATCG 497

Db 453 AGCAAAATGCGGGATATGTACCGCAAGTCTGTGATCATCAGGGGCTGTCTATCG 512

QY 498 CTTTGGCGGGTACAGTCTTCTGCTTCCAGGAAATGAACTAGTTGATCAGCT 557

Db 513 CTTTGGCGGGTACAGTCTTCTGCTTCCAGGAAATGAACTAGTTGATCAGCT 572

QY 558 GCTGCAACACCCCTTTTGTAGAGGGGCAAGGCCCAAGAAAGGGAGTTTGCCTCG 617

Db 573 GCTGCAACACCCCTTTTGTAGAGGGGCAAGGCCCAAGAAAGGGAGTTTGCCTCG 632

QY 618 CCTTCAGGCGAGGGCTCCGACACCATCTGTTCTCAATTAAGCCCTTCTCGGAC 677

Db 633 CCTTCAGGCGAGGGCTCCGACACCATCTGTTCTCAATTAAGCCCTTCTCGGAC 692

QY 678 ACTGCTGAAGTGAAGAGATGCCACCCCTCTGCAATTTCTTCAGAGCCCTCGCC 737

Db 693 ACTGCTGAAGTGAAGAGATGCCACCCCTCTGCAATTTCTTCAGAGCCCTCGCC 752

QY 738 AACGCCACCTCCCTGAGTGTGTTCTTGGGTGTCCTTTATTTGAGGAGGAG 797

Db 753 AACGCCACCTCCCTGAGTGTGTTCTTGGGTGTCCTTTATTTGAGGAGGAG 812





Db 633 CCTCAGGCGCAGGCTCCGACACACACATCTGTTCTCAATTTAGCCCTCTCTCGGCAC 692  
 QY 678 ACTGCTGAGCTGAAGAGATGCCACCCCTGTCATTTGTTCCAGCCCTCGCCCC 737  
 Db 693 ACTGCTGAAGCTGAAGAGATGCCACCCCTGTCATTTGTTCCAGCCCTCGCCCC 752  
 QY 738 AACCCCGACCTCCCTGAGTGTCTCTGAGGTCCTTTTATNTCTGGGTAGGAGCG 797  
 Db 753 AACCCCGACCTCCCTGAGTGTCTCTGAGGTCCTTTTATNTCTGGGTAGGAGCG 812  
 QY 798 GGAGTCGCTGTTCTCTTCTTCTGTCGCAATATGAAAGAGCTCGGTAAAGCATTCG 857  
 Db 813 GGAGTCGCTGTTCTCTTCTTCTGTCGCAATATGAAAGAGCTCGGTAAAGCATTCG 872  
 QY 858 AATTAATTCAGCTGTGACGATTTTTCATATGTTTAAAGAGAGGTGGAGTGAAG 917  
 Db 873 AATTAATTCAGCTGTGACGATTTTTCATATGTTTAAAGAGAGGTGGAGTGAAG 932  
 QY 918 TTTCACCCCATGTCGTGTAAACCGGAGTCAGGCGGAGAGTCAGTCTGTTAGAA 977  
 Db 933 TTTCACCCCATGTCGTGTAAACCGGAGTCAGGCGGAGAGTCAGTCTGTTAGAA 992  
 QY 978 GTCACTGAGGTGGGATCTGCTTTTGTAAAGCCCTCCAGTGTCCATTCCTGATGG 1037  
 Db 993 GTCACTGAGGTGGGATCTGCTTTTGTAAAGCCCTCCAGTGTCCATTCCTGATGG 1052  
 QY 1038 GGGCATATGTTGAGACTGACAGATGAGTACGTTTCTTAAAGGCTGGAGGCGCATTC 1097  
 Db 1053 GGGCATATGTTGAGACTGACAGATGAGTACGTTTCTTAAAGGCTGGAGGCGCATTC 1112  
 QY 1098 CCACCTAAGAGCTCCCTGCTTGTACATTTCAAACTTCCTCTGAAACCATTCCTGCA 1157  
 Db 1113 CCACCTAAGAGCTCCCTGCTTGTACATTTCAAACTTCCTCTGAAACCATTCCTGCA 1172  
 QY 1158 GCAGATATGCTGTTGTCGCGCTGAGTGTGGGCTCTAGTGAAGTCAATGATGG 1217  
 Db 1173 GCAGATATGCTGTTGTCGCGCTGAGTGTGGGCTCTAGTGAAGTCAATGATGG 1232  
 QY 1218 GACTTAAGTATGGGCTCGGCTCTGAAAGTCTTAAAGTCTTAAAGTCTGCTGTC 1277  
 Db 1233 GACTTAAGTATGGGCTCGGCTCTGAAAGTCTTAAAGTCTTAAAGTCTGCTGTC 1292  
 QY 1278 CTTGCAAGAGATGTCGCGCGGAGCGCAAGCAAGGCGCTGCAACAAGCGGCGCTG 1337  
 Db 1293 CTTGCAAGAGATGTCGCGCGGAGCGCAAGCAAGGCGCTGCAACAAGCGGCGCTG 1352  
 QY 1338 TCGGTGTGTGAGTGTGCGCATGTACGCGCAAGGCGCTTCTGTTGGCTGTGCAAGCAC 1397  
 Db 1353 TCGGTGTGTGAGTGTGCGCATGTACGCGCAAGGCGCTTCTGTTGGCTGTGCAAGCAC 1412  
 QY 1398 AGGCGGACACAGACACGTCGCAAGCAACCCGCGAACTGCTGCGAGAGACCGGTGAC 1457  
 Db 1413 AGGCGGACACAGACACGTCGCAAGCAACCCGCGAACTGCTGCGAGAGACCGGTGAC 1472  
 QY 1458 AGGAGGGGTTGATGACGAGCTGAGGTAGAAAAGCTCTCGAGAAAGGAGAGATGTC 1517  
 Db 1473 AGGAGGGGTTGATGACGAGCTGAGGTAGAAAAGCTCTCGAGAAAGGAGAGATGTC 1532  
 QY 1518 ATGTACGCGCGGAGAGTGAAGTCTGTCATGTCGTTGGTTGGCGGACCATGATC 1577  
 Db 1533 ATGTACGCGCGGAGAGTGAAGTCTGTCATGTCGTTGGTTGGCGGACCATGATC 1592  
 QY 1578 CTCCGGAATGTGTTGGGATCTCCAGATAGGCGCATGTCAACAATAGCCCTGGGAG 1637  
 Db 1593 CTCCGGAATGTGTTGGGATCTCCAGATAGGCGCATGTCAACAATAGCCCTGGGAG 1652  
 QY 1638 ACACGAGCAG 1697  
 Db 1653 ACACGAGCAG 1712  
 QY 1698 ATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1757  
 Db 1713 ATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1772

QY 1758 ATTTTCAGTGTGACTTGACAGCTTCTTTTGGCCAGAGAGAGATTTAACTG 1817  
 Db 1773 ATTTTCAGTGTGACTTGACAGCTTCTTTTGGCCAGAGAGAGATTTAACTG 1832  
 QY 1818 TTTCAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGCATTAATGCTTTAGAGTGT 1877  
 Db 1833 TTTCAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGCATTAATGCTTTAGAGTGT 1892  
 QY 1878 A 1878  
 Db 1893 A 1893  
 RESULT 22  
 US-09-801-833-7188  
 ; Sequence 7188, Application US/09801833  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Glucksmann, M. Alexandra  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
 ; TITLE OF INVENTION: HUMAN BRAIN LIBRARY  
 ; FILE REFERENCE: 1600.1037-005  
 ; CURRENT APPLICATION NUMBER: US/09/801,833  
 ; PRIOR FILING DATE: 2001-03-13  
 ; PRIOR APPLICATION NUMBER: 09/371,168  
 ; PRIOR FILING DATE: 1999-08-10  
 ; PRIOR APPLICATION NUMBER: 60/095,907  
 ; PRIOR FILING DATE: 1998-08-10  
 ; PRIOR APPLICATION NUMBER: 60/103,145  
 ; PRIOR FILING DATE: 1998-10-05  
 ; NUMBER OF SEQ ID NOS: 8285  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7188  
 ; LENGTH: 1917  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-801-833-7188  
 Query Match 83.7%; Score 1587; DB 31; Length 1917;  
 Best Local Similarity 99.8%; Pred. No. 1.2e-298;  
 Matches 1857; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 19 GGTGCTGGGCGCGGAGCGGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 78  
 Db 33 GGTGCTGGGCGCGGAGCGGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 92  
 QY 79 CGGCGATGACAGGTCCTCGGAGCGGCGACCTCGGCTCTCTTAAGTACAGACGCTGCTC 138  
 Db 93 CGGCGATGACAGGTCCTCGGAGCGGCGACCTCGGCTCTCTTAAGTACAGACGCTGCTC 152  
 QY 139 CGGCGAGCAGCGGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 198  
 Db 153 CGGCGAGCAGCGGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 212  
 QY 199 CTCCGCTGCTGTGCGCTCTCTGATGCGCTTGGCTTCCGCGCGCGGAGCTCGGGAG 258  
 Db 213 CTCCGCTGCTGTGCGCTCTCTGATGCGCTTGGCTTCCGCGCGCGGAGCTCGGGAG 272  
 QY 259 AATGTGGTCTTACGATTCGCGGCACTTTTGGCGATTTTCTTCTTCCAGGCTTTCG 318  
 Db 273 AATGTGGTCTTACGATTCGCGGCACTTTTGGCGATTTTCTTCTTCCAGGCTTTCG 332  
 QY 319 GCTCAATTCAGTGTACAGAGTGTGAAGATTTCCAGCT-GAACAAGACTGTCTCTCC 377  
 Db 333 GCTCAATTCAGTGTACAGAGTGTGAAGATTTCCAGCTGAACAAGACTGTCTCTCC 392  
 QY 378 CCGAGTTCATTTGTAATTTGACAGGTGAAGCTTCAAGCATGTGTCAAGAAAGAGATGG 437  
 Db 393 CCGAGTTCATTTGTAATTTGACAGGTGAAGCTTCAAGCATGTGTCAAGAAAGAGATGG 452  
 QY 438 AGCAAAAGTCCGGGATATGTACCGCAAGTCTGTGTATATACAGGCGCTGTCTATCG 497  
 Db 453 AGCAAAAGTCCGGGATATGTACCGCAAGTCTGTGTATATACAGGCGCTGTCTATCG 512





OY	319	GCATCAATCCAGGCGTACACAGGCTGTAAGAAATTCACAGCTGAACCAACGACTGCTCCTCCC	378
Db	1635	GCTCCAAATCCAGTGGCTTACAGCTGTGAAGAAATTCACAGCTGAACCAACGACTGCTCCTCCC	1576
OY	379	CGAGTTGATTTGTGAATTTGCACGGGTGAAGCTTCAGACATGTGTCTGAGAAAGAAAGTGTATGA	438
Db	1575	CGAGTTGATTTGTGAATTTGCACGGGTGAAGCTTCAGACATGTGTCTGAGAAAGAAAGTGTATGA	1516
OY	439	GCAAAATGCCGGGATTCATGTACCCGCAAAATCTGTGATCATACAGGGGCTGTGCATATGC	498
Db	1515	GCAAAATGCCGGGATTCATGTACCCGCAAAATCTGTGATCATACAGGGGCTGTGTATATGC	1456
OY	499	CTTCGCGGGATACCAATGCTCTTGTCTGCCAGAGGAAATCAAGTCTGATTTGCATCAGCTG	558
Db	1455	CTTCGCGGGATACCAATGCTCTTGTCTGCCAGAGGAAATCAAGTCTGATTTGCATCAGCTG	1396
OY	559	CTGCACACACCCCTCTTTGTATAGGGGCCAAGGCCAAGAAAGGGGAATTTGCTCGCCG	618
Db	1395	CTGCACACACCCCTCTTTGTATAGGGGCCAAGGCCAAGAAAGGGGAATTTGCTCGCTCGC	1336
OY	619	CCTCAGGCGCAGGGGCTCGGCAACCAATCCGTTCCCAATTAATGACCCCTTCTCGGCACA	678
Db	1335	CCTCAGG - CAGGGCTCGGCAACCAATCCTGTTCTCCTCAATTAATGACCCCTTCTCGGCACA	1277
OY	679	CTGCTGAAGCTGAAGAGATGCCACACCCCTCTGTGATTTGTTCCAGACCCCTCGCCCCA	738
Db	1276	CTGCTGAAGCTGAAGAGATGCCACACCCCTCTGTGATTTGTTCCAGACCCCTCGCCCCA	1217
OY	739	ACCCCCCACTCCTGTAGTGAATTTCTCTGGGTGTCCTTTATCTGGGTAGGGAAGGG	798
Db	1216	ACCCCCCACTCCTGTAGTGAATTTCTCTGGGTGTCCTTTATCTGGGTAGGGAAGGG	1157
OY	799	GAGTCCGCTTCTCTTTGTTCCTGTGCAATTAATAAAGAGCTGCTTAACATTTGCA	858
Db	1156	GAGTCCGCTTCTCTTTGTTCCTGTGCAATTAATAAAGAGCTGCTTAACATTTGCA	1097
OY	859	ATAATTTAGCTTACATGAAATTTTCAATATGTACTTGAAGGAAGAGGTGAGTGAAGT	918
Db	1096	ATAATTTAGCTTACATGAAATTTTCAATATGTACTTGAAGGAAGAGGTGAGTGAAGT	1037
OY	919	TCACCCCATCTCTGTATTAACCGGAGTCAGAGGCGAGGCTGGCAGATCTGCTTTAGAG	978
Db	1036	TCACCCCATCTCTGTATTAACCGGAGTCAGAGGCGAGGCGAGGCTGGCAGATCTGCTTTAGAG	977
OY	979	TCACCTGAGGTGGGCACTGCTCTTTTGTAAAGCTCCAAGTGTCCATTTCACTCCCTATGGG	1038
Db	976	TCACCTGAGGTGGGCACTGCTCTTTTGTAAAGCTCCAAGTGTCCATTTCACTCCCTATGGG	917
OY	1039	GGCATAGTTTAAAGCTGAGAGTGAAGTGAACGTTTCTTAAAGGCTGGAGGGCCAGATTCC	1098
Db	916	GGCATAGTTTAAAGCTGAGAGTGAAGTGAACGTTTCTTAAAGGCTGGAGGGCCAGATTCC	857
OY	1099	CACCTAAGGCTCCCTCGCTTGACATTTCAAACTTCATGCTCTGAAAAACCATTTCTGCA	1157
Db	856	CACCTAAGGCTCCCTCGCTTGACATTTCAAACTTCATGCTCTGAAAAACCATTTCTGCA	797
OY	1159	CAGATTTGGCGTTTGGCCGCTGAGTGTGGGGCTATGATGATCTGAGACATCAATGATGGG	1218
Db	796	CAGATTTGGCGTTTGGCCGCTGAGTGTGGGGCTATGATGATCTGAGACATCAATGATGGG	737
OY	1219	ACTTACAGTGGGGGCTCGGCTCTGCTGAAAGAGTCTTATGAAGAAATCTTCTCAGTTCTCC	1278
Db	736	ACTTACAGTGGGGGCTCGGCTCTGCTGAAAGAGTCTTATGAAGAAATCTTCTCAGTTCTCC	677
OY	1279	TTTGAGAGAGACTGGCGCCGGGAGCGCAAGACAAAGGGCGCTCCACAAAGCGGGCGCTGT	1338
Db	676	TTTGAGAGAGACTGGCGCCGGGAGCGCAAGAGCAACGGGCGCTCCACAAAGCGGGCGCTGT	617
OY	1339	CGGTGTGGAGTGGCAATGTACGGGCAAGGGGCTTCTGTGGTTGGGCTGTGAGAGACA	1398
Db	616	CGGTGTGGAGTGGCAATGTACGGGCAAGGGGCTTCTGTGGTTGGGCTGTGAGAGACA	557

Qy	1399	GGAGCGAGCAGACACACTGTGACGAAACACCGCGCGAAACGTGCTGCGAGGACACACCGGTACCA	1458
Db	556	GGCGGCGACACAGACACTGCACGACAACACCGCGCGAAACGTGCTGCGAGGACACACCGGTACCA	497
Qy	1459	GGAGCGGGTGTGATGACCGAGCTAGGTAGAAAAACGTCCTCCGAGAAGGGAGAGAGATCA	1518
Db	496	GGAGCGGGTGTGATGACCGAGCTAGGTAGAAAAACGTCCTCCGAGAAGGGAGAGAGATCA	437
Qy	1519	TGTACGCGCCGGAAGTAGGACCTGTCCATCTCGTGCCTGGGCTTGGCCCGCAGCATGATCC	1578
Db	436	TGTACGCGCCGGAAGTAGGACCTGTCCATCTCGTGCCTGGGCTTGGCCCGCAGCATGATCC	377
Qy	1579	TCCCAATCTGTGGTGGCGATCCAGCATACGCGCCATGTCTCAACAACATCAAGCCCTGGCGAGA	1638
Db	376	TCCCAATCTGTGGTGGCGATCCAGCATACGCGCCATGTCTCAACAACATCAAGCCCTGGCGAGA	317
Qy	1639	CACGACGAGGAGGAGAGACAGACAGAAAAAACAACACATGACAGACACAGTAATATGA	1698
Db	316	CACGACGAGGAGGAGAGACAGACAGAAAAAACAACACATGACAGACACAGTAATATGA	257
Qy	1699	TAAACCATTAATATTTTACCCCTCGTCTGCTTACTGGCCAGGAAATGTACCAA	1758
Db	256	TAAACCATTAATATTTTACCCCTCGTCTGCTTACTGGCCAGGAAATGTACCAA	197
Qy	1759	TTTTTCAGTGTGGACCTTGACAGCTTCTTTGGCCACAGCAAGAGAAATTTACACTGT	1818
Db	196	TTTTTCAGTGTGGACCTTGACAGCTTCTTTGGCCACAGCAAGAGAAATTTACACTGT	137
Qy	1819	TTTCAACCCCGGGAGTGTGGCTGCTGTAAAGAAAGCATTAATAGCTTTAGACAGTGA	1878
Db	136	TTTCAACCCCGGGAGTGTGGCTGCTGTAAAGAAAGCATTAATAGCTTTAGACAGTGA	77
RESULT 24			
US-09-950-083-1914/c			
Sequence 1914, Application US/09950083			
GENERAL INFORMATION:			
APPLICANT: Rosen, et. al			
TITLE OF INVENTION: Human Secreted Proteins			
FILE REFERENCE: PS805			
CURRENT APPLICATION NUMBER: US/09/950,083			
CURRENT FILING DATE: 2001-09-12			
PRIOR APPLICATION NUMBER: 60/278,650			
PRIOR FILING DATE: 2001-03-27			
PRIOR APPLICATION NUMBER: 09/833,245			
PRIOR FILING DATE: 2001-04-12			
PRIOR APPLICATION NUMBER: PCT/US01/11988			
PRIOR FILING DATE: 2001-04-12			
PRIOR APPLICATION NUMBER: PCT/US00/06043			
PRIOR FILING DATE: 2000-03-09			
PRIOR APPLICATION NUMBER: PCT/US00/06012			
PRIOR FILING DATE: 2000-03-09			
PRIOR APPLICATION NUMBER: PCT/US00/06058			
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PRIOR FILING DATE: 2000-03-09			
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PRIOR APPLICATION NUMBER: PCT/US00/06824			
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PRIOR APPLICATION NUMBER: PCT/US00/06765			
PRIOR FILING DATE: 2000-03-16			
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7	PRIOR FILING DATE: 2000-03-16	PCT/US00/06791
8	PRIOR APPLICATION NUMBER: PCT/US00/06791	
9	PRIOR FILING DATE: 2000-03-16	PCT/US00/06828
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11	PRIOR FILING DATE: 2000-03-16	PCT/US00/06833
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13	PRIOR FILING DATE: 2000-03-16	PCT/US00/06781
14	PRIOR APPLICATION NUMBER: PCT/US00/06781	
15	PRIOR FILING DATE: 2000-03-16	PCT/US00/07505
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17	PRIOR FILING DATE: 2000-03-22	PCT/US00/07440
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21	PRIOR FILING DATE: 2000-03-22	PCT/US00/07507
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29	PRIOR FILING DATE: 2000-03-22	PCT/US00/07527
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31	PRIOR FILING DATE: 2000-03-22	PCT/US00/07661
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35	PRIOR FILING DATE: 2000-03-23	PCT/US00/07723
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37	PRIOR FILING DATE: 2000-03-23	PCT/US00/07724
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39	PRIOR FILING DATE: 2000-03-23	PCT/US00/14929
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43	PRIOR FILING DATE: 2000-03-23	PCT/US00/07578
44	PRIOR APPLICATION NUMBER: PCT/US00/07578	
45	PRIOR FILING DATE: 2000-03-23	PCT/US00/09070
46	PRIOR APPLICATION NUMBER: PCT/US00/09070	
47	PRIOR FILING DATE: 2000-04-06	PCT/US00/08982
48	PRIOR APPLICATION NUMBER: PCT/US00/08982	
49	PRIOR FILING DATE: 2000-04-06	PCT/US00/08983
50	PRIOR APPLICATION NUMBER: PCT/US00/08983	
51	PRIOR FILING DATE: 2000-04-06	PCT/US00/09067
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53	PRIOR FILING DATE: 2000-04-06	PCT/US00/09066
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55	PRIOR FILING DATE: 2000-04-06	PCT/US00/09068
56	PRIOR APPLICATION NUMBER: PCT/US00/09068	
57	PRIOR FILING DATE: 2000-04-06	PCT/US00/08981
58	PRIOR APPLICATION NUMBER: PCT/US00/08981	
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61	PRIOR FILING DATE: 2000-04-06	PCT/US00/09071
62	PRIOR APPLICATION NUMBER: PCT/US00/09071	
63	PRIOR FILING DATE: 2000-04-06	

PRIOR APPLICATION NUMBER: PCT/US/00/09069	PRIOR FILING DATE: 2000-04-06	PRIOR APPLICATION NUMBER: PCT/US/00/15136	PRIOR FILING DATE: 2000-06-01	PRIOR APPLICATION NUMBER: PCT/US/00/14926	PRIOR FILING DATE: 2000-06-01	PRIOR APPLICATION NUMBER: PCT/US/00/14963	PRIOR FILING DATE: 2000-06-01	PRIOR APPLICATION NUMBER: PCT/US/00/15137	PRIOR FILING DATE: 2000-06-01	PRIOR APPLICATION NUMBER: PCT/US/00/14928	PRIOR FILING DATE: 2000-06-01	PRIOR APPLICATION NUMBER: PCT/US/00/14934	PRIOR FILING DATE: 2000-06-01	PRIOR APPLICATION NUMBER: PCT/US/00/14933	PRIOR FILING DATE: 2000-06-01	PRIOR APPLICATION NUMBER: PCT/US/00/14964	PRIOR FILING DATE: 2000-06-01	PRIOR APPLICATION NUMBER: PCT/US/00/26376	PRIOR FILING DATE: 2000-09-26	PRIOR APPLICATION NUMBER: PCT/US/00/26371	PRIOR FILING DATE: 2000-09-26	PRIOR APPLICATION NUMBER: PCT/US/00/26324	PRIOR FILING DATE: 2000-09-26	PRIOR APPLICATION NUMBER: PCT/US/00/26323	PRIOR FILING DATE: 2000-09-26	PRIOR APPLICATION NUMBER: PCT/US/00/26337	PRIOR FILING DATE: 2000-09-26	PRIOR APPLICATION NUMBER: PCT/US/01/13318	PRIOR FILING DATE: 2001-04-27	PRIOR APPLICATION NUMBER: US 60/124,146	PRIOR FILING DATE: 1999-03-12	PRIOR APPLICATION NUMBER: US 60/167,061	PRIOR FILING DATE: 1999-11-23	PRIOR APPLICATION NUMBER: US 60/124,093	PRIOR FILING DATE: 1999-03-12	PRIOR APPLICATION NUMBER: US 60/166,989	PRIOR FILING DATE: 1999-11-23	PRIOR APPLICATION NUMBER: US 60/124,145	PRIOR FILING DATE: 1999-03-12	PRIOR APPLICATION NUMBER: US 60/168,654	PRIOR FILING DATE: 1999-12-03	PRIOR APPLICATION NUMBER: US 60/124,099	PRIOR FILING DATE: 1999-03-12	PRIOR APPLICATION NUMBER: US 60/168,661	PRIOR FILING DATE: 1999-12-03	PRIOR APPLICATION NUMBER: US 60/124,096	PRIOR FILING DATE: 1999-03-12	PRIOR APPLICATION NUMBER: US 60/168,622	PRIOR FILING DATE: 1999-12-03	PRIOR APPLICATION NUMBER: US 60/138,598	PRIOR FILING DATE: 1999-06-11	PRIOR APPLICATION NUMBER: US 60/168,665	PRIOR FILING DATE: 1999-12-03	PRIOR APPLICATION NUMBER: US 60/125,360	PRIOR FILING DATE: 1999-03-19	PRIOR APPLICATION NUMBER: US 60/138,626	PRIOR FILING DATE: 1999-06-11	PRIOR APPLICATION NUMBER: US 60/168,662	PRIOR FILING DATE: 1999-12-03	PRIOR APPLICATION NUMBER: US 60/124,144	PRIOR FILING DATE: 1999-03-12	PRIOR APPLICATION NUMBER: US 60/138,574
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DB 256 TAAACCAATTAATTTAGCCCCCTGCTGTCTTACTTACTGCGCAGCAAGAAATGATACCA 197
OY 1759 TTTTTCAGTGTGGACTTGGACAGCTTTCTTTGCCACAGCAAGAGAAATTAACACTGT 1818
DB 196 TTTTTCAGTGTGGACTTGGACAGCTTTCTTTGCCACAGCAAGAGAGAAATTAACACTGT 137
OY 1819 TTTCAACCCGGGGAGTTGGCTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 1878
DB 136 TTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 77

RESULT 27
US-09-950-083-1915/C
: Sequence 1915, Application US/09950083
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al
: TITLE OF INVENTION: Human Secreted Proteins
: FILE REFERENCE: PS805
: CURRENT APPLICATION NUMBER: US/09/950,083
: CURRENT FILING DATE: 2001-09-12
: PRIOR APPLICATION NUMBER: 60/278,650
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 09/833,245
: PRIOR FILING DATE: 2001-04-12
: PRIOR APPLICATION NUMBER: PCT/US01/11988
: PRIOR FILING DATE: 2001-04-12
: PRIOR APPLICATION NUMBER: PCT/US00/06043
: PRIOR FILING DATE: 2000-03-09
: PRIOR APPLICATION NUMBER: PCT/US00/06012
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12	PRIOR FILING DATE: 2001-04-27
13	PRIOR APPLICATION NUMBER: US 60/124,146
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15	PRIOR APPLICATION NUMBER: US 60/167,061
16	PRIOR FILING DATE: 1999-11-23
17	PRIOR APPLICATION NUMBER: US 60/124,093
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19	PRIOR APPLICATION NUMBER: US 60/166,989
20	PRIOR FILING DATE: 1999-11-23
21	PRIOR APPLICATION NUMBER: US 60/124,145
22	PRIOR FILING DATE: 1999-03-12
23	PRIOR APPLICATION NUMBER: US 60/168,654
24	PRIOR FILING DATE: 1999-12-03
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64	PRIOR FILING DATE: 1999-12-03
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66	PRIOR FILING DATE: 1999-03-23
67	PRIOR APPLICATION NUMBER: US 60/169,906

Query Match	Score	DB	Length
Best Local Similarity	99.8%	Pred. No.1.9e-298	
Matches 1856; Conservative	0;	Mismatches 3;	Indels 1; Gaps 1

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Db	1935	GGTCTCTGGCCCGGAGGCGCGAGGCGGAGGAGACAGAGACCCGACGCGGGAGCCCGACGG	1876
Qy	79	CGGGGATGACAGGCTCTCCGGAAGCGGCACCTCTCGGGCTCCTTAAGCTTAACAGACGCTGTCTTC	138
Db	1875	CGGGCGATGACAGGCTCTCCGGAAGCGGCACCTCTCGGGCTCCTTAAGCTTAACAGACGCTGTCTTC	1816
Qy	139	CGGGGACGACGCGCGGGGCCCGACAGCCCTCGGGACGACACAGCCGCTGACACCGCGGGACACG	198
Db	1815	CGGGGACGACGCGCGGGGCCCGACAGCCCTCGGGACGACACAGCCGCTGACACCGCGGGACACG	1756
Qy	199	CTCCGCTGCTGTCCGCTCCTCTGATGCGCTGTCCCTCTCCCGGGCCCGGGACCTCCGGAG	258
Db	1755	CTCCGCTGCTGTCCGCTCCTCTGATGCGCTGTCCCTCTCCCGGGCCCGGGACCTCCGGAG	1696
Qy	259	AATGTGGGTCCTTAGGATCGCGGCAACTTTTGGCGATTGTTCTTTCGCTTCAGGACTTTGC	318
Db	1695	AATGTGGGTCCTTAGGATCGCGGCAACTTTTGGCGATTGTTCTTTCGCTTCAGGACTTTGC	1636
Qy	319	GCTGCAATCCAGTCTACCAAGTGTGAGAAATTCACGCTGAACACAGACTGTCTTCC	378
Db	1635	GCTGCAATCCAGTCTACCAAGTGTGAGAAATTCACGCTGAACACAGACTGTCTTCC	1576
Qy	379	CGAATTCAATGTGAATTTGACAGCGGTGAAGCTTAAACATGTGTGAGAAAGAGTATGA	438
Db	1575	CGAATTCAATGTGAATTTGACAGCGGTGAAGCTTAAACATGTGTGAGAAAGAGTATGA	1516
Qy	439	GCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATACGCGGCTGTCTATCGC	498
Db	1515	GCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATACGCGGCTGTCTATCGC	1456
Qy	499	CTCTGCGGGTACCAAGTCTTCTGCTCCCGCAGGAAACGAACTCAGTTTGCATCAGCTG	558
Db	1455	CTCTGCGGGTACCAAGTCTTCTGCTCCCGCAGGAAACGAACTCAGTTTGCATCAGCTG	1396
Qy	559	CTGCAACACCCCTCTTGTGTACGCGGCCAAGGCCCAAGAAAAGGGAAATTCTGCTCGGC	618
Db	1395	CTGCAACACCCCTCTTGTGTACGCGGCCAAGGCCCAAGAAAAGGGAAATTCTGCTCGGC	1336
Qy	619	CCTCAGGCCAGGGCTCCGCAACACATCCTGTCTTCTCAAAATTAAGCCCTCTCTCGGACA	678
Db	1335	CCTCAGGCCAGGGCTCCGCAACACATCCTGTCTTCTCAAAATTAAGCCCTCTCTCGGACA	1277
Qy	679	CTGCGAAGCTGAAGGAGATGCCACCCCTCGCATGTTGTTCTTCACAGCCCTCGCCCCA	738
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Qy	739	ACCCCCCACTCCCTGAGTGAAGTTTCTTGCGGTCTCTTTATCTCGGTGAGGACCG	798
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Qy	859	ATAAATTACAGCTACGTGAATTTTCAATATGACTTGAAGAAAGAGGTGAGTGAAGT	918
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Db	976	TCACGTAGAGTGGGCACTGCTTTTGAAGCCCTCAGATGCTCATCTCATCCCTGATGG	917
Qy	1039	GCGATAGTTGAGACTGACAGTGAAGTGAAGTCTTTTGAAGGCGTGAAGGCGCAGTTC	1098
Db	916	GCGATAGTTGAGACTGACAGTGAAGTGAAGTCTTTTGAAGGCGTGAAGGCGCAGTTC	857
Qy	1099	CATCAAGGCTCCCGGTTGACATTAACCTCATGCTCTCTAAACCATCTCTCGAC	1158



Db	856	CACCTCAAGGCTCCCTCGCTTGACATTTCAAACTTCATGCTCTCGTAAGAACCATTTCTCGACG	797
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Db	796	CAGAAATTGGCTGGTTTGGCGCCCTGATAGTTGGGCTCTATGACTCGAGACTCAATGACTGGG	737
Qy	1219	ACTTAGACTGGGGCTCGGGCCCTGCGCTCGTAAGAAAGTGCTTAAAGAAATCTTCAGTTCTCC	1278
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Qy	1279	TTTCAGAGACTGGCGCCCGGGAGCGAAGAGCAACGGGGCTTCACAAAGCGGGCGCTGT	1338
Db	676	TTTCAGAGAGACTGGCGCCCGGGAGCGAAGAGCAACGGGGCTTCACAAAGCGGGCGCTGT	617
Qy	1339	CGGTGTGTGAGTGGCGCATGTATACGGGAGCGGCTTCTCTGTGTGGTGGCGTCTCGACGACA	1398
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Qy	1399	GGCGGACAGCAGACACCTTCGACAGCAACCCCGCGGAATGCTGCGAGGACACCGTGTACA	1458
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Qy	1759	TTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAAGAGAGAAATTTACACTGT	1818
Db	196	TTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAAGAGAGAAATTTACACTGT	137
Qy	1819	TTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAATGCTTTAGACAGTGA	1878
Db	136	TTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAATGCTTTAGACAGTGA	77
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US-10-105-299-2415/c			
Sequence 2415, Application US/10105299			
GENERAL INFORMATION:			
APPLICANT: Rosen, et. al			
TITLE OF INVENTION: Human Secreted Proteins			
FILE REFERENCE: PS950			
CURRENT APPLICATION NUMBER: US/10/105,299			
CURRENT FILING DATE: 2002-03-26			
NUMBER OF SEQ ID NOS: 15197			
Prior Application removed - See File Wrapper or Palm			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 2415			
LENGTH: 1956			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (1362)..(1636)			
OTHER INFORMATION: n equals a,t,g, or c			
US-10-105-299-2415			

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Dd	1935	GGTGCTCGGCCCGGGAGCCGCAGACGGGAGAGACAGACCCTCCGAGCCGGAGCCGAGCG	1876			
OY	79	CGGGGATTCAGAGCTCCCGGAGCGGCACTGGGGCTCCTTAAGTAGACCTGCTCTC	138			
Dd	1875	CGGGGATTCAGAGCTCCCGGAGCGGCACTGGGGCTCCTTAAGTAGACCTGCTCTC	1816			
OY	139	CGCGGAGCAGCGCGGGCCCCCAGACGCTCGGACAGCACAGCCGCTGCAGCCGGGACAC	198			
Dd	1815	CGCGGAGCAGCGCGGGGCCCCAGACGCTCGGACAGCANAGCCGCTGCAGCCGGGACAC	1756			
OY	199	CTCCGCTGTCTCGCCTCTCTGAATGCGCTTCCCTCCCGGCCCGGGACTCCGGGAG	258			
Dd	1755	CTCCGCTGTCTCGCCTCTCTGAATGCGCTTCCCTCCCGGCCCGGGACTCCGGGAG	1696			
OY	259	AATGTGGTCTCAGGCATCGCGCAACTTTTGGCGAATTGTCCTTGCTTCAGAGGCTTGC	318			
Dd	1695	AATGTGGTCTCAGGCATCGCGCAACTTTTGGCGAATTGTCCTTGCTTCAGAGGCTTGC	1636			
OY	319	GCTGCAATTCAGTGTCTACAGTGTGAAGAATTCCAGCTGAACAACAGACTGCTCTCCC	378			
Dd	1635	GCTGCAATTCAGTGTCTACAGTGTGAAGAATTCCAGCTGAACAACAGACTGCTCTCCC	1576			
OY	379	CGAGTTCATTGGAAATTGACGGGTAAAGCTTAAACANCTGTCAGAAAAGAGTAGATGA	438			
Dd	1575	CGAGTTCATTGGAAATTGACGGGTAAAGCTTAAACANCTGTCAGAAAAGAGTAGATGA	1516			
OY	439	GCAAAGTCCCGGATCATGTACCGCAAGTCTCTGCATCATAGAGGCTCTCTCATGC	498			
Dd	1515	GCAAAGTCCCGGATCATGTATACCGCAAGTCTCTGCATCATAGAGGCTCTCTCATGC	1456			
OY	499	CTCTCGCGGGTACAGTCTCTTCTGCCCTCCGAGGAACTGAACCTAGTTGCATACCTG	558			
Dd	1455	CTCTCGCGGGTACAGTCTCTTCTGCCCTCCGAGGAACTGAACCTAGTTGCATACCTG	1396			
OY	559	CTGCAACACCCCTCTTGTGAACGGGCGCAAGGCCCAAGAAAAAGGGGAAGTTGCTCGCGC	618			
Dd	1395	CTGCAACACCCCTCTTGTGAACGGGCGCAAGGCCCAAGAAAAAGGGGAAGTTGCTCGCGC	1336			
OY	619	CCTCAGGCCAGGGCTCCGCAACCATCTCTCTCTCAAAATTAGCCCTCTCTCGGCACA	678			
Dd	1335	CCTCAGG--CAGGGCTCCGCAACCATCTCTCTCTCAAAATTAGCCCTCTCTCGGCACA	1277			
OY	679	CTGCTGAAGCTAAAGAGATGCGACCCCTCTCTGATGTCTTCCACGCCCTCGGCCCA	738			
Dd	1276	CTGCTGAAGCTAAAGAGATGCGACCCCTCTCTGATGTCTTCCACGCCCTCGGCCCA	1217			
OY	739	ACCCCCCACTCCGAGTAGATTCTTCTGGGTCCTTTTATCTGGGTAGGAGCGG	798			
Dd	1216	ACCCCCCACTCCGAGTAGATTCTTCTGGGTCCTTTTATCTGGGTAGGAGCGG	1157			
OY	799	GAGTCCGTTCTCTTTGTCTCTGTCCTGCAAAATAAAGAAAGAGCTGGTAAGCATTTGCA	858			
Dd	1156	GAGTCCGTTCTCTTTGTCTCTGTCCTGCAAAATAAAGAAAGAGCTGGTAAGCATTTGCA	1097			
OY	859	ATAAATTCAGCTGACTGAATTTTCAATGATGACTTGAAGGAGAGGTGAGTGAAGT	918			
Dd	1096	ATAAATTCAGCTGACTGAATTTTCAATGATGACTTGAAGGAGAGGTGAGTGAAGT	1037			
OY	919	TCACCCCCATGTCTGTGTAACCGGAGTCAAGGCCAGGCTGGCAGAGTGTGCTTGAAG	978			
Dd	1036	TCACCCCCATGTCTGTGTAACCGGAGTCAAGGCCAGGCTGGCAGAGTGTGCTTGAAG	977			
OY	979	TCACTGAGGTGGGCACTTCGCTTTTGTAAAGCCTTCAATGTTCATTCCTCCATATGG	1038			
Dd	976	TCACTGAGGTGGGCACTTCGCTTTTGTAAAGCCTTCAATGTTCATTCCTCCATATGG	917			
OY	1039	GGCATAGTTTTAGAGTCGAGAGTGAAGTGAACGTTTCTTAAGGCTGGAGGCCAGTTC	1098			

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Oy 1099 CACTCAGAGCTCCCTCGCTTGACATTCAAACTCTCTCTGAAAACCACTTCTGTGAG 1158
Db 856 CACTCAGAGCTCCCTCGCTTGACATTCAAACTCTCTCTGAAAACCACTTCTGTGAG 797
Oy 1159 CAGAAATGGCTGGTTGCGGCTGAGTTGGGCTGAGTACGAGCTCATGACTGAGTGG 1218
Db 796 CAGAAATGGCTGGTTGCGGCTGAGTTGGGCTGAGTACGAGCTCATGACTGAGTGG 737
Oy 1219 ACTTAGACTGGGGCTCGGCTCGCTGAAAAGTCTTGAAGAAATCTTCTCAGTTTCC 1278
Db 736 ACTTAGACTGGGGCTCGGCTCGCTGAAAAGTCTTGAAGAAATCTTCTCAGTTTCC 677
Oy 1279 TTGCAAGAGACTGGGCGCGGAGACGGGAAGAGCAAGGGGCGCTGCAGCAAAAGCGGCGCTGT 1338
Db 676 TTGCAAGAGACTGGGCGCGGAGACGGGAAGAGCAAGGGGCGCTGCAGCAAAAGCGGCGCTGT 617
Oy 1339 CGGTGGTGGAGTGGCGATGTACGCGCAGGCGCTTCTCGTGGTTGGCGTGTGCAGCGACA 1398
Db 616 CGGTGGTGGAGTGGCGATGTACGCGCAGGCGCTTCTCGTGGTTGGCGTGTGCAGCGACA 557
Oy 1399 GCGCGGACAGACAGCACTGACAGAAACACCGCGGAACTGCTGCGAGAGACACCGTGTACA 1458
Db 556 GCGCGGACAGACAGCACTGACAGAAACACCGCGGAACTGCTGCGAGAGACACCGTGTACA 497
Oy 1459 GAGGCGGGTGTATGACCCGAGCTGAGGTAGAAAACGTCTCCGAGAAAGGGAGAGAGATCA 1518
Db 496 GAGGCGGGTGTATGACCCGAGCTGAGGTAGAAAACGTCTCCGAGAAAGGGAGAGAGATCA 437
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Db 436 TGTACGCCCGGAAGTGTAGACCTGTGTCAAGTCTGCTTGGGTTGGCGGAGCCAGATATCC 377
Oy 1579 TCCGAATCTGTGGGATTCACAGCATAGCGCAATGTCAACAATTCAGCCCTGGGAGAGA 1638
Db 376 TCCGAATCTGTGGGATTCACAGCATAGCGCAATGTCAACAATTCAGCCCTGGGAGAGA 317
Oy 1639 CACGAGCAGAGGAGAGAGACAGAGAAAAGAAAACACAGCATGAGAACAGTAATATGA 1698
Db 316 CACGAGCAGAGGAGAGAGACAGAGAAAAGAAAACACAGCATGAGAACAGTAATATGA 257
Oy 1699 TAAACCATATAATATTAGCCCTCTGTCTGTGCTTACTGCGCAGGAATGTATCCAA 1758
Db 256 TAAACCATATAATATTAGCCCTCTGTCTGTGCTTACTGCGCAGGAATGTATCCAA 197
Oy 1759 TTTTTCAGTGTGAGCTTTCACAGCTTCTTTTGGCACAAGAGAGAAATTTAACACTGT 1818
Db 196 TTTTTCAGTGTGAGCTTTCACAGCTTCTTTTGGCACAAGAGAGAAATTTAACACTGT 137
Oy 1819 TTCAAAACCCGGGAGTGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 1878
Db 136 TTCAAAACCCGGGAGTGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA 77

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RESULT 29  
US-10-108-260A-197  
Sequence 197, Application US/10108260A

GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: H1-A0106  
CURRENT APPLICATION NUMBER: US/10/108,260A  
CURRENT FILING DATE: 2002-03-27  
NUMBER OF SEQ ID NOS: 5458  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 197  
LENGTH: 1832  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-108-260A-197

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Query Match      80.4%; Score 1526; DB 40; Length 1832;
Best Local Similarity 99.8%; Pred. No. 8e-287;
Matches 1676; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 154 CTCGGCTGCTGTGGCTCTCTGTATGAGCTTGGCCCTCTCCCGGCGGAGACTCGGGAG 213
Oy 259 AATGTGGTCTTAGCATTCGCGGCACTTTTGGCGATTTTGTCTTGTCCAGAGCTTTCG 318
Db 214 AATGTGGTCTTAGCATTCGCGGCACTTTTGGCGATTTTGTCTTGTCCAGAGCTTTCG 273
Oy 319 GCTGCAATCCAGTGTACAGAGTGAAGAATTCACAGTGAACAGAGCTGCTCCGCC 378
Db 274 GCTGCAATCCAGTGTACAGAGTGAAGAATTCACAGTGAACAGAGCTGCTCCGCC 333
Oy 379 CAGATTATTTGTAATTCAGAGTGAAGACGTTCAAGACATGTGTCAAGAAAGATGATGA 438
Db 334 CAGATTATTTGTAATTCAGAGTGAAGACGTTCAAGACATGTGTCAAGAAAGATGATGA 393
Oy 439 GCAAGTGGCGGATCATGTATACGCAAGTCTGTGATCATACAGGCGCTGTCTATCCG 498
Db 394 GCAAGTGGCGGATCATGTATACGCAAGTCTGTGATCATACAGGCGCTGTCTATCCG 453
Oy 499 CTCTGCGGGGTACCAAGTCTTGTGCTCCCGAGGAACTGACACTGTTGATCAGCTG 558
Db 454 CTCTGCGGGGTACCAAGTCTTGTGCTCCCGAGGAACTGACACTGTTGATCAGCTG 513
Oy 559 CTGCAACACCCCTTTTGTATAGGGGCCCAAGGCCCAAGAAAGGGAAAGTCTCCGCG 618
Db 514 CTGCAACACCCCTTTTGTATAGGGGCCCAAGGCCCAAGAAAGGGAAAGTCTCCGCG 573
Oy 619 CCTCAGGCAAGGGCTCCGACACCATCTGTCTCAAAATTAAGCCCTCTTCTCGGACA 678
Db 574 CCTCAGGCAAGGGCTCCGACACCATCTGTCTCAAAATTAAGCCCTCTTCTCGGACA 633
Oy 679 CTGCTGAAGCTGAAGAGATCCACCCCTCTGCAATGTTCTTCCAGCCCTGCCCCA 738
Db 634 CTGCTGAAGCTGAAGAGATCCACCCCTCTGCAATGTTCTTCCAGCCCTGCCCCA 693
Oy 739 ACCGCCCACTCCCTGAGTGTCTTCTGCGGTCTCTTATTTGCGGTAGGAGACGG 798
Db 694 ACCGCCCACTCCCTGAGTGTCTTCTGCGGTCTCTTATTTGCGGTAGGAGACGG 753
Oy 799 GAGTCCGTTCTCTTTTGTCTCTGTGCAAAATTAAGAGCTCGGTAAGCATTCGA 858
Db 754 GAGTCCGTTCTCTTTTGTCTCTGTGCAAAATTAAGAGCTCGGTAAGCATTCGA 813
Oy 859 ATTAATTTAGCTGACAGTGAATTTTCAATGATGTACTGAAGAGAGAGTGAAGTGAAGT 918
Db 814 ATTAATTTAGCTGACAGTGAATTTTCAATGATGTACTGAAGAGAGAGTGAAGTGAAGT 873
Oy 919 TCACCCCATGTCTGTGTAACCGAGTCAAGGCCAGGCTGGCAGAGTCAAGTCTTAGAG 978
Db 874 TCACCCCATGTCTGTGTAACCGAGTCAAGGCCAGGCTGGCAGAGTCAAGTCTTAGAG 933
Oy 979 TCACGAGTGGGATCTGCTTTTGTAAAGCTCCAGTGTCAATTCATCCGTATGG 1038
Db 934 TCACGAGTGGGATCTGCTTTTGTAAAGCTCCAGTGTCAATTCATCCGTATGG 993
Oy 1039 GGCATAGTTTGAAGCTGACAGAGTGAAGTGAAGTCTTTCTTAAGGCTGGAGGCCAGTTC 1098
Db 994 GGCATAGTTTGAAGCTGACAGAGTGAAGTGAAGTCTTTCTTAAGGCTGGAGGCCAGTTC 1053
Oy 1099 CACTCAGAGCTCCCTCGCTTACATTCAAACTTATGCTCTGAAAAACATTTCTCTGAG 1158
Db 1054 CACTCAGAGCTCCCTCGCTTACATTCAAACTTATGCTCTGAAAAACATTTCTCTGAG 1113
Oy 1159 CAGAAATGGCTGGTTGCGGCTGAGTTGGGCTGTAGTGCAGACTCAATGACTGG 1218
Db 1114 CAGAAATGGCTGGTTGCGGCTGAGTTGGGCTGTAGTGCAGACTCAATGACTGG 1173
Oy 1219 ACTTAGACTGGGGCTCGGCTCGCTGTGAAAAGTGTCTTAAGAAATCTTCTCAGTTCC 1278

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Db 1174 ACTTACACTGGGGCTCGGGCTCGCTGTGAANAATGCTTAAGAAATCTTCTCAGTTCTCC 1233

Qy 1279 TTGCAGAGACTGTGCCCCGGGAGCGGACAGACAGCGGGCGCTGCACAAAGCGGGCGCTGT 1338

Db 1234 TTGCAGAGACTGTGCCCCGGGAGCGGACAGCAAGCAAGCGGGCGCTGCACAAAGCGGGCGCTGT 1293

Qy 1339 CGGTGGTGAAGTGGCGATGTGTACGGCGGAGCGCTTCTCTGTGTGTGGGTGTGTGACAGGACA 1398

Db 1294 CGGTGGTGAAGTGGCGATGTGTACGGCGGAGCGCTTCTCTGTGTGTGGGTGTGTGACAGGACA 1353

Qy 1399 GCGCGAGACAGACACACTCTCAGCAACACCCGCCGAATAGCTCGAGAGACACCGTGTACA 1458

Db 1354 GCGCGAGACAGACACACTCTCAGCAACACCCGCCGAATAGCTCGAGAGACACCGTGTACA 1413

Qy 1459 GGACGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCCTCCGAGAAAGGGAGAGAGATCA 1518

Db 1414 GGAGGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCCTCCGAGAAAGGGAGAGAGATCA 1473

Qy 1519 TGTAGCGCCGGGAAGTGAAGCACTGTGTCAATCTGTGTGTGGTTTGGCCGACCATATGCC 1578

Db 1474 TGAAGCGCCGGGAAGTGAAGCACTGTGTCAATCTGTGTGTGGTTTGGCCGACCATATGCC 1533

Qy 1579 TCCGATCTGTGTGGCATCCAGCATACGGCCAAATGTCAACAAATCAGCGCCGTGGGCAGA 1638

Db 1534 TCCGATCTGTGTGGCATCCAGCATACGGCCAAATGTCAACAAATCAGCGCCGTGGGCAGA 1593

Qy 1639 CACGAGCAGAGAGAGAGACAGAGAAAAAACAACAGCATGAGAAACAGTAAATGAA 1698

Db 1594 CACGAGCAGAGAGAGAGAGACAGAGAAAAAACAACAGCATGAGAAACAGTAAATGAA 1653

Qy 1699 TAAACCAATAAATATTTTGGCCCTCTGTCTGTGTACTGTGGCCAGGAATGTACCAA 1758

Db 1654 TAAACCAATAAATATTTTGGCCCTCTGTCTGTGTGTACTGTGGCCAGGAATGTACCAA 1713

Qy 1759 TTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAAGAGAGAAATTTAACACTGT 1818

Db 1714 TTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAAGAGAGAAATTTAACACTGT 1773

Qy 1819 TTCAAAACCCGGGGAGTGTGGCTGTGTTAAAGAAAGCAATTAAATGCTTTAGACAGTGT 1877

Db 1774 TTCAAAACCCGGGGAGTGTGGCTGTGTTAAAGAAAGCAATTAAATGCTTTAGACAGTGT 1832

RESULT 30

US-09-526-994-1070/c

: Sequence 1070, Application US/09526994

: GENERAL INFORMATION:

: APPLICANT: Shyjan, Andrew M.

: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A

: TITLE OF INVENTION: HUMAN OVARY LIBRARY

: FILE REFERENCE: 1600.1090-001

: CURRENT APPLICATION NUMBER: US/09/526.994

: CURRENT FILING DATE: 2000-03-15

: EARLIER APPLICATION NUMBER: 60/125.564

: EARLIER FILING DATE: 1999-03-22

: EARLIER APPLICATION NUMBER: 60/135.678

: EARLIER FILING DATE: 1999-05-24

: NUMBER OF SEQ ID NOS: 1304

: SOFTWARE: FastSeq for Windows Version 3.0

: SEQ ID NO 1070

: LENGTH: 2535

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-526-994-1070

Query Match	79.5%	Score 1509	DB 19	Length 2535
Best Local Similarity	99.9%	Pred. No. 1.4e-283		
Matches 1609	Conservative	0	Mismatches 2	Indels 0
			Gaps	0
0y	19	6GTGCTCGCGCCGGGAGCGCCGAGCGGAGACAGACAGACCCGAGCCGGAGCCGAGCGG	78	
Db	2503	GGTGCTTCGGCCCGGGAGCGCGAGCGGAGACAGACAGACCCGAGCCGGAGACCCGAGCGG	2444	

OY	79	CGGGGATGCGAGGCTCCGCGAGCGGCAACCTCGGGCTCCTCCTAAACCTAGACGCGCTC	138
Db	2443	CGGGGATGCGAGGCTCCGCGAGCGGCAACCTCGGGCTCCTCCTAAACCTAGACGCGCTC	238
OY	139	CGCGGACAGACGGGGGGCCCGACAGCCTCGGCGGCCACAGCCGCTCACCGGGGACG	198
Db	2383	CGCGGACAGACGGGGGGCCCGACAGCCTCGGCGGCCACAGCCGCTCACCGGGGACG	232
OY	139	CTCCGCTCTGTGCGCTCTCTGTATGGGCTTGCCCTCTCCCGGGCCCGGAGCTCCGGAG	258
Db	2323	CTCCGCTCTGTGCGCTCTCTGTATGGGCTTGCCCTCTCCCGGGCCCGGAGCTCCGGAG	226
OY	259	AATGGGGTCTTAGGCATCGGGCAACTTTTGGGAGTGTCTGCTTCAGAGCTTTGC	318
Db	2263	AATGGGGTCTTAGGCATCGGGCAACTTTTGGGAGTGTCTGCTTCAGAGCTTTGC	220
OY	319	GCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGACACAGACGTCTCTCC	378
Db	2203	GCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGACACAGACGTCTCTCC	214
OY	379	CGAGTTCATTGTGAATTGACAGGGAACGTTCAAGACATGTGTGACGAAGAATAATGTGA	438
Db	2143	CGAGTTCATTGTGAATTGACAGGGAACGTTCAAGACATGTGTGACGAAGAATAATGTGA	208
OY	439	GCAAAGTCCGGGATCATGTACCCGAAGTCTGTGCATCATACGCGGCTGTCTCATCC	498
Db	2083	GCAAAGTCCGGGATCATGTACCCGAAGTCTGTGCATCATACGCGGCTGTCTCATCC	202
OY	499	CTCTGCGGGGATACGAGTCTCTCTCTCCCGAGGAACTAGACTCACTGTGCTACAGCTG	558
Db	2023	CTCTGCGGGGATACGAGTCTCTCTCTCCCGAGGAACTAGACTCACTGTGCTACAGCTG	196
OY	559	CTGCAACACCCCTTTTGTAAACGGGGCCAAAGGCCAAAGAAAGGGGAAGTCTCTCTCGG	618
Db	1963	CTGCAACACCCCTTTTGTAAACGGGGCCAAAGGCCAAAGAAAGGGGAAGTCTCTCTCGG	190
OY	619	CCTCAGGCGAGGCTCCGGACACACCATCTGTCTCTAAATTAGCCCTCTTCTCGGCACA	678
Db	1903	CCTCAGGCGAGGCTCCGGACACACCATCTGTCTCTAAATTAGCCCTCTTCTCGGCACA	184
OY	679	CTGCTGAAGCTGAAGAGAGATCCACCCCTCTGCAATGTATCTTCAAGCCCTCGGCCCA	738
Db	1843	CTGCTGAAGCTGAAGAGAGATCCACCCCTCTGCAATGTATCTTCAAGCCCTCGGCCCA	178
OY	739	ACCCCCACCTCTCTGAGTAGATTTCTTGGGTGTCCTTTATTCGTGGGTAGGAGCGG	798
Db	1783	ACCCCCACCTCTCTGAGTAGATTTCTTGGGTGTCCTTTATTCGTGGGTAGGAGCGG	172
OY	799	GAGTCCGGTCTCTTTTGTTCCTGTGTCCAATTAATGAAGAAGCTCGGTAAAGCATCTGA	858
Db	1723	GAGTCCGGTCTCTTTTGTTCCTGTGTCCAATTAATGAAGAAGCTCGGTAAAGCATCTGA	166
OY	859	ATAAATTCAGCTGACTGAATTTTCACTATGTACTTGAAAGAGAGAGGTGAGATGAAAT	918
Db	1663	ATAAATTCAGCTGACTGAATTTTCACTATGTACTTGAAAGAGAGAGGTGAGATGAAAT	160
OY	919	TCACCCCCATGTCTGTGTAAACCGGAGTCAAGGCCAGGCTGGCAGAGTCWTGCTTGAAG	978
Db	1603	TCACCCCCATGTCTGTGTAAACCGGAGTCAAGGCCAGGCTGGCAGAGTCWTGCTTGAAG	154
OY	979	TCACTGAGGTGGGATGTGCTTTTGTGAAGCCTCCAGTGTCCATTCATCCCTGATGGG	1033
Db	1543	TCACTGAGGTGGGATGTGCTTTTGTGAAGCCTCCAGTGTCCATTCATCCCTGATGGG	148
OY	1039	GGCATAGTTTGAGACTGCGAGAGTGAAGTAGAGTGTTCCTTAAAGGCTGGAGGGCCACTTCC	1091
Db	1483	GGCATAGTTTGAGACTGCGAGAGTGAAGTAGAGTGTTCCTTAAAGGCTGGAGGGCCACTTCC	142
OY	1099	CACATCAAGGCTCCCTGCTTGACATTTCAAACTTCATGCTCTGTAAAAACCATTTCTGCGAG	1155
Db	1423	CACATCAAGGCTCCCTGCTTGACATTTCAAACTTCATGCTCTGTAAAAACCATTTCTGCGAG	136







QY	1340	GGTGGTGAAGTGGCATTGACGGGCGAGGGCCCTCTGTGGTGGGGTGGTGCAGGAGAC	1399
Db	1201	GGTGGTGAATGCGCATGTACGGCCAGGGCGCTTCTGTGTGGCGGTCTGCAGGAGAC	1260
QY	1400	GCGGCAGCAGCAGCACCCCTGCAGAACCCCGCGAAACTCTCTCGAGAGACCCGTATACG	1459
Db	1261	GCGGCAGCAGCAGCAGCCTGCGACAGAAACCCCGCGAAACTCTCTCGAGAGACCCGTATACG	1320
QY	1460	GAGCGGGTTGATGACCCGAGCTGAGGTAGAAAAACGTCCTCGAGGAAGGGAGAGGATCAT	1519
Db	1321	GAGCGGGTTGATGACCCGAGCTGAGGTAGAAAAACGTCCTCGAGGAAGGGAGAGGATCAT	1380
QY	1520	GTCAGCCCCGGAAGTAGAGCACTGCTCCAGTGTGTCCTTGSGTTTGGCCGACCCATGATCCT	1579
Db	1381	GTCAGCCCCGGAAGTAGAGCACTGCTCCAGTGTGTCCTTGSGTTTGGCCGACCCATGATCCT	1440
QY	1580	CCGAATCTGGTTGGGCAATCCAGCATACGGCCAAATGTCAACAACAATCAGCCCTGGGCGAC	1639
Db	1441	CCGAATCTGGTTGGGCAATCCAGCATACGGCCAAATGTCAACAACAATCAGCCCTGGGCGAC	1500
QY	1640	ACGAGCAGAGGAGGAGACACAGACA	1663
Db	1501	ACGAGCAGAGGAGGAGACACAGACA	1524

```

: RESULT 34
: US-10-216-162-15
: Sequence 15. Application US/10216162
: GENERAL INFORMATION:
:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Matanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530PIC2
: CURRENT APPLICATION NUMBER: US/10/216,162
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079566
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 15

```

Query Match		Similarity	95.0%	Score	1422	DB	426	Length	1524:	
Best Local		Similarity	99.9%	Pred.	No.1.2e-26	26:				
Matches		1522:	Conservative	0:	Mismatches	2:	Indels	0:	Gaps	0
QY	140	GGGCGAGCAGCCCGGGCCCCCAGCAGCCTTCGGGAGCCACAGCCGCTGCACCCGGGCGACCC	199							
Db	1	GGGGGAGCAGCGCGGGCCCCCAGCAGCCTTCGGGAGCCACAGCCGCTGCACCCGGGCGACCC	60							
QY	200	TCCGCTGCTGTGCGCTCCTCTGATGCGCTTTCGCCCTTCGCCGCCCGGGAGCTCCGGGAGA	259							
Db	61	TCCGCTGCTGTGCGCTCCTCTGATGCGCTTTCGCCCTTCGCCGCCCGGGAGCTCCGGGAGA	120							
QY	260	ATGTGGGTCTTAGCATGCCGGCACTTTTTCGGGATTTTCTTGTCTTCAGGCTTTGGC	319							
Db	121	ATGTGGGTCTTAGCATGCCGGCACTTTTTCGGGATTTTCTTGTCTTCAGGCTTTGGC	180							
QY	320	CTGCAAAATCCATGCTACACAGTGTGAAGAAATTCACGCTAACAGACATGCTCTCCCC	379							
Db	181	CTGCAAAATCCATGCTACACAGTGTGAAGAAATTCACGCTAACAGACATGCTCTCCCC	240							
QY	380	GAGTTCATTGTGAATTTGCAAGGTGAACGTTCAAGACATGTGTACAGAAAGATGATGAG	439							
Db	241	GAGTTCATTGTGAATTTGCAAGGTGAACGTTCAAGACATGTGTACAGAAAGATGATGAG	300							
QY	440	CAAAATGCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCC	499							
Db	301	CAAAATGCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCC	360							
QY	500	TCTGGCGGGTACAGTCCCTTGTGCTCCCGAGGAAATCACTCAAGTTTGCATCAGCTCC	559							
Db	361	TCTGGCGGGTACAGTCCCTTGTGCTCCCGAGGAAATCACTCAAGTTTGCATCAGCTCC	420							
QY	560	TGCAACACCCCTCTTTGTAAACGGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCTCCGCGC	619							
Db	421	TGCAACACCCCTCTTTGTAAACGGGCGCAAGGCCCAAGAAAAGGGAAGTTCTGCTCCGCGC	480							
QY	620	CTCAGGCCAGGGCTCCGCAACCACTCTGTTCCTCAATTTAGCCCTCTTCTCGGCACAC	679							
Db	481	CTCAGGCCAGGGCTCCGCAACCACTCTGTTCCTCAATTTAGCCCTCTTCTCGGCACAC	540							
QY	680	TGCTGAAGCTGAAGAGATGCCACCCCTCCGCAATGTGTTTCCAGGCTCGGCCCCCA	739							
Db	541	TGCTGAAGCTGAAGAGATGCCACCCCTCCGCAATGTGTTTCCAGGCTCGGCCCCCA	600							
QY	740	CCCCCACCCTCCCTAGTAGTAGTTTCTTGGGTGTCTTTTATTTGCGGTAGGAGCGGG	799							
Db	601	CCCCCACCCTCCCTAGTAGTAGTTTCTTGGGTGTCTTTTATTTGCGGTAGGAGCGGG	660							
QY	800	AGTCGGTGTCTCTTTTGTCTGTGCAAAATATGAAGAGCTCGGTAAAGCATTTCTGAA	859							
Db	661	AGTCGGTGTCTCTTTTGTCTGTGCAAAATATGAAGAGCTCGGTAAAGCATTTCTGAA	720							
QY	860	TAAATTCAGCTGATGAAATTTTACGTATGTACTTGAAAGAGAGGTGAGATGAAGTT	919							
Db	721	TAAATTCAGCTGATGAAATTTTACGTATGTACTTGAAAGAGAGGTGAGATGAAGTT	780							
QY	920	CACCCCATGTCTGTGTAAACCGAGTCAAGGCGAGGCTGGCAGAGTCTGTCCTTGAAGT	979							
Db	781	CACCCCATGTCTGTGTAAACCGAGTCAAGGCGAGGCTGGCAGAGTCTGTCCTTGAAGT	840							
QY	980	CAGTGAAGTGGGCATCTGCTTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGG	1039							
Db	841	CAGTGAAGTGGGCATCTGCTTTTGTAAAGCTCCAGTGTCCATTCATCCCTGATGGGG	900							
QY	1040	GCATGTTTGAAGTGCAGAGTGAAGAGTGAAGCTTTTCTTAAGGCTGAGAGGCAATTGCC	1099							
Db	901	GCATGTTTGAAGTGCAGAGTGAAGAGTGAAGCTTTTCTTAAGGCTGAGAGGCAATTGCC	960							
QY	1100	ACTCAAGGCTCCCTGCTGTGATCAATCAAACTTCATGCTCTGTAAGAACCATTTCTGCAGC	1159							
Db	961	ACTCAAGGCTCCCTGCTGTGATCAATCAAACTTCATGCTCTGTAAGAACCATTTCTGCAGC	1020							
QY	1160	AGAAATGGCTGTTCGCGCCTGAAGTTGGGCTCTAATGATCTGAGACTCAATGACTGGGA	1219							



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Db 1021 AGAATTGGCTGGTTCGGCCGCTGATTTGGCTCTAGTACTCGAGACTCATGTGATGCGGA 1080
Qy 1220 CTTAGACTGGGCTCGGCTGCTCTGTAAGAGTCTTAAAGAAATCTTCTGATTTCTCT 1279
Db 1081 CTTAGACTGGGCTCGGCTGCTCTGTAAGAGTCTTAAAGAAATCTTCTGATTTCTCT 1140
Qy 1280 TGCAGAGGCTGGGCGCGGAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1339
Db 1141 TGCAGAGGCTGGGCGCGGAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
Qy 1340 GGTGTGTAGTGTGCGATGTACGCGGAGCGGCTTCTGCTGTTGGCTGCTGAGGAGGAG 1399
Db 1201 GGTGTGTAGTGTGCGATGTACGCGGAGCGGCTTCTGCTGTTGGCTGCTGAGGAGGAG 1260
Qy 1400 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1459
Db 1261 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1330
Qy 1460 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1519
Db 1321 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
Qy 1520 GTACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1579
Db 1381 GTACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Qy 1580 CCGAATCTGTGTGGGCTTCAGCATACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1639
Db 1441 CCGAATCTGTGTGGGCTTCAGCATACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
Qy 1640 ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1663
Db 1501 ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1524

RESULT 35
US-10-216-163-15
: Sequence 15, Application US/10216163
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530PIC3
: CURRENT APPLICATION NUMBER: US/10/216.163
: PRIOR FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656

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: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 15
: LENGTH: 1524
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-216-163-15

Query Match 75.0%; Score 1422; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 1.2e-266;
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 140 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 199
Db 1 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
Qy 200 TCGGCTGCTGTGCGCTCTCTGATGCGCTTGCCTGCTCCGCGCGCGGAGCTCCGAGAG 259
Db 61 TCGGCTGCTGTGCGCTCTCTGATGCGCTTGCCTGCTCCGCGCGCGGAGCTCCGAGAG 120
Qy 260 ATGTGGGCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 319
Db 121 ATGTGGGCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Qy 320 CTGGAATCCAGTCTACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 379
Db 181 CTGGAATCCAGTCTACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Qy 380 GAGTCAATGTGAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 439
Db 241 GAGTCAATGTGAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Qy 440 CAAAGTCCGCGGATCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 499
Db 301 CAAAGTCCGCGGATCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Qy 500 TCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 559
Db 361 TCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 560 TGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 619
Db 421 TGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Qy 620 CTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 679
Db 481 CTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
Qy 680 TGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 739
Db 541 TGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
Qy 740 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 799
Db 601 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Qy 800 AGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 859
Db 661 AGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Qy 860 TAAATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 919
Db 721 TAAATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Qy 920 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 979
Db 781 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Qy 980 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1039

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Db	841	CACATGAGTGGGCATCTGCCCTTTGTAAAGCCTCAGTGTCATTCATCCCTGATGGGG	900
Qy	1040	GCATAGTTTGAGACTGCAGAGATGAGATGACGTTTCTTAGGGCTGAGAGGCCACTTCCC	10999
Db	901	GCATAGTTTGAGACTGCAGAGATGAGATGACGTTTTCTTAGGGCTGAGAGGCCACTTCCC	960
Qy	1100	ACTCAAGGCTCCCTCGCGTTCTACATTCACAACTTATCTCTCTGTAAGAAACCATCTCTCGAGC	1159
Db	961	ACTCAAGGCTCCCTCGCGTTCTACATTCACAACTTATCTCTCTGTAAGAAACCATCTCTCGAGC	10200
Qy	1160	AGAAATGGCTGTGTTTCCCGCCCTGAGTTGGGCTCTAGTGACTCGAGACTCAATGACTGGA	1219
Db	1021	AGAAATGGCTGTGTTTCCCGCCCTGAGTTGGGCTCTAGTGACTCGAGACTCAATGACTGGA	1080
Qy	1220	CTTAGACAGGGGGCTCGGCGCTCGCGTCTGAAAGGCTTAGAAATCTTCTCAGTTCTCT	1279
Db	1081	CTTAGACAGGGGGCTCGGCGCTCGCGTCTGAAAGGCTTAGAAATCTTCTCAGTTCTCT	1140
Qy	1280	TGCAGAGACTGCGCGCGGGAGCGCGAAGACACGCGCGCTGCACACAAAGCGGCGCTGTC	1339
Db	1141	TGCAGAGACTGCGCGCGGGAGCGCGAAGACACGCGCGCTGCACACAAAGCGGCGCTGTC	1200
Qy	1340	GGTGTGGAGTGGCGCATGTACGGGCGAGCGGCTTCTCTGTGTGTGGCTGTGACGACAG	1399
Db	1201	GGTGTGGAGTGGCGCATGTACGGGCGAGCGGCTTCTCTGTGTGTGGCTGTGACGACAG	1260
Qy	1400	CGCGCAGCACAGCACCTGCACGAACACCGCGCAAACTGCTCGAGAGCACCGTGTACAG	1459
Db	1261	CGCGCAGCACAGCACCTGCACGAACACCGCGCAAACTGCTCGAGAGCACCGTGTACAG	1320
Qy	1460	GAGCGGGTTGATGACGAGACTGAGGTAGAAAAAGTCTCCGAAAGGAGGAGAGATCAT	1519
Db	1321	GAGCGGGTTGATGACGAGACTGAGGTAGAAAAAGTCTCCGAAAGGAGGAGAGATCAT	1380
Qy	1520	GTACGCCCGGGAAGAGGACCTCTCCAGTCTGCTGGTGGCTGGCGGAGCATGATGCT	1579
Db	1381	GTACGCCCGGGAAGAGGACCTCTCCAGTCTGCTGGTGGCTGGCGGAGCATGATGCT	1440
Qy	1580	CCGAAATCTGTTGGGCGATCCAGCATACGGCCCAATGTCAACAACTACGCTTGGGCGAC	1639
Db	1441	CCGAAATCTGTTGGGCGATCCAGCATACGGCCCAATGTCAACAACTACGCTTGGGCGAC	1500
Qy	1640	ACGAGCAGGAGGGAGAGACAGAGAA	1663
Db	1501	ACGAGCAGGAGGGAGAGACAGAGAA	1524
RESULT 36			
US-10-216-164-15			
: Sequence 15, Application US/10216164			
: GENERAL INFORMATION:			
: APPLICANT: Baker, Kevin P.			
: APPLICANT: Desnoyers, Luc			
: APPLICANT: Geriltsen, Mary			
: APPLICANT: Goddard, Audrey			
: APPLICANT: Godowski, Paul J.			
: APPLICANT: Grimaldi, J Christopher			
: APPLICANT: Gurney, Austin L.			
: APPLICANT: Smith, Victoria			
: APPLICANT: Stephan, Jean-Philippe F.			
: APPLICANT: Watanabe, Colin L.			
: APPLICANT: Wood, William I.			
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
: FILE REFERENCE: P350P1C5			
: CURRENT APPLICATION NUMBER: US/10/216.164			
: CURRENT FILING DATE: 2002-08-09			
: PRIOR APPLICATION NUMBER: 10/119,480			
: PRIOR FILING DATE: 2002-04-09			
: PRIOR APPLICATION NUMBER: 60/059113			
: PRIOR FILING DATE: 1997-09-17			
: PRIOR APPLICATION NUMBER: 60/062287			
: PRIOR FILING DATE: 1997-10-17			

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? PRIOR APPLICATION NUMBER: 60/063549
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/064103
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/069873
? PRIOR FILING DATE: 1997-12-17
? PRIOR APPLICATION NUMBER: 60/076910
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/079294
? PRIOR FILING DATE: 1998-03-25
? PRIOR APPLICATION NUMBER: 60/079656
? PRIOR FILING DATE: 1998-03-26
? PRIOR APPLICATION NUMBER: 60/079728
? PRIOR FILING DATE: 1998-03-27
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 246
? SEQ ID NO 15
? LENGTH: 1524
? TYPE: DNA
? ORGANISM: Homo Sapien
US-10-216-164-15

Query Match          75.0%   Score 1422:   DB 42:   Length 1524:
Best Local Similarity 99.9%:   Pred. No. 1.2e-266:
Matches 1522, Conservative 0:   Mismatches 2:   Indels 0:   Gaps 0:

```

Query Match	75.0%	Score 1422:	DB 42:	Length 1524:
Best Local Similarity	99.9%	Pred. No. 1.2e-26:		
Matches 1522:	Conservative	0:	Mismatches 26:	Indels 0:
			Gaps	0:
QY 140	GCGCAGACAGCGCGGGCCCGACAGCCTTCGCGACGACAGCGCGCTGCAGCGCGGGGACGC	199		
Db 1	GCGCAGACAGCGCGGGCCCGACAGCCTTCGCGACGACAGCGCGCTGCAGCGCGGGGACGC	60		
QY 200	TCCGCTGCTGTGCGCTTCCTCTGTATGCGCTTGCCCTTCGCCGGGCCGGGACTCCGGGAGA	259		
Db 61	TCCGCTGCTGTGCGCTTCCTCTGTATGCGCTTGCCCTTCGCCGGGCCGGGACTCCGGGAGA	120		
QY 260	ATGAGGTGCTCCTAGGCAATCGCGGCAACTTTTGGGATGTTCTTTCGCTTCCAGGCTTTGGG	319		
Db 121	ATGAGGTGCTCCTAGGCAATCGCGGCAACTTTTGGGATGTTCTTTCGCTTCCAGGCTTTGGG	180		
QY 320	CTGCAATATCCAGTGTCTACGAGTGTAAAGAAATTCAGCGTGAACAACGAGCTCTCTCCCC	379		
Db 181	CTGCAATATCCAGTGTCTACGAGTGTAAAGAAATTCAGCGTGAACAACGAGCTCTCTCCCC	240		
QY 380	GAGTTCAATTGTGAATTTGCAGGCTGAAGCTTGAAGACATGTGTGCAGAAAGATGATGGAG	439		
Db 241	GAGTTCAATTGTGAATTTGCAGGCTGAAGCTTGAAGACATGTGTGCAGAAAGATGATGGAG	300		
QY 440	CAAGTGCAGCGGGATCATGTACCGCAAGTCTGTGCATCATACAGCGGCTGTCTCATCGCC	499		
Db 301	CAAGTGCAGCGGGATCATGTACCGCAAGTCTGTGCATCATACAGCGGCTGTCTCATCGCC	360		
QY 500	TCTAGCGGGTACAGTCTTCTGTGCTCCCGACAGGAACGTGAACACTAGTTTGCATCACTGCG	559		
Db 361	TCTAGCGGGTACAGTCTTCTGTGCTCCCGACAGGAACGTGAACACTAGTTTGCATCACTGCG	420		
QY 560	TGCAACACCCCTTTTGTAAAGCGGCCAAGGCCAAGAAAAGGGGAAGTTCTGCTTGCGCC	619		
Db 421	TGCAACACCCCTTTTGTAAAGCGGCCAAGGCCAAGAAAAGGGGAAGTTCTGCTTGCGCC	480		
QY 620	CTCAGGCCAGGGCTCCGCAACCACTCTGTCTCTCAAAATTAACCTCTTCTCGGCACAC	679		
Db 481	CTCAGGCCAGGGCTCCGCAACCACTCTGTCTCTCAAAATTAACCTCTTCTCGGCACAC	540		
QY 680	TGCTGAAGCTGAAGAGATGCGACCCCTCCCTGATGTTCTTCAGGCGCTCGCCCCCA	739		
Db 541	TGCTGAAGCTGAAGAGATGCGACCCCTCCCTGATGTTCTTCAGGCGCTCGCCCCCA	600		
QY 740	CCCCCACCCTCCCTAGTGAAGTTTCTTGTGGTGTCTCTTATTTCTGGGTAGGAGCGGG	799		
Db 601	CCCCCACCCTCCCTAGTGAAGTTTCTTGTGGTGTCTCTTATTTCTGGGTAGGAGCGGG	660		
QY 800	AGTCGCTGTTCTCTTTTGTCTCTGTCGAATAATGAAGAGCTCGGTAAAGCATTTCTGA	859		
Db 661	AGTCGCTGTTCTCTTTTGTCTCTGTCGAATAATGAAGAGCTCGGTAAAGCATTTCTGA	720		

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QY 860 TAAATTCAGCTGACTGAATTTTCTAGTATGTAAGTGAAGAGAGTGGAGTAAAGT 919
    |||||
Db 721 TAAATTCAGCTGACTGAATTTTCTAGTATGTAAGTGAAGAGAGTGGAGTAAAGT 780
QY 920 CACCCCATGCTGTGTAAACCGAGTCAAGGCGAGGAGAGTGTCTCTTGAAGT 979
    |||||
Db 781 CACCCCATGCTGTGTAAACCGAGTCAAGGCGAGGAGAGTGTCTCTTGAAGT 840
QY 980 CACTAGGTGGGCACTGTGCTTTTGTAAAGCTCCAGTGTCCATTCATCCCTGAGG 1039
    |||||
Db 841 CACTAGGTGGGCACTGTGCTTTTGTAAAGCTCCAGTGTCCATTCATCCCTGAGG 900
QY 1040 GCATAGTTGAAGTCAAGAGTGAAGAGTGTCTTTTGAAGGCTGGAGGCGAGTCC 1099
    |||||
Db 901 GCATAGTTGAAGTCAAGAGTGAAGAGTGTCTTTTGAAGGCTGGAGGCGAGTCC 960
QY 1100 ACTCAAGGCTCCCTGCTGTGACATTCAAACTTCATGCTCTGAAAAACCATTCCTGCAGC 1159
    |||||
Db 961 ACTCAAGGCTCCCTGCTGTGACATTCAAACTTCATGCTCTGAAAAACCATTCCTGCAGC 1020
QY 1160 AGAATGCTGCTGTTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGGA 1219
    |||||
Db 1021 AGAATGCTGCTGTTTGGCGCTGAGTGGGCTCTAGTACTGAGACTCAATGACTGGA 1080
QY 1220 CTTAGACTGGGCTGGGCTGCTGCTGAAAGTGTCTTAAAGAAATCTTCTGAGTTCCT 1279
    |||||
Db 1081 CTTAGACTGGGCTGGGCTGCTGCTGAAAGTGTCTTAAAGAAATCTTCTGAGTTCCT 1140
QY 1280 TGCAGAGACTGGCGCGCGGAGCGAGAGCAACGGCGCTGACACAAAGCGGCGCTGTC 1339
    |||||
Db 1141 TGCAGAGACTGGCGCGCGGAGCGAGAGCAACGGCGCTGACACAAAGCGGCGCTGTC 1200
QY 1340 GGTGTGGAGTGGCGCTGACGCTGACGCGAGGCGCTTCTGTGTGGTGGTGTCTGAGGAG 1399
    |||||
Db 1201 GGTGTGGAGTGGCGCTGACGCTGACGCGAGGCGCTTCTGTGTGGTGGTGTCTGAGGAG 1260
QY 1400 GCGGCGAGCAGACCTGTGACAGAACACCGCGGAACTGCTCGAGAGACACGCTGTACAG 1459
    |||||
Db 1261 GCGGCGAGCAGACCTGTGACAGAACACCGCGGAACTGCTCGAGAGACACGCTGTACAG 1320
QY 1460 GAGCGGTTGATGACCGAGCTGAGTAGAAAACTCTCCGAGAGAGGAGAGATCAT 1519
    |||||
Db 1321 GAGCGGTTGATGACCGAGCTGAGTAGAAAACTCTCCGAGAGAGGAGAGATCAT 1380
QY 1520 GATAGCGCGGAGATGAGACTGCTGACGCTGTGGTGGTGGGCGAGGAGATGCT 1579
    |||||
Db 1381 GATAGCGCGGAGATGAGACTGCTGACGCTGTGGTGGTGGGCGAGGAGATGCT 1440
QY 1580 CCGAATCTGTTGGGCACTACAGCATACGGCAATGTACACAAATCAGCCCTGGGCAAGC 1639
    |||||
Db 1441 CCGAATCTGTTGGGCACTACAGCATACGGCAATGTACACAAATCAGCCCTGGGCAAGC 1500
QY 1640 ACGAGCAGAGGAGAGAGAGAGA 1663
    |||||
Db 1501 ACGAGCAGAGGAGAGAGAGA 1524

```

RESULT 37  
US-10-216-165-15

Sequence 15, Application US/10216165  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerlielsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Collin L.  
APPLICANT: Wood, William I.

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C7
; CURRENT APPLICATION NUMBER: US/10/216,165
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-165-15

```

Query Match 75.0%; Score 1422; DB 42; Length 1524;  
Best Local Similarity 99.9%; Pred. No. 1.2e-266;  
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 140 GCGGCGAGGCGCGGCGCGGAGAGCTTGGGCAAGCCAGCCGCGGAGCGGAGGCC 199
    |||||
Db 1 GCGGCGAGGCGCGGCGCGGAGAGCTTGGGCAAGCCAGCCGCGGAGCGGAGGCC 60
QY 200 TCCGCTGCTGTGCGCTCTCTGATGCGCTTCCCTTCCCGGCGCGGAGACTCCGGAGA 259
    |||||
Db 61 TCCGCTGCTGTGCGCTCTCTGATGCGCTTCCCTTCCCGGCGCGGAGACTCCGGAGA 120
QY 260 ATGTGGGCTCAGGATGCGGCAACTTTTGGCGATTGTTGCTTCCAGGCTTTGGC 319
    |||||
Db 121 ATGTGGGCTCAGGATGCGGCAACTTTTGGCGATTGTTGCTTCCAGGCTTTGGC 180
QY 320 CTGCAATCCAGTCTACCAAGTGAAGAATTCCAGCTGAACAAGCACTGCTCTCC 379
    |||||
Db 181 CTGCAATCCAGTCTACCAAGTGAAGAATTCCAGCTGAACAAGCACTGCTCTCC 240
QY 380 GAGTTCAATGTAATGACGAGGTGAAGTCAACATGATGTCGAAGAAGTGAAGAG 439
    |||||
Db 241 GAGTTCAATGTAATGACGAGGTGAAGTCAACATGATGTCGAAGAAGTGAAGAG 300
QY 440 CAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATCATCAGGCGCTGTCTATGCC 499
    |||||
Db 301 CAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATCATCAGGCGCTGTCTATGCC 360
QY 500 TCTGCGGGGTACCAAGTCTTGTCTCCCAAGGAAACTGAATCAGTTTGCATCAGTGC 559
    |||||
Db 361 TCTGCGGGGTACCAAGTCTTGTCTCCCAAGGAAACTGAATCAGTTTGCATCAGTGC 420
QY 560 TGCACACCCCTCTTTGTAAGGCGCAAGGCGCAAGAAAGGGAATTTGCTGCGGCC 619
    |||||
Db 421 TGCACACCCCTCTTTGTAAGGCGCAAGGCGCAAGAAAGGGAATTTGCTGCGGCC 480
QY 620 CTCAGGCGGAGGCTCGGACCAACATCTGTTCTCAAAATTAGCCCTTCTCGGACAC 679
    |||||
Db 481 CTCAGGCGGAGGCTCGGACCAACATCTGTTCTCAAAATTAGCCCTTCTCGGACAC 540

```

OY	680	TGCTCAACCTCAAGSAGATGCGACCCCCCTCCTCGATTGTTCTTCACAGCCCTGGCCCCCA	733
Db	541	TGCTGMACTCAAGSAGATGCGACCCCCCTCCTCGATTGTTCTTCACAGCCCTGGCCCCCA	600
OY	740	CCCCCACCTCCCTGAGTGAGTTCCTCTGSGGTGTCCTTTATCTTGGGTAGGAGCGGG	799
Db	601	CCCCCACCTCCCTGAGTGAGTTCCTCTGSGGTGTCCTTTATCTTGGGTAGGAGCGGG	660
OY	800	AGTCGCTTCCTCTTTTGTCCTGTGCAATTAATGAAAGAGCGGTGAAGATCTGAA	859
Db	661	AGTCGCTTCCTCTTTTGTCCTGTGCAATTAATGAAAGAGCGGTGAAGATCTGAA	720
OY	860	TAAATTGAGCTGACTGAATTTTCAGTATGTACTTGAAGAGAGAGGTGAGTGAAGTT	919
Db	721	TAAATTGAGCTGACTGAATTTTCAGTATGTACTTGAAGAGAGAGGTGAGTGAAGTT	780
OY	920	CACCCCACTGTCTGTGTAACCGGAGTCGAAGCGAGCTGGCAGAGTCMCTCTTGAAGT	979
Db	781	CACCCCACTGTCTGTGTAACCGGAGTCGAAGCGAGCTGGCAGAGTCMCTCTTGAAGT	840
OY	980	CACTGAGGTGGGCATCTGCCCTTTTGTAAGACCTCCAGGTGCAATTCATCCCTGATGGGG	1033
Db	841	CACTGAGGTGGGCATCTGCCCTTTTGTAAGACCTCCAGGTGCAATTCATCCCTGATGGGG	900
OY	1040	GCATAGTTTGAGACTGTGAGAGTGAAGTGAAGTGAAGCTTTCTTAGGCTCTGAGAGGCCAGTTCCC	1099
Db	901	GCATAGTTTGAGACTGTGAGAGTGAAGTGAAGTGAAGCTTTCTTAGGCTCTGAGAGGCCAGTTCCC	960
OY	1100	ACTCAAGGCTCCCTGCGTTGATACATTCAAACTTCATGCTCCTGTAAACCACTTCCTGCAAC	1155
Db	961	ACTCAAGGCTCCCTGCGTTGATACATTCAAACTTCATGCTCCTGTAAACCACTTCCTGCAAC	1020
OY	1160	AGAAATGGCTGGTTTGGCGGCTAGTGTGGGCTCTACTGACTGAGACTGAATGACTGGGA	1215
Db	1021	AGAAATGGCTGGTTTGGCGGCTAGTGTGGGCTCTACTGACTGAGACTGAATGACTGGGA	1080
OY	1220	CTTAGACTGGGGCTCGGCGCTCGCTCTGTAAAGTGTCTTAGAAATCTTCTCAGTCTCCT	1279
Db	1081	CTTAGACTGGGGCTCGGCGCTCGCTCTGTAAAGTGTCTTAGAAATCTTCTCAGTCTCCT	1140
OY	1280	TGCAAGAGACTGGGCGGGGAGCGGAAGACACAGGGGGCTGTGACAAAGCGGGCGCTGTG	1333
Db	1141	TGCAAGAGACTGGGCGGGGAGCGGAAGACACAGGGGGCTGTGACAAAGCGGGCGCTGTG	1200
OY	1340	GGTGGTGGAGTGCAGATGTACGGGACGGGCTTCTGTGTGGGTGGCGTGTGACGAGAC	1399
Db	1201	GGTGGTGGAGTGCAGATGTACGGGACGGGCTTCTGTGTGGGTGGCGTGTGACGAGAC	1260
OY	1400	GGGGACAGACGACCTGTGCACAAACCCGGCCGAACCTGCTGCGAGAGACCCGTATAC	1455
Db	1261	GGGGACAGACGACCTGTGCACAAACCCGGCCGAACCTGCTGCGAGAGACCCGTATAC	1320
OY	1460	GAGCGGGTTGATGACCGAGCTGAGGTAGAAAAAGCTCTCGAGAAAGGAGGAGAGATCAT	1519
Db	1321	GAGCGGGTTGATGACCGAGCTGAGGTAGAAAAAGCTCTCGAGAAAGGAGGAGAGATCAT	1380
OY	1520	GTAGAGCCCGGAAGTAGACCTCGTCCAGTGTGTCTTGGTGTTGGCCGACGCATGATCT	1579
Db	1381	GTAGAGCCCGGAAGTAGACCTCGTCCAGTGTGTCTTGGTGTTGGCCGACGCATGATCT	1440
OY	1580	CCGAATCTGTGTTGGGCATCCAGCATACGGGCATATGTCAACAACATCAGCCCTGGGCACAC	1639
Db	1441	CCGAATCTGTGTTGGGCATCCAGCATACGGGCATATGTCAACAACATCAGCCCTGGGCACAC	1500
OY	1640	ACGAGCAGAGAGGAGACACGAGAA 1663	
Db	1501	ACGAGCAGAGAGGAGACACGAGAA 1524	

RESULT 38  
US-10-216-166-15  
; Sequence 15, Application US/10216166  
; GENERAL INFORMATION:

```

1 / APPLICANT: Baker, Kevin P.
2 / APPLICANT: Desnoyers, Luc
3 / APPLICANT: Gerritsen, Mary
4 / APPLICANT: Goddard, Audrey
5 / APPLICANT: Godowski, Paul J.
6 / APPLICANT: Grimaldi, J. Christopher
7 / APPLICANT: Gurney, Austin L.
8 / APPLICANT: Smith, Victoria
9 / APPLICANT: Stephan, Jean-Philippe F.
10 / APPLICANT: Watanabe, Colin L.
11 /
12 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
13 / TITLE OF INVENTION: ACIDS ENCODING THE SAME
14 / FILE REFERENCE: P3530PIC9
15 / CURRENT APPLICATION NUMBER: US/10/216,166
16 /
17 / CURRENT FILING DATE: 2002-08-09
18 / PRIOR APPLICATION NUMBER: 10/119,480
19 / PRIOR FILING DATE: 2002-04-09
20 / PRIOR APPLICATION NUMBER: 60/059113
21 / PRIOR FILING DATE: 1997-09-17
22 / PRIOR APPLICATION NUMBER: 60/062287
23 / PRIOR FILING DATE: 1997-10-17
24 / PRIOR APPLICATION NUMBER: 60/063549
25 / PRIOR FILING DATE: 1997-10-28
26 / PRIOR APPLICATION NUMBER: 60/064103
27 / PRIOR FILING DATE: 1997-10-31
28 / PRIOR APPLICATION NUMBER: 60/069873
29 / PRIOR FILING DATE: 1997-12-17
30 / PRIOR APPLICATION NUMBER: 60/078910
31 / PRIOR FILING DATE: 1998-03-20
32 / PRIOR APPLICATION NUMBER: 60/079294
33 / PRIOR FILING DATE: 1998-03-25
34 / PRIOR APPLICATION NUMBER: 60/079656
35 / PRIOR FILING DATE: 1998-03-26
36 / PRIOR APPLICATION NUMBER: 60/079728
37 / PRIOR FILING DATE: 1998-03-27
38 / Remaining Prior Application data removed - See file Wrapper or PALM.
39 / NUMBER OF SEQ ID NOS: 246
40 /
41 / SEQ ID NO 15
42 /
43 / LENGTH: 1524
44 /
45 / TYPE: DNA
46 /
47 / ORGANISM: Homo Sapien
48 /
49 / US-10-216-166-15

```

Query Match	Similarity	75.0%	Score 1422:	DB 42:	Length 1524:
Best Local	Similarity	99.9%	Pred. No. 1.2e-265:		
Matches 1522:	Conservative	0:	Mismatches	2:	Indels
					Gaps
					0:
QY	140	GGGCGAGCAGCGCGGGGCCCCAGCAGCCTTGCGAGGCACACAGCCGCTGCAGGCCGCGGCGAGCC	199		
Db	1	GGGCGAGCAGCGCGGGGCCCCAGCAGCCTTGCGAGGCACACAGCCGCTGCAGGCCGCGGCGAGCC	199		
QY	200	TCCGCTGCCTTCGCGCTCCTCTGATCGCTGCGCTCTCCGGGCCCGGAGCTCCGGGAGA	259		
Db	61	TCCGCTGCCTTCGCGCTCCTCTGATCGCTGCGCTCTCCGGGCCCGGAGCTCCGGGAGA	259		
QY	260	ATGTGGGTCCTTAGGCGATCGCGGCACTTTTTCGGGATGTTTGGCTTCCTTCAGGCTTTGGG	319		
Db	121	ATGTGGGTCCTTAGGCGATCGCGGCACTTTTTCGGGATGTTTGGCTTCCTTCAGGCTTTGGG	319		
QY	320	CTGCAATTCAGATGCTACCAAGTGTGAAGAATTCAGCTGAACMACGAGCTGCCTCCGCC	379		
Db	181	CTGCAATTCAGATGCTACCAAGTGTGAAGAATTCAGCTGAACMACGAGCTGCCTCCGCC	379		
QY	380	GAGTTCATTGTGAATTTGCAAGGTGAACGTTCAAGCAATGTGTCAAGAAAGATGTAGAG	439		
Db	241	GAGTTCATTGTGAATTTGCAAGGTGAACGTTCAAGCAATGTGTCAAGAAAGATGTAGAG	439		
QY	440	CAAAATGCCGGGATATGTACCGCAAGTCTGTGTGATATATCAGCGGCGCTGTCTATTCGCC	499		
Db	301	CAAAATGCCGGGATATGTACCGCAAGTCTGTGTGATATATCAGCGGCGCTGTCTATTCGCC	499		
QY	500	TCTGCGGCGATACCACTCCTTGTCTCTCCCGAGGAAACTGAACCTCAGTTTGCATCAGCTGC	559		

Db	361	TCCTCGGGATACAGAGCTCTTCTGCTCCGCCAGGAAACTGAATCAGTTTGCATCAGCTGC	420
Qy	560	TGCACACCCCTCTTTTGTAACTGGGCCAAGGCCCAAGAAAGGGGAATTTCTGCTCGGCC	619
Db	421	TGCACACCCCTCTTTGTAACTGGGCCCAAGGCCCAAGAAAGGGGAATTTCTGCTCGGCC	480
Qy	620	CTCAGGCGAGGGCCGACACCACTATCTGTTCTCTAAATTTAGCCCTCTTCTCGGCACAC	679
Db	481	CTCAGGCGAGGGCTCCGCACTACCACTCTGTTCTCTAAATTTAGCCCTCTTCTCGGCACAC	540
Qy	680	TGCTGAAGCTGAAGAGATGCCACCCCTCTGCTCATTTGTTCTTCCAGCCCTCGCCCCAA	739
Db	601	CCCCCACTCCCTGAGTGAATTTCTTCTGCGGTCTCTTTATCTCGGGTTAGGAGCGGG	799
Qy	740	CCCCCACTCCCTGAGTGAATTTCTTCTGCGGTCTCTTTATCTCGGGTTAGGAGCGGG	660
Db	800	AGTCCGTGTTCTTCTTGTATCTGCTGCAATAATGAAGAGCTCGGTAAAGCATCTTGAA	859
Db	661	AGTCCGTGTTCTCTTTTGTCTCTGTGAATAATGAAGAGCTCGGTAAAGCATCTTGAA	720
Qy	860	TAAATTCAGCTTACTCAATTTTCAGTATGTACTTAAAGAAAGAGGTGAGTGAATTT	919
Db	721	TAAATTCAGCTCTGACTCAATTTTCAGTATGTACTTAAAGAAAGAGGTGAGTGAATTT	780
Qy	920	CACCCCATGCTGTGTAAACCGGAGTCAAGAGCGAGCGCTGGCAGATCTGTCCTTGAAGT	979
Db	781	CACCCCATGCTGTGTAAACCGGAGTCAAGAGCGAGCGCTGGCAGATCTGTCCTTGAAGT	840
Qy	980	CACGTGAGTGGGCATCTGCTCTTTTGTAAAGCTTCAGTGTCCATTCATCCTGATGGGG	1039
Db	841	CACGTGAGTGGGCATCTGCTCTTTTGTAAAGCTTCAGTGTCCATTCATCCTGATGGGG	900
Qy	1040	GCATAGTTTGGAGTGTGAGAGTGAAGTGAGTGACGTTTTCTTAAGGCTGGAGGGCCACTTCC	1099
Db	901	GCATAGTTTGGAGTGTGAGAGTGAAGTGAGTGACGTTTTCTTAAGGCTGGAGGGCCACTTCC	960
Qy	1100	ACTCAAGGCTCCCTCGGTGACATTCACAACTTCATGCTCTGAAAAACCATTCCTGTGACG	1159
Db	961	ACTCAAGGCTCCCTCGGTGACATTCACAACTTCATGCTCTGAAAAACCATTCCTGTGACG	1020
Qy	1160	AGAAATGGCTGTGGCGGCTGAGTTGGGCTGTATGACTGAGACTCAATGACTGTGGA	1219
Db	1021	AGAAATGGCTGTGGCGGCTGAGTTGGGCTGTATGACTGAGACTCAATGACTGTGGA	1080
Qy	1220	CTTAGACTGGGGCTCGGCTCTGCTGTAAGAAAGTGTCTTAAGAAATCTTCTCAGTTCTCT	1279
Db	1081	CTTAGACTGGGGCTCGGCTCTGCTGTAAGAAAGTGTCTTAAGAAATCTTCTCAGTTCTCT	1140
Qy	1280	TGCAGAGGACTGCGCGCGCGGAGCGGAAGGACACGGGCGCTGTGCACAAAGCGGGCCCTGT	1339
Db	1141	TGCAGAGGACTGCGCGCGCGGAGCGGAAGGACACGGGCGCTGTGCACAAAGCGGGCCCTGT	1200
Qy	1340	GGTGGTGGAGTGGCCATGTACGGCGAGGGCTCTGTGTGTTGGCTGTGTGAGGAGACAG	1399
Db	1201	GGTGGTGGAGTGGCCATGTACGGCGAGGGCTCTGTGTGTTGGCTGTGTGAGGAGACAG	1260
Qy	1400	GGCGAGCAGACACCTGTACAGCAACACCGCGAAACTGCTCGAGAGACACCGTGTACAG	1459
Db	1261	GGCGAGCAGACACCTGTGTGAGCAAGCAACCCCGCAAACTCTCGAGAGACACCGTGTACAG	1320
Qy	1460	GAGCGGTTGTATGACGAGCTGAGGTGAAGAAACGTTCTCGAAGAGGGAGGAGGATCAT	1519
Db	1321	GAGCGGTTGTATGACGAGCTGAGGTGAAGAAACGTTCTCGAAGAGGGAGGAGGATCAT	1380
Qy	1520	GTAGCGCCGGAGTAGAGACCTGTGTCAAGTGTGTCCTTGGGTTTGGCGGACAGCCATGATCT	1579
Db	1381	GTAGCGCCGGAGTAGAGACCTGTGTCAAGTGTGTCCTTGGGTTTGGCGGACAGCCATGATCT	1440
Qy	1580	CCGAATCTGGTTGGGCAATCCAGCATACGGCAATGTTCACACAATCAGCCTTGGCGAGAC	1639

```

Db      1441 CCGAATTCGTGGTGGGCATATCCAGCATACCGGCCCAATGTCAACAATACAGCCTCTGGCGAGAC 1500
QY      1640 ACGAGCAGAGGAGGAGACAGACAGA 1663
        |||
Db      1501 ACGAGCAGAGGAGGAGACAGACAGA 1524
        |||

RESULT 39
US-10-216-167-15
; Sequence 15, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin T.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C4
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/211,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/068873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-167-15

Query Match      75.0%; Score 1422; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 1.2e+266;
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      140 GCGGCAGCAGCGCGGGCCCCAGCAGCCTTGCGCAGCCACAGCCCGCTGCGACCGGGGCGAGCC 199
        |||
Db      1 GCGGCAGCAGCGCGGGCCCCAGCAGCCTTGCGCAGCCACAGCCCGCTGCGACCGGGGCGAGCC 60
        |||

QY      200 TCCGCGCTGTGGCCCTCCCTGATGCGGCTTGCGCCTCTCCCGGGCCCCGGGAGCTCCGGGAGA 259
        |||
Db      61 TCCGCGCTGTGGCCCTCCCTGATGCGGCTTGCGCCTCTCCCGGGCCCCGGGAGCTCCGGGAGA 120
        |||

QY      260 ATGTGGGTCTTAGGATCGCGGCAACTTTTTCGGATTGTCTTGCTTCCAGGCTTTGCG 319
        |||
Db      121 ATGTGGGTCTTAGGATCGCGGCAACTTTTTCGGATTGTCTTGCTTCCAGGCTTTGCG 180
        |||

QY      320 CTGCAATTCAGTCTACCAATGTGAAGAAATTCACAGCTGACACAGAGACTGCTTCCTCCCC 379
        |||

```



OY	200	TCGCCTCTGCGCCTCCCTGATGAGCGTTGGCCCTCCCGGCCCCCGGAGACTCCGGGAGA	255
Db	61	TCGCCTCTGTGCGCTCTCTCTGATGCGCTTGCCCTCTCCCGGCCCGGAGACTCCGGGAGA	120
OY	260	ATGTGGGTCTGAGGCATCGCGGCACTTTTGTGCGGATTTGTTCTTGCTTCAGGCTTTGGC	319
Db	121	ATGTGGGTCTGAGGCATCGCGGCACTTTTGTGCGGATTTGTTCTTGCTTCAGGCTTTGGC	180
OY	320	CTGAATTCAGTGCATACAGTGTGAAGAAATTCAGCTGAGAACACAGCTGCTCCGCCCC	379
Db	181	CTGAATTCAGTGCATACAGTGTGAAGAAATTCAGCTGAGAACACAGCTGCTCCGCCCC	240
OY	380	GAGTTCAATTGTAATTCAGAGTGAACGTTTCAAGAAGATGTGCAGAAAAGATGATGAG	439
Db	241	GAGTTCAATTGTAATTCAGAGTGAACGTTTCAAGAAGATGTGCAGAAAAGATGATGAG	300
OY	440	CAAAAGTCCGGGATCATATACCCCAAGTCTGTGCATCATACGCGCCTGTCTATGCC	499
Db	301	CAAAAGTCCGGGATCATATACCCCAAGTCTGTGCATCATACGCGCCTGTCTATGCC	360
OY	500	TCCTGCGGGATACAGTCTCTGCTGCCCAAGGAAATCAATCAAGTTTGCATGAGCTGC	559
Db	361	TCCTGCGGGATACAGTCTCTGCTGCCCAAGGAAATCAATCAAGTTTGCATGAGCTGC	420
OY	560	TGCAACACCCCTCTTTGTAAAGGGGCCAAGGCCCAAGAAAAGGGGAATTTCTGCTCGGC	619
Db	421	TGCAACACCCCTCTTTGTAAAGGGGCCAAGGCCCAAGAAAAGGGGAATTTCTGCTCGGC	480
OY	620	CTCAGGCGCAGGGCCCGGCACACATCTGTTCTCAAAATTTAGCCCTCTCTCGCGGCACAC	679
Db	481	CTCAGGCGCAGGGCCCGGCACACATCTGTTCTCAAAATTTAGCCCTCTCTCGCGGCACAC	540
OY	680	TGCTGAAGCTGAAGAGATGCCAACCCCTCTGTCATTTGTTCTTCAGCCCTCGCCCCAA	739
Db	541	TGCTGAAGCTGAAGAGATGCCAACCCCTCTGTCATTTGTTCTTCAGCCCTCGCCCCAA	600
OY	740	CCCCCACTCCCGAGTGAATTTCTTCTGCGGTCCTTTTATCTCGGATAGGAGCGGG	799
Db	601	CCCCCACTCCCGAGTGAATTTCTTCTGCGGTCCTTTTATCTCGGATAGGAGCGGG	660
OY	800	AGTCGCTGTTCTCTTTTGTGTCCTGTGCAATAATGAAGAGCTCGTAAAGCATCTGAA	859
Db	661	AGTCGCTGTTCTCTTTTGTGTCCTGTGCAATAATGAAGAGCTCGTAAAGCATCTGAA	720
OY	860	TAAATTCAGCTGACTCAATTTTCAGTATGTACTTAAGAAAGAGGTGAGTGAAGTT	919
Db	721	TAAATTCAGCTGACTCAATTTTCAGTATGTACTTAAGAAAGAGGTGAGTGAAGTT	780
OY	920	CACCCCATGTCTGTATACCCGAGTCAAGGCGAGGCTGGAGAGTCMGTCTTGAAGT	979
Db	781	CACCCCATGTCTGTATACCCGAGTCAAGGCGAGGCTGGAGAGTCAATCTTGAAGT	840
OY	980	CAGTGAAGTGGGCATGTGCCCTTTTGTAAAGCTTCAGTGTCCATTCATCCCTGATGGGG	1039
Db	841	CAGTGAAGTGGGCATGTGCCCTTTTGTAAAGCTTCAGTGTCCATTCATCCCTGATGGGG	900
OY	1040	GCATGCTTTGAGACTGAGAGGTGAGAGTGAAGCTTTTCTTAAGGGCTGGAGGCGCAATGCC	1099
Db	901	GCATGCTTTGAGACTGAGAGGTGAGAGTGAAGCTTTTCTTAAGGGCTGGAGGCGCAATGCC	960
OY	1100	ACTCAAGGCTCCCTCGGCTGTACATCAATCAATTCATCTCTCAAAAACATTTCTGCGAGC	1159
Db	961	ACTCAAGGCTCCCTCGGCTGTACATCAATCAATTCATCTCTCTCAAAAACATTTCTGCGAGC	1020
OY	1160	AGAATTTGGCTGTGTTCCGCGCTGAGTTGGGCTCTAATGACTGAGACTCAATGACTGGGA	1219
Db	1021	AGAATTTGGCTGTGTTCCGCGCTGAGTTGGGCTCTAATGACTGAGACTCAATGACTGGGA	1080
OY	1220	CTTAGAGACGGGGCTCGGCGCTCGCTCAAAAAGTGTCTTAAGAAAATCTTTCAGTTCTCT	1279
Db	1081	CTTAGAGACGGGGCTCGGCGCTCGCTCTBAAAAGTGTCTTAAGAAAATCTTTCAGTTCTCT	1140

QY	1280	TGAGAGACTCGGCGCCGGGACGGAAAGACACGGGCGCTGCACAAACGGGGCGCTGC	1339
Db	1141	TGCAGAGACTGGGCGCGGAGCCGAGAGACACAGGGCGCTGCACAAACGGGGCGCTGC	1200
QY	1340	GGTAGTGAAGTGGCCATGTACGGGCAGAGGCGCTTCTCGTGGTGGCGTGTGCAGCGACAG	1399
Db	1201	GGTGGTGAAGTGGCCATGTACGGGCAGAGGCGCTTCTCGTGGTGGCGTGTGTGCAGCGACAG	1260
QY	1400	CGGGCAGCACAGCACCTGCGACGAACACCCGCCAAACTCTCTCGAGAGAACCCGTGTACAG	1459
Db	1261	CGCGAGCAGCACAGCCTGCGACGAACACCCGCCAAACTCTCTCGAGAGAACCCGTGTACAG	1320
QY	1460	GAGCGGGTTGATGACCCGACAGCTGAGAGTGAAGAAACGTCCTCCGAAAGGAGGAGGATCAT	1519
Db	1321	GAGCGGGTTGATGACCCGACAGCTGAGAGTGAAGAAACGTCCTCCGAAAGGAGGAGGATCAT	1380
QY	1520	GTACGCCCGGGAAGTAGACCTCGTCACGTGCTTGGGTTTGGCCCGACGCATGATCCT	1579
Db	1381	GTACGCCCGGGAAGTAGACCTCGTCACGTGCTTGGGTTTGGCCCGACGCATGATCCT	1440
QY	1580	CCGAATCTGGTTGGGGCATCCAGCATACGGCCATGTGCACAACATATACGCCCTGGGCAAGC	1639
Db	1441	CCGAATCTGGTTGGGGCATCCAGCATACGGCCATGTGCACAACATATACGCCCTGGGCAAGC	1500
QY	1640	ACGAGCAGAGGAGGAGACAGAGA 1663	
Db	1501	ACGAGCAGAGGAGGAGACAGAGA 1524	

```

1      RESULT 41
2      US-10-218-612-15
3      ; Sequence 15, Application US/10218612
4      ; GENERAL INFORMATION:
5      ; APPLICANT: Baker, Kevin P.
6      ; APPLICANT: Desnoyers, Luc
7      ; APPLICANT: Gerritsen, Mary
8      ; APPLICANT: Goddard, Audrey
9      ; APPLICANT: Godowski, Paul J.
10     ; APPLICANT: Grimaldi, J. Christopher
11     ; APPLICANT: Gurney, Austin L.
12     ; APPLICANT: Smith, Victoria
13     ; APPLICANT: Stephan, Jean-Philippe F.
14     ; APPLICANT: Watanabe, Colin L.
15     ; APPLICANT: Wood, William I.
16     ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
17     ; FILE REFERENCE: P3530P1C21
18     ; CURRENT APPLICATION NUMBER: US/10/218, 612
19     ; CURRENT FILING DATE: 2002-08-12
20     ; PRIOR APPLICATION NUMBER: 10/119, 480
21     ; PRIOR FILING DATE: 2002-04-09
22     ; PRIOR APPLICATION NUMBER: 60/059113
23     ; PRIOR FILING DATE: 1997-09-17
24     ; PRIOR APPLICATION NUMBER: 60/062287
25     ; PRIOR FILING DATE: 1997-10-17
26     ; PRIOR APPLICATION NUMBER: 60/065549
27     ; PRIOR FILING DATE: 1997-10-28
28     ; PRIOR APPLICATION NUMBER: 60/064103
29     ; PRIOR FILING DATE: 1997-10-31
30     ; PRIOR APPLICATION NUMBER: 60/069873
31     ; PRIOR FILING DATE: 1997-12-17
32     ; PRIOR APPLICATION NUMBER: 60/078910
33     ; PRIOR FILING DATE: 1998-03-20
34     ; PRIOR APPLICATION NUMBER: 60/079294
35     ; PRIOR FILING DATE: 1998-03-25
36     ; PRIOR APPLICATION NUMBER: 60/079656
37     ; PRIOR FILING DATE: 1998-03-26
38     ; PRIOR APPLICATION NUMBER: 60/079728
39     ; PRIOR FILING DATE: 1998-03-27
40     ; Remaining Prior Application data removed - See File Wrapper or PALM.
41     ; NUMBER OF SEQ ID NOS: 246
42     ; SEQ ID NO 15
43     ; LENGTH: 1524

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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-612-15

Query Match      75.0%   Score 1422:   DB 42:   Length 1524:
Best Local Similarity 99.9%:   Pred. No. 1.2e-266:
Matches 1522:   Conservative 0:   Mismatches 2:   Indels 0:   Gaps 0:

QY  140 GCGGAGCAGAGCGGGGCGCCAGCAGAGCCTCGGAGCAGCAGCCGCTGACAGCCGGGAGCC 199
    1 GCGGAGCAGAGCGGGGCGCCAGCAGAGCCTCGGAGCAGCAGCCGCTGACAGCCGGGAGCC 60
QY  200 TCGCGTGTGTGCGCTCTCTCTGATGCGCTTGCCTCCCGCGCGCGGAGCTCCGGAGCA 259
    61 TCGCGTGTGTGCGCTCTCTCTGATGCGCTTGCCTCCCGCGCGCGGAGCTCCGGAGCA 120
QY  260 ATGTGGTCTTAGCATGCGAGCGGCACTTTTGGGATGTTGTTGCTTGCCTCAGGCTTTGG 319
    121 ATGTGGTCTTAGCATGCGAGCGGCACTTTTGGGATGTTGTTGCTTGCCTCAGGCTTTGG 180
QY  320 CTGCAAAATCCAGTGTACAGAGTGTGAAGATTCCAGCTGACAGACTGCTCTCCGCC 379
    181 CTGCAAAATCCAGTGTACAGAGTGTGAAGATTCCAGCTGACAGACTGCTCTCCGCC 240
QY  380 GAGTTATTGTGAATTGCAAGCGGTGAACGTTCAAGACATGTTCAGAAAGAGTATGAG 439
    241 GAGTTATTGTGAATTGCAAGCGGTGAACGTTCAAGACATGTTCAGAAAGAGTATGAG 300
QY  440 CAAAGTCCGCGGATCATGTATCCGCAAGCTCTGTGATCATCAGCGCGCTGTCTCATCGCC 499
    301 CAAAGTCCGCGGATCATGTATCCGCAAGCTCTGTGATCATCAGCGCGCTGTCTCATCGCC 360
QY  500 TCTGCGGCTTACCAAGTCTTCTGCTCCCGAGGAAACTGAACTGATTCATCAGCTGC 559
    361 TCTGCGGCTTACCAAGTCTTCTGCTCCCGAGGAAACTGAACTGATTCATCAGCTGC 420
QY  560 TCGAAGACCCCTTCTGTAAAGCGGCGCAAGCGCCAGAGAAAGGGGAAAGTTCTCGCGCC 619
    421 TCGAAGACCCCTTCTGTAAAGCGGCGCAAGCGCCAGAGAAAGGGGAAAGTTCTCGCGCC 480
QY  620 CTCAGGCGCAGGCTCCGCGACCAACATCTGTTCTCTCAATTAATTAAGCCCTTCTCGGACAC 679
    481 CTCAGGCGCAGGCTCCGCGACCAACATCTGTTCTCTCAATTAATTAAGCCCTTCTCGGACAC 540
QY  680 TGTGTAAGTGAAGAGATGCCACCCCTCTGATTTGTTCTTCCAGCCCTCGCCCAA 739
    541 TGTGTAAGTGAAGAGATGCCACCCCTCTGATTTGTTCTTCCAGCCCTCGCCCAA 600
QY  740 CCCCCACCTCCCTGATGAGTTTCTTGGGCTGCTCTTTATTCGGGTAGGAGCGGG 799
    601 CCCCCACCTCCCTGATGAGTTTCTTGGGCTGCTCTTTATTCGGGTAGGAGCGGG 660
QY  800 AGTCGCTGTTCTTCTTCTTCTCTGTCGCAATATGATGAAGAGCTGGTAAAGATTCTGAA 859
    661 AGTCGCTGTTCTTCTTCTTCTCTGTCGCAATATGATGAAGAGCTGGTAAAGATTCTGAA 720
QY  860 TAAATTACACCTGACTGAATTTTCAATATGATGTAAGAGAGAGGTGAGTGAAGTT 919
    721 TAAATTACACCTGACTGAATTTTCAATATGATGTAAGAGAGAGGTGAGTGAAGTT 780
QY  920 CAGCCCAATGTCGTGTAGTACCGGAGTCAAGGCGGAGCTGGAGAGTCTGTAAGT 979
    781 CAGCCCAATGTCGTGTAGTACCGGAGTCAAGGCGGAGTCAAGTCTGTAAGT 840
QY  980 CACTGAGTGGGATCTGCTTCTTGTAAAGCTTCCAGTGTTCATTCATCCCTGATGGGG 1039
    841 CACTGAGTGGGATCTGCTTCTTGTAAAGCTTCCAGTGTTCATTCATCCCTGATGGGG 900
QY  1040 GCATAGTTTGAAGCTGACAGAGTGAAGAGTGAAGTCTTTTGGGCTGAGAGGCGCAGTTCC 1099
    901 GCATAGTTTGAAGCTGACAGAGTGAAGAGTGAAGTCTTTTGGGCTGAGAGGCGCAGTTCC 960
QY  1100 ACTCAAGGCTCCCTGCTTGCATTCATCAACCTTCATGCTCTCTCAAAACCATTTCTGCGAC 1159

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Db  961 ACTCAAGGCTCCCTGCTTGCATTCATCAACCTTCATGCTCTGAAACCATTCCTGCGAC 1020
QY  1160 AGAATTGGCTGGTTTCCGCGCTGAGTTGGGCTCTAGTACTCGAGACTCATGACTGGA 1219
    1021 AGAATTGGCTGGTTTCCGCGCTGAGTTGGGCTCTAGTACTCGAGACTCATGACTGGA 1080
QY  1220 CTTAGACTGGGGCTCGGCTGCTCTGTAAGAGTCTTAAGAAATCTTCTCAGTTCTCT 1279
    1081 CTTAGACTGGGGCTCGGCTGCTCTGTAAGAGTCTTAAGAAATCTTCTCAGTTCTCT 1140
QY  1280 TCGAGAGACTTGGGCGCGGAGCGGAAAGAGCAACGGGCGCTGCACAAAGCGGCGTCTC 1339
    1141 TCGAGAGAGTGGGCGCGGAGCGGAAAGAGCAACGGGCGCTGCACAAAGCGGCGTCTC 1200
QY  1340 GGTGGTGGAGTGGCGATATAGCGCGGCGCTTCTCTGTTGGCTGCTGCTGCTGCTGCT 1399
    1201 GGTGGTGGAGTGGCGATATAGCGCGGCGCTTCTCTGTTGGCTGCTGCTGCTGCTGCT 1260
QY  1400 GCGGAGCAGACAGCACTTGCACAGAACACCCGCGAAACTGCTGCGAGAGACACCGTACAG 1459
    1261 GCGGAGCAGACAGCACTTGCACAGAACACCCGCGAAACTGCTGCGAGAGACACCGTACAG 1320
QY  1460 GAGCGGTTGATGACCGAGCTGAGGTAGAAAACGTTCTCGAGAGAGGAGAGAGATCAT 1519
    1321 GAGCGGTTGATGACCGAGCTGAGGTAGAAAACGTTCTCGAGAGAGGAGAGAGATCAT 1380
QY  1520 GTAGCGCGGAGAGTACGACCTGTCGATGCTGCTGGCTTGGCTTGGCGCCAGCATGATCT 1579
    1381 GTAGCGCGGAGAGTACGACCTGTCGATGCTGCTGGCTTGGCTTGGCGCCAGCATGATCT 1440
QY  1580 CCGAATCTGTTGGGCTACAGCATACGCGCAATGTCAACAATTCAGCCCTGGGCGAGAC 1639
    1441 CCGAATCTGTTGGGCTACAGCATACGCGCAATGTCAACAATTCAGCCCTGGGCGAGAC 1500
QY  1640 ACGAGCAGAGAGGAGACAGACAGA 1663
    1501 ACGAGCAGAGAGGAGAGACAGAGA 1524

RESULT 42
US-10-218-631-15
; Sequence 15, Application US/10218631
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218, 631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910

```







[illegible]



Sequence 15, Application US/10218784  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerltsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC18  
CURRENT APPLICATION NUMBER: US/10/218,784  
CURRENT FILING DATE: 2002-08-12  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089905  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
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PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/095302  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095318  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095916

PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096146  
PRIOR FILING DATE: 1998-08-11  
PRIOR APPLICATION NUMBER: 60/096791  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/097986  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098544  
PRIOR FILING DATE: 1998-08-31  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099811  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100038  
PRIOR FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101786  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12

1	PRIOR APPLICATION NUMBER: 60/119549
2	PRIOR FILING DATE: 1999-02-10
3	PRIOR APPLICATION NUMBER: 60/12618
4	PRIOR FILING DATE: 1999-03-10
5	PRIOR APPLICATION NUMBER: 60/125259
6	PRIOR FILING DATE: 1999-03-19
7	PRIOR APPLICATION NUMBER: 60/125775
8	PRIOR FILING DATE: 1999-03-23
9	PRIOR APPLICATION NUMBER: 60/126773
10	PRIOR FILING DATE: 1999-03-29
11	PRIOR APPLICATION NUMBER: 60/127887
12	PRIOR FILING DATE: 1999-04-05
13	PRIOR APPLICATION NUMBER: 60/130232
14	PRIOR FILING DATE: 1999-04-21
15	PRIOR APPLICATION NUMBER: 60/131022
16	PRIOR FILING DATE: 1999-04-26
17	PRIOR APPLICATION NUMBER: 60/131270
18	PRIOR FILING DATE: 1999-04-27
19	PRIOR APPLICATION NUMBER: 60/131291
20	PRIOR FILING DATE: 1999-04-27
21	PRIOR APPLICATION NUMBER: 60/131445
22	PRIOR FILING DATE: 1999-04-28
23	PRIOR APPLICATION NUMBER: 60/134287
24	PRIOR FILING DATE: 1999-05-14
25	PRIOR APPLICATION NUMBER: 60/140650
26	PRIOR FILING DATE: 1999-06-22
27	PRIOR APPLICATION NUMBER: 60/140723
28	PRIOR FILING DATE: 1999-06-22
29	PRIOR APPLICATION NUMBER: 60/141037
30	PRIOR FILING DATE: 1999-06-23
31	PRIOR APPLICATION NUMBER: 60/144758
32	PRIOR FILING DATE: 1999-07-20
33	PRIOR APPLICATION NUMBER: 60/145698
34	PRIOR FILING DATE: 1999-07-26
35	PRIOR APPLICATION NUMBER: 60/146222
36	PRIOR FILING DATE: 1999-07-28
37	PRIOR APPLICATION NUMBER: 60/146963
38	PRIOR FILING DATE: 1999-08-03
39	PRIOR APPLICATION NUMBER: 60/149320
40	PRIOR FILING DATE: 1999-08-17
41	PRIOR APPLICATION NUMBER: 60/146638
42	PRIOR FILING DATE: 1999-08-17
43	PRIOR APPLICATION NUMBER: 60/151733
44	PRIOR FILING DATE: 1999-08-31
45	PRIOR APPLICATION NUMBER: 60/164418
46	PRIOR FILING DATE: 1999-11-09
47	PRIOR APPLICATION NUMBER: 60/166361
48	PRIOR FILING DATE: 1999-11-16
49	PRIOR APPLICATION NUMBER: 60/169445
50	PRIOR FILING DATE: 1999-12-07
51	PRIOR APPLICATION NUMBER: 60/169495
52	PRIOR FILING DATE: 1999-12-07
53	PRIOR APPLICATION NUMBER: 60/169835
54	PRIOR FILING DATE: 1999-12-07

Query Match	75.0%	Score 1422	DB 42	Length 1524
Best Local Similarity	99.9%	Pred. 10.12e-266		
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QY	140	GGGCGACGACGCGCGGCCCGCCAGCAGCCTTGCGACGACCGCGGGGACGC	199	
Db	1	GGGGACGACGCGCGCGGCCCGCCAGCAGCCTTGCGACGACCGCGGGGACGC	60	
QY	200	TCCGCTGCTGTGCGCTCTCTGTGATCGGCTTGCGCTCTCCCGGCGCGGAGCTCCGGGAGA	259	
Db	61	TCCGCTGCTGTGCGCTCTCTGTGATCGGCTTGCGCTCTCCCGGCGCGGAGCTCCGGGAGA	120	
QY	260	ATGTGGGTCCTATGAGGATGCGCGCACTTTTTCGGATGTTCTTGCCTCCAGGCTTTGGG	319	
Db	121	ATGTGGGTCCTATGAGGATGCGCGCACTTTTTCGGATGTTCTTGCCTCCAGGCTTTGGG	180	
QY	320	CTGCAGATTCAGTGTACCACTGTGAGAGATTCCAGCTGAGACAGCACTGCTCTCCGCC	379	

Db	181	CTGGAATCCAGTGTCTACAGTGTGAAGAAATTCACGTGAACAAACGACTGCTCTCC	240
QY	380	GAGTTCATTGTGAATTTCACGGTGGAAAGCTTCAAGACATGTGTACAGAAAGAAATGTGAG	439
Db	241	GAGTTCATTGTGAATTTCACGGTGGAAAGCTTCAAGACATGTGTACAGAAAGAAATGTGAG	300
QY	440	CAAAAGTGGCGGATCATGTACCCCAAGTCCGTGCATCATCAGCGGCGTCTCATGCC	499
Db	301	CAAAAGTGGCGGATCATGTACCCCAAGTCCGTGCATCATCAGCGGCGTCTCATGCC	360
QY	500	TCCTGGCGGATACAGTCTTCTGTCTCCACAGGAAACTAAGTCACTCACTTGCATCAGCTGC	559
Db	361	TCCTGGCGGATACAGTCTTCTGTCTCCACAGGAAACTAAGTCACTCACTTGCATCAGCTGC	420
QY	560	TGCAACACCCCTCTTTGTAACGGGGCCAAAGGCCCAAAAAAGGGAGAAATCTCTCAGCGCC	619
Db	421	TGCAACACCCCTCTTTGTAACGGGGCCAAAGGCCCAAAAAAGGGAGAAATCTCTCAGCGCC	480
QY	620	CTCAGGCCAGGGCTCCGACACCATCTCTGTTCTCAAAATTAAGCCCTCTTCTCGGACAC	679
Db	481	CTCAGGCCAGGGCTCCGACACCATCTCTGTTCTCAAAATTAAGCCCTCTTCTCGGACAC	540
QY	680	TGCTGAAGCTGAAGAGATGCAACCCCTCTGATCTGTTCTTCAAGCCCTCGGCCCA	739
Db	541	TGCTGAAGCTGAAGAGATGCAACCCCTCTGATCTGTTCTTCAAGCCCTCGGCCCA	600
QY	740	CCCCCACTCCCTGAGCTGATTTCTTCTGGGTCTCTTTTATCTGGGTAGAGACGG	799
Db	601	CCCCCACTCCCTGAGCTGATTTCTTCTGGGTCTCTTTTATCTGGGTAGAGACGG	660
QY	800	AGTCCGTCTCTTTTGTTCCTGTGTGAATTAATGAAGCTCGGTAAAGATCTCTGA	859
Db	661	AGTCCGTCTCTTTTGTTCCTGTGTGAATTAATGAAGCTCGGTAAAGATCTCTGA	720
QY	860	TAAATTCAGCTGACATTAATTTTCAGATATCTTGAAGAGAGAGTGTGATGAAAT	919
Db	721	TAAATTCAGCTGACATTAATTTTCAGATATCTTGAAGAGAGAGTGTGATGAAAT	780
QY	920	CACCCCATGTCTGTGTAAACCGGAGTCAAGCCAGGCTGGCAGAGTCTTGAAGT	979
Db	781	CACCCCATGTCTGTGTAAACCGGAGTCAAGCCAGGCTGGCAGAGTCTTGAAGT	840
QY	980	CACGTAGGTGGGCAATCTGACCTTTTGTAAACCTCCAGTGTCCATTCATCCCTGATGGG	1039
Db	841	CACGTAGGTGGGCAATCTGACCTTTTGTAAACCTCCAGTGTCCATTCATCCCTGATGGG	900
QY	1040	GCATAGTTGAGACTGCAGAGTGAAGTACGTTTTCTTAGGGCTGGAGGGCCAGTTCC	1099
Db	901	GCATAGTTGAGACTGCAGAGTGAAGTACGTTTTCTTAGGGCTGGAGGGCCAGTTCC	960
QY	1100	ACTCAAGCTTCCCTCGCTTGTACATTAACCTTCATCTCTGAAAACTTCTGTGCAGC	1159
Db	961	ACTCAAGCTTCCCTCGCTTGTACATTAACCTTCATCTCTGAAAACTTCTGTGCAGC	1020
QY	1160	AGAAATTTGGCTGTTTCCCGCTAGTGTGGGCTCTAGTGACTGAGACCTCAATGACTGGGA	1219
Db	1021	AGAAATTTGGCTGTTTCCCGCTAGTGTGGGCTCTAGTGACTGAGACCTCAATGACTGGGA	1080
QY	1220	CTTAGACTGGGGCTCGGCTCGCTCTGTAAAGTGTCTTAAGAAATCTTCTCAGTCTCT	1279
Db	1081	CTTAGACTGGGGCTCGGCTCGCTCTGTAAAGTGTCTTAAGAAATCTTCTCAGTCTCT	1140
QY	1280	TGCAGAGGACTGGGGCCGGGACCGGAAAGCAACGGGGCTCTCACAAAAGCGGGCTGTCT	1339
Db	1141	TGCAGAGGACTGGGGCCGGGACCGGAAAGCAACGGGGCTCTCACAAAAGCGGGCTGTCT	1200
QY	1340	GGTGGTGGAGTGCAGATGTACGGGACGGGCTTCTGTGTGGCTGTCTGACGACAG	1399
Db	1201	GGTGGTGGAGTGCAGATGTACGGGACGGGCTTCTGTGTGGCTGTCTGACGACAG	1260
QY	1400	GGCGGACGACAGCACTGTGCACAAACCCGCGAAACTCTCTGAGAGACACCGTCTACAG	1459
Db	1261	GGCGGACGACAGCACTGTGCACAAACCCGCGAAACTCTCTGAGAGACACCGTCTACAG	1320

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OY 1460 GAGCGGGTTGATGACCGAGCTGAGTGAAGAAAAACGTCCTCCGAGAGGGGAGAGATTCAT 1519
DB 1321 GAGCGGGTTGATGATACCGAGCTGAGTGAAGAAAAACGTCCTCCGAGAGGGGAGAGATTCAT 1380
OY 1520 GTACGCCCGGGAAGTGAAGACCTGTCAGTCAAGTGTGGTGGTGGGCGGAGCCATGATTCCT 1579
DB 1381 GTACGCCCGGGAAGTGAAGACCTGTCAGTCAAGTGTGGTGGTGGGCGGAGCCATGATTCCT 1440
OY 1580 CCGAATCTGCTGGTGGGCATCCAGCATATCGGSCCAATGTCAACAATCAGCCCTGGCGAGAC 1639
DB 1441 CCGAATCTGCTGGTGGGCATCCAGCATATCGGSCCAATGTCAACAATCAGCCCTGGCGAGAC 1500
OY 1640 ACGAGCAGGAGGAGAGAGACAGAGA 1663
DB 1501 ACGAGCAGGAGGAGAGAGACAGAGA 1524

RESULT 45
US-10-218-849-15
: Sequence 15, Application US/10218849
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P1C11
: CURRENT APPLICATION NUMBER: US/10/218,849
: CURRENT FILING DATE: 2002-08-12
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 15
: LENGTH: 1524
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-218-849-15

Query Match 75.0%; Score 1422; DB 42; Length 1524;
Best Local Similarity 99.9%; Pred. No. 1.2e-266;
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 140 GCGGAGCAGCAGCGGGGGCCCGACAGACCTCGCGAGCAGACAGCGCGTGCAGCCGGGACGCC 199
DB 1 GCGGAGCAGCAGCGGGGGCCCGACAGACCTCGCGAGCAGACAGCGCGTGCAGCCGGGACGCC 60
OY 200 TCCTGCTGTCGCCCTCTCTCTGATGCGCTTGCCCTCTCCCGGCCCGGGAGCTCCGGAGAGA 259
DB 61 TCCTGCTGTCGCCCTCTCTCTGATGCGCTTGCCCTCTCCCGGCCCGGGAGCTCCGGAGAGA 120
OY 260 ATGTGGGGTCTCAAGCATGCGCGGCAACTTTTGGGATTTGTTCTTCTCCAGAGCTTTGGC 319
DB 121 ATGTGGGGTCTCAAGCATGCGCGGCAACTTTTGGGATTTGTTCTTCTCCAGAGCTTTGGC 180
OY 320 CTGCAAATCCAGTGTACAGTGTGAAGAAATTCACAGTGAACAAAGACATGCTCTCCGCC 379
DB 181 CTGCAAATCCAGTGTACAGTGTGAAGAAATTCACAGTGTGAACAAAGACATGCTCTCCGCC 240
OY 380 GAGTTCAATTGTGAATTTGACAGCGGTACAGCTTCAAGACATGTGTCAAGAAAGATGTAGAG 439
DB 241 GAGTTCAATTGTGAATTTGACAGCGGTACAGCTTCAAGACATGTGTCAAGAAAGATGTAGAG 300
OY 440 CAAAGTGGCGGGATCATATACCGCAAGTCTGTGCATCATACAGGGGCGCTGTCTATCCGCC 499
DB 301 CAAAGTGGCGGGATCATATACCGCAAGTCTGTGCATCATACAGGGGCGCTGTCTATCCGCC 360

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QY	500	TCGCGGGGTACAGATCTCTTCGTCTCCCGCAGGGAACTGAACCTCACTTGGCATCAGCTGC	559
Db	361	TCCTGCGGGGTACAGATCTCTTCGTCTCCCGCAGGGAACTGAACCTCACTTGGCATCAGCTGC	420
QY	560	TGCAACACCCCTCTTTTGTAAACGGGGCCAAAGGCCCAAGAAAAAGGGAGATTCTGCCTCGGCC	619
Db	421	TGCAACACCCCTCTTTTGTAAAGGGGCCAAGGCCCAAGAAAAAGGGAGATTCTGCCTCGGCC	480
QY	620	CTCAGGCCAGGGGCTTCGACCACCATCTGTCTCAAAATTAGCCCTCTTCTCGGCACAC	679
Db	481	CTCAGGCCAGGGGCTTCGACCACCATCTGTCTCAAAATTAGCCCTCTTCTCGGCACAC	540
QY	680	TGCTCAACCTGAAGAGATGCGACACCCCTCTGCATTTGTTCTTCCAGCCCTCGCCCCCA	739
Db	541	TGCTCAACCTGAAGAGATGCGACACCCCTCTGCATTTGTTCTTCCAGCCCTCGCCCCCA	600
QY	740	CCCCCACCCTCCCTGAGTGAAGTTCTTCTGGGTGTCCTTTTATTCTGGGTAGAGACGG	799
Db	601	CCCCCACCCTCCCTGAGTGAAGTTCTTCTGGGTGTCCTTTTATTCTGGGTAGAGACGG	660
QY	800	AGTCGCTCTCTCTTTTGTTCCTGTGTGAATAATGAAAGCTCGTTAAAGCATTTCTGA	859
Db	661	AGTCGCTCTCTCTTTTGTTCCTGTGTGAATAATGAAAGCTCGTTAAAGCATTTCTGA	720
QY	860	TAAATTACGCTGACATAATTTTCAGTATGTACTTTGAAGAAAGAGAGTGGAGTGAAGTT	919
Db	721	TAAATTACGCTGACATAATTTTCAGTATGTACTTTGAAGAAAGAGAGTGGAGTGAAGTT	780
QY	920	CACCCCATCTCTGTGTAAACCGAGTCAAGGCCAGGCTGCGACAGCTCWTGCTTGAAGT	979
Db	781	CACCCCATCTCTGTGTAAACCGAGTCAAGGCCAGGCTGCGACAGCTCWTGCTTGAAGT	840
QY	980	CACGTAGGTGGGCAATCTGCCCTTTTGTAAACCCCGAGTGCATTCACCTCGATGGGG	10399
Db	841	CACGTAGGTGGGCAATCTGCCCTTTTGTAAACCCCGAGTGCATTCACCTCGATGGGG	900
QY	1040	GCAATGTTTGAGACTGCGAGAGTGAAGTACGTTTTCTTAAAGGCTGAGAGGCCCACTTCCC	10999
Db	901	GCAATGTTTGAGACTGCGAGAGTGAAGTACGTTTTCTTAAAGGCTGAGAGGCCCACTTCCC	960
QY	1100	ACTCAAGGCTCCCGGCTGTACAAATTCAAACTTCATCTCTGAAAAACATTTCTCTGCAGC	11599
Db	961	ACTCAAGGCTCCCGGCTGTACAAATTCAAACTTCATCTCTGAAAAACATTTCTCTGCAGC	10200
QY	1160	AGAATTGGCTGTTCGCGCTAGTATGGGCTCTAGTACTGAGACCTCAATGACTGTGGGA	12199
Db	1021	AGAATTGGCTGTTCGCGCTAGTATGGGCTCTAGTACTGAGACCTCAATGACTGTGGGA	10800
QY	1220	CTTAGACTGGGGGCTTCGGCTCTCTGAAAAGTGTCTTAAAGAAATCTTCTCAGTTCTCT	12799
Db	1081	CTTAGACTGGGGGCTTCGGCTCTCTGAAAAGTGTCTTAAAGAAATCTTCTCAGTTCTCT	11400
QY	1280	TGCAGAGGACTGCGGCGCGGGAGCCGAAAGCAACGGGGCCCTGCACAAAAGCGGGCCCTGC	13399
Db	1141	TGCAGAGGACTGCGGCGCGGGAGCCGAAAGCAACGGGGCCCTGCACAAAAGCGGGCCCTGC	12000
QY	1340	GGTGTGGAATGCGCATGTATACGCGCAGAGGGCTTCTCTGTGTGGGTGCTCTGCAGCAG	13999
Db	1201	GGTGTGGAATGCGCATGTATACGCGCAGAGGGCTTCTCTGTGTGGGTGCTCTGCAGCAG	12600
QY	1400	GCGGACGACAGCAACCTGTGCAGAAACCCGCGGAAACTCTGCGAGGACACCGTGTACAG	14599
Db	1261	GCGGACGACAGCAACCTGTGCAGAAACCCGCGGAAACTCTGCGAGGACACCGTGTACAG	13200
QY	1460	GAGCGGCTTGATGACCGAGCTGAGGTAGAAAAAGCTTCCGAGAAAGGGAGAGAGATCAT	15199
Db	1321	GAGCGGCTTGATGACCGAGCTGAGGTAGAAAAAGCTTCCGAGAAAGGGAGAGAGATCAT	13800
QY	1520	GTACGCGCGGGAAGAGAACTGCTCCAGTCTGTGTTGGGTTTGGCGGACATGATGCT	15799
Db	1381	GTACGCGCGGGAAGAGAACTGCTCCAGTCTGTGTTGGGTTTGGCGGACATGATGCT	14400

OY 1580 CCGAATCTGGTTGGGCATCCAGCATACGGCCATGTCTCAACATTCAGCCCTGGGCAAGAC 1639  
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Db 1441 CCGAATCTGGTTGGGCATCCAGCATACGGCCATGTCTCAACAAATCAAGCCCTGGGCAAGAC 1500  
|||||  
OY 1640 ACGACGAGGAGGAGAGACAGAGA 1663  
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Db 1501 ACGACGAGGAGGAGAGACAGAGA 1524  
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Search completed: November 8, 2002, 02:00:50  
Job time : 4268.69 secs

697

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:16:33 ; Search time 52.9982 Seconds  
(without alignments)  
3937.596 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897  
Sequence: 1 gccaaactccgagcgtctgg.....aaaaaaaaaaaaaaaaaa 1897

Scoring table: OLIGO.MNC  
Gapop 60.0 , Gapext 60.0

Searched: 193892 seqs, 55004114 residues

Word size : 10

Total number of hits satisfying chosen parameters: 75239

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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3: /cgn2\_6/pdata/1/pna/US07\_NEW\_COMB.seq.\*  
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7: /cgn2\_6/pdata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1422	75.0	1524	6 US-10-230-437-15	Sequence 15, App1
2	24	1.3	1337	6 US-10-125-928A-215	Sequence 215, App
3	24	1.3	2057	6 US-10-266-829-15	Sequence 15, App1
4	24	1.3	2305	6 US-10-240-425-1530	Sequence 1530, App
5	23	1.2	102	5 US-09-513-999C-20982	Sequence 20982, A
6	23	1.2	198	5 US-09-907-907A-23	Sequence 23, App1
7	23	1.2	286	6 US-10-266-131-1361	Sequence 1361, App
8	23	1.2	315	5 US-09-907-907A-21	Sequence 31, App1
9	23	1.2	504	6 US-10-240-425-758	Sequence 758, App
10	23	1.2	523	6 US-10-240-425-555	Sequence 525, App
11	23	1.2	574	6 US-10-264-237-114	Sequence 114, App
12	23	1.2	785	6 US-10-264-237-1055	Sequence 1055, App
13	23	1.2	1001	6 US-10-264-237-687	Sequence 687, App
14	23	1.2	1040	1 PCR-US02-33408-5	Sequence 5, App1
15	23	1.2	1092	6 US-10-264-237-553	Sequence 563, App
16	23	1.2	1326	6 US-10-264-237-40	Sequence 40, App1
17	23	1.2	1539	6 US-10-264-237-995	Sequence 995, App
18	23	1.2	1571	6 US-10-264-237-1007	Sequence 1007, App
19	23	1.2	1593	6 US-09-602-472A-1	Sequence 1, App1
20	23	1.2	1689	6 US-10-264-237-457	Sequence 457, App
21	23	1.2	1740	6 US-10-260-046-19	Sequence 19, App1
22	23	1.2	1765	6 US-10-264-237-890	Sequence 890, App
23	23	1.2	1998	6 US-10-145-087A-136	Sequence 136, App
24	23	1.2	1998	6 US-10-143-031A-136	Sequence 136, App
25	23	1.2	1998	6 US-10-145-092A-136	Sequence 136, App
26	23	1.2	1998	6 US-10-162-522A-136	Sequence 136, App

27	23	1.2	1998	6 US-10-165-038A-136	Sequence 136, App
28	23	1.2	1998	6 US-10-165-353-136	Sequence 136, App
29	23	1.2	1998	6 US-10-170-461A-136	Sequence 136, App
30	23	1.2	1998	6 US-10-172-039A-136	Sequence 136, App
31	23	1.2	1998	6 US-10-145-016A-136	Sequence 136, App
32	23	1.2	1998	6 US-10-145-088A-136	Sequence 136, App
33	23	1.2	1998	6 US-10-145-129A-136	Sequence 136, App
34	23	1.2	1998	6 US-10-125-923A-53	Sequence 53, App1
35	23	1.2	1998	6 US-10-165-353A-136	Sequence 136, App
36	23	1.2	2136	6 US-10-125-923A-227	Sequence 227, App
37	23	1.2	2680	6 US-10-145-087A-136	Sequence 136, App
38	23	1.2	2680	6 US-10-143-031A-156	Sequence 156, App
39	23	1.2	2680	6 US-10-145-092A-156	Sequence 156, App
40	23	1.2	2680	6 US-10-162-522A-156	Sequence 156, App
41	23	1.2	2680	6 US-10-165-038A-156	Sequence 156, App
42	23	1.2	2680	6 US-10-165-353-156	Sequence 156, App
43	23	1.2	2680	6 US-10-170-481A-156	Sequence 156, App
44	23	1.2	2680	6 US-10-172-039A-156	Sequence 156, App
45	23	1.2	2680	6 US-10-145-016A-156	Sequence 156, App

#### ALIGNMENTS

RESULT 1  
US-10-230-437-15  
Sequence 15, Application US/10230437  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C94  
CURRENT FILING DATE: US/10/230,437  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-230-437-15  
Query Match 75.0%; Score 1422; DB 6; Length 1524;





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;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 215
;; LENGTH: 1337
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-125-923A-215

Query Match
Best Local Similarity 1.3%; Score 24; DB 6; Length 1337;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897
DB 1298 GTGTAACAAAAA 1321

RESULT 3
US-10-266-829-15
; Sequence 15, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266,829
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756,168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145,220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2057
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-266-829-15

Query Match
Best Local Similarity 1.3%; Score 24; DB 6; Length 2057;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897
DB 1907 GTGTAACAAAAA 1930

RESULT 4
US-10-240-425-1530/c
; Sequence 1530, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Metzger, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1530
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;; LENGTH: 2305
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. X06374
US-10-240-425-1530

Query Match
Best Local Similarity 1.3%; Score 24; DB 6; Length 2305;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 GTGTAACAAAAA 1897
DB 1626 GTGTAACAAAAA 1603

RESULT 5
US-09-513-999C-20982
; Sequence 20982, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59,US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent. pm
; SEQ ID NO 20982
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20982

Query Match
Best Local Similarity 1.2%; Score 23; DB 5; Length 102;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
DB 73 TGTAAAAA 95

RESULT 6
US-09-907-907A-23
; Sequence 23, Application US/09907907A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Ieszyńska, Magdalena
; TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESECE
; FILE REFERENCE: A34584-A-PCT-USA (070050,1664)
; CURRENT APPLICATION NUMBER: US/09/907,907A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US 09/243,277
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 21
; OTHER INFORMATION: a or c or g or t
US-09-907-907A-23

Query Match
Best Local Similarity 1.2%; Score 23; DB 5; Length 198;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
|||||  
Db 160 TGTAAAAAAAAAAAAAAAAA 182

RESULT 7  
US-10-266-131-1361/C  
; Sequence 1361, Application US/10266131  
; GENERAL INFORMATION:  
; APPLICANT: Friedlich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: Novel Murine Polynucleotide Tags and  
; FILE REFERENCE: LEX-0030-USA  
; CURRENT APPLICATION NUMBER: US/10/266.131  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: US/09/617, 675  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/143, 878  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 2908  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1361  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)-(286)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-266-131-1361

Query Match 1.2%; Score 23; DB 6; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.08;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
|||||  
Db 24 TGTAAAAAAAAAAAAAAAAA 2

RESULT 8  
US-09-907-907A-31  
; Sequence 31, Application US/09907907A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Paul B.

; APPLICANT: Leszczynska, Magdalena  
; TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESCENCE A  
; FILE REFERENCE: A34584-A-PCT-USA (070050.1664)  
; CURRENT APPLICATION NUMBER: US/09/907, 907A  
; PRIOR FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: US 09/243, 277  
; PRIOR FILING DATE: 1999-02-02  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-907-907A-31

Query Match 1.2%; Score 23; DB 5; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.08;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
|||||  
Db 290 TGTAAAAAAAAAAAAAAAAA 312

RESULT 9  
US-10-240-425-758/C  
; Sequence 758, Application US/10240425  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe

; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240, 425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193, 446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 758  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AI675419  
US-10-240-425-758

Query Match 1.2%; Score 23; DB 6; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897  
|||||  
Db 23 TGTAAAAAAAAAAAAAAAAA 1

RESULT 10  
US-10-240-425-525/C  
; Sequence 525, Application US/10240425  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240, 425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193, 446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 525  
; LENGTH: 523  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AI262104  
US-10-240-425-525

Query Match 1.2%; Score 23; DB 6; Length 523;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAA 1897

DB 52 TGTAAAAAAAAAAAAAAAAAAAA 30

RESULT 11  
US-10-264-237-114

; Sequence 114, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 114  
; LENGTH: 574  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-264-237-114

Query Match 1.2%; Score 23; DB 6; Length 574;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
DB 551 TGTAAAAAAAAAAAAAAAAAAAA 573

RESULT 12  
US-10-264-237-1055

; Sequence 1055, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 1055  
; LENGTH: 785  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc-feature  
; LOCATION: (74)..(74)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-264-237-1055

Query Match 1.2%; Score 23; DB 6; Length 785;  
Best Local Similarity 100.0%; Pred. No. 0.077;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
DB 734 TGTAAAAAAAAAAAAAAAAAAAA 756

RESULT 13  
US-10-264-237-687  
; Sequence 687, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 687  
; LENGTH: 1001  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-264-237-687

Query Match 1.2%; Score 23; DB 6; Length 1001;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
DB 974 TGTAAAAAAAAAAAAAAAAAAAA 996

RESULT 14  
PCT-US02-33408-5/c

; Sequence 5, Application PC/TUS0233408  
; GENERAL INFORMATION:  
; APPLICANT: HAYASHI, Yasunori  
; TITLE OF INVENTION: NR3B Receptor Subunit Compositions and Related Methods  
; FILE REFERENCE: M00656/70068 WO  
; CURRENT APPLICATION NUMBER: PCT/US02/33408  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: US 60/344,545  
; PRIOR FILING DATE: 1999-10-19  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 1040  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
PCT-US02-33408-5

Query Match 1.2%; Score 23; DB 1; Length 1040;  
Best Local Similarity 100.0%; Pred. No. 0.076;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
DB 42 TGTAAAAAAAAAAAAAAAAAAAA 20

RESULT 15  
US-10-264-237-563  
; Sequence 563, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 563  
; LENGTH: 1092  
; TYPE: DNA  
; ORGANISM: Homo sapiens

Query Match 1.2%; Score 23; DB 6; Length 1092;  
Best Local Similarity 100.0%; Pred. No. 0.077;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (57)..(57)
: OTHER INFORMATION: n equals a,t,g, or c
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (227)..(227)
: OTHER INFORMATION: n equals a,t,g, or c
:
: NAME/KEY: misc_feature
: LOCATION: (1078)..(1078)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-563

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? RESULT 20
? US-10-264-237-457
? Sequence 457, Application US/10264237
? GENERAL INFORMATION:
? APPLICANT: Birst et al..
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: P41311
? CURRENT APPLICATION NUMBER: US/10/264,237
? PRIOR FILING DATE: 2002-10-04
? PRIOR APPLICATION NUMBER: PCT/US01/16450
? PRIOR FILING DATE: 2001-05-18
? PRIOR APPLICATION NUMBER: US 60/205,515
? PRIOR FILING DATE: 2000-05-19
? NUMBER OF SEQ ID NOS: 2876
? SOFTWARE: PatentIn Ver. 3.1
? SEQ ID NO 457
? LENGTH: 1669
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-264-237-457

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Query Match	1.28;	Score 23;	DB 6;	Length 1689;
Best Local Similarity	100.08;	Pred. No. 0.074;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1875	TCGTA	AAAAAAAAAAAAAAAAAAAA	1897
Db	1654	TGTA <td>AAAAAAAAAAAAAAAAAAAA</td> <td>1676</td>	AAAAAAAAAAAAAAAAAAAA	1676

```

RESULT 21
US-10-260-046-19
: Sequence 19, Application US/10260046
: GENERAL INFORMATION:
: APPLICANT: Dhugga, Kanwarpal S.
: APPLICANT: Tomes, Dwight
: TITLE OF INVENTION: Manipulation of Plant Polysaccharide
: TITLE OF INVENTION: Syntheses
: FILE REFERENCE: 1296
: CURRENT APPLICATION NUMBER: US/10/260.046
: CURRENT FILING DATE: 2002-09-27
: PRIOR APPLICATION NUMBER: 60/325,614
: PRIOR FILING DATE: 2001-09-27
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 19
: LENGTH: 1740
: TYPE: DNA
: ORGANISM: Zea mays
: US-10-260-046-19

```

Query Match 1.28; Score 23; DB 6; Length 1740;  
Best Local Similarity 100.0%; Pred. No. 0.074;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1875	TCATAAAAAAAAAAAAAA	1897
Db	1711	TGTAATAAAAAAAAAAAAAA	1733

```

RESULT 22
US-10-264-237-890
; Sequence 890, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA134P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18

```

```

?
? PRIOR APPLICATION NUMBER: US 60/205,515
?
? PRIORITY DATE: 2000-05-19
?
? FILING DATE: 2000-05-19
?
? NUMBER OF SEQ ID NOS: 2876
?
? SOFTWARE: PatentIn Ver. 3.1
?
? SEQ ID NO: 890
?
? LENGTH: 1765
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
US-10-264-237-890
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Query Match	1.2%;	Score 23;	DB 6;	Length 1765;
Best Local Similarity	100.0%;	Pred. No. 0.074;		
Matches	23;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1875	TGTA	1897
Db	1739	TGTA	1761

```

RESULT 23
US-10-145-087A-136
; Sequence 136, Application US/10145087A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C47
; CURRENT APPLICATION NUMBER: US/10/145,087A
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11

```

PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 136  
LENGTH: 1998  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-145-087A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

## RESULT 24

US-10-143-031A-136  
Sequence 136, Application US/10143031A  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C39  
CURRENT APPLICATION NUMBER: US/10/143.031A  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 136  
LENGTH: 1998  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-143-031A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

## RESULT 25

US-10-145-092A-136  
Sequence 136, Application US/10145092A  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C45  
CURRENT APPLICATION NUMBER: US/10/145.092A  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11

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;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 624
;; SEQ ID NO 136
;; LENGTH: 1998
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-145-092A-136

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1998;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996

RESULT 26
US-10-162-522A-136
; Sequence 136, Application US/10162522A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC56
; CURRENT APPLICATION NUMBER: US/10/162,522A
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
```

```
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 624
;; SEQ ID NO 136
;; LENGTH: 1998
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-162-522A-136

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1998;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996

RESULT 27
US-10-165-038A-136
; Sequence 136, Application US/10165038A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC29
; CURRENT APPLICATION NUMBER: US/10/165,038A
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
```

PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 136  
LENGTH: 1998  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-165-038A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

## RESULT 28

US-10-165-353-136  
Sequence 136, Application US/10165353

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C40  
CURRENT APPLICATION NUMBER: US/10/165.353  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 136  
LENGTH: 1998  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-165-353-136

Query Match 1.2%; Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

## RESULT 29

US-10-170-481A-136  
Sequence 136, Application US/10170481A

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C53  
CURRENT APPLICATION NUMBER: US/10/170.481A  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11



```
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 624
;; SEQ ID NO 136
;; LENGTH: 1998
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-170-481A-136
```

```
Query Match          1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
    |||
Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996
```

## RESULT 30

```
US-10-172-039A-136
; Sequence 136, Application US/10172039A
; GENERAL INFORMATION:
```

```
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC30
;; CURRENT APPLICATION NUMBER: US/10/172,039A
;; PRIOR FILING DATE: 2002-10-10
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077641
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
;; PRIOR FILING DATE: 1998-03-11
```

```
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 624
;; SEQ ID NO 136
;; LENGTH: 1998
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-172-039A-136
```

```
Query Match          1.2%; Score 23; DB 6; Length 1998;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
    |||
Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996
```

## RESULT 31

```
US-10-145-016A-136
; Sequence 136, Application US/10145016A
; GENERAL INFORMATION:
```

```
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC32
;; CURRENT APPLICATION NUMBER: US/10/145,016A
;; PRIOR FILING DATE: 2001-10-18
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077641
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
;; PRIOR FILING DATE: 1998-03-11
```

PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See file Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 136  
LENGTH: 1998  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-145-016A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 32  
US-10-145-088A-136  
Sequence 136, Application US/10145088A  
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC49  
CURRENT APPLICATION NUMBER: US/10/145.088A  
PRIOR FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See file Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 136  
LENGTH: 1998  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-145-088A-136

Query Match 1.2%; Score 23; DB 6; Length 1998;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||  
DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

RESULT 33  
US-10-145-129A-136  
Sequence 136, Application US/10145129A  
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC51  
CURRENT APPLICATION NUMBER: US/10/145.129A  
PRIOR FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11

```

; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 136
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-145-129A-136

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1998;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996

RESULT 34
US-10-125-923A-53
; Sequence 53, Application US/10125923A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C79
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 53
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-923A-53

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1998;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
```

```

Db 1974 TGTAAAAAAAAAAAAAAAAAAAAA 1996

RESULT 35
US-10-165-353A-136
; Sequence 136, Application US/10165353A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C40
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 136
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-165-353A-136

Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 1998;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
|||||
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DB 1974 TGTAAAAAAAAAAAAAAAAAAAA 1996

## RESULT 36

US-10-125-923A-227  
Sequence 227, Application US/10125923A

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C79  
CURRENT FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 227  
LENGTH: 2136  
TYPE: DNA  
ORGANISM: Homo Saplen  
US-10-125-923A-227

Query Match 1.2%; Score 23; DB 6; Length 2136;  
Best Local Similarity 100.0%; Pred. No. 0.073;

Matches 23; Conservative 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||

DB 2061 TGTAAAAAAAAAAAAAAAAAAAA 2083

## RESULT 37

US-10-145-087A-156

Sequence 156, Application US/10145087A

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630P1C47  
CURRENT APPLICATION NUMBER: US/10/145,087A

CURRENT FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/07450

PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/07632

PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/07641

PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/07791

PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 156

LENGTH: 2680  
TYPE: DNA

ORGANISM: Homo sapiens  
US-10-145-087A-156

Query Match 1.2%; Score 23; DB 6; Length 2680;  
Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897  
|||||

DB 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677

## RESULT 38

US-10-143-031A-156

Sequence 156, Application US/10143031A

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang

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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC39
: CURRENT APPLICATION NUMBER: US/10/143,031A
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-143-031A-156

Query Match
Best Local Similarity 1.2%; Score 23; DB 6; Length 2680;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

RESULT 39
US-10-145-092A-156
: Sequence 156, Application US/10145092A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC45
: CURRENT APPLICATION NUMBER: US/10/145,092A
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-145-092A-156

Query Match
Best Local Similarity 1.2%; Score 23; DB 6; Length 2680;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

RESULT 40
US-10-162-522A-156
: Sequence 156, Application US/10162522A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC56
: CURRENT APPLICATION NUMBER: US/10/162,522A
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-162-522A-156

Query Match 1.2%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
Db 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677

RESULT 41
US-10-165-038A-156
: Sequence 156, Application US/10165038A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC29
: CURRENT APPLICATION NUMBER: US/10/165,038A
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-165-038A-156

Query Match 1.2%: Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1875 TGTAAAAAAAAAAAAAAAAAAAA 1897
Db 2655 TGTAAAAAAAAAAAAAAAAAAAA 2677

RESULT 42
US-10-165-353-156
: Sequence 156, Application US/10165353
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC40
: CURRENT APPLICATION NUMBER: US/10/165,353
: PRIOR FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-165-353-156

Query Match      1.2%; Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

RESULT 43
US-10-170-481A-156
: Sequence 156, Application US/10170481A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC53
: CURRENT APPLICATION NUMBER: US/10/170,481A
: PRIOR FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450
: PRIOR FILING DATE: 1998-03-10
: PRIOR APPLICATION NUMBER: 60/077632
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077641
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077649
: PRIOR FILING DATE: 1998-03-11
: PRIOR APPLICATION NUMBER: 60/077791
: PRIOR FILING DATE: 1998-03-12
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 624
: SEQ ID NO 156
: LENGTH: 2680
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-170-481A-156

Query Match      1.2%; Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAAAAAAAAAAAAAAAAAA 1897
Db 2655 TGTAAAAAAAAAAAAAAAAAAAAA 2677

RESULT 44
US-10-172-039A-156
: Sequence 156, Application US/10172039A
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C30
CURRENT APPLICATION NUMBER: US/10/172.039A
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-172-039A-156

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2655 TGTAAAAA 2677
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US-10-145-016A-156
Sequence 156, Application US/10145016A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C52
CURRENT APPLICATION NUMBER: US/10/145.016A
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 156
LENGTH: 2680
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-016A-156

Query Match 1.2%; Score 23; DB 6; Length 2680;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1875 TGTAAAAA 1897
DB 2655 TGTAAAAA 2677
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

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Title: US-09-970-966-214

Perfect score: 1897

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Searched: 2054640 seqs, 14551402878 residues

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

## SUMMARIES

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7	908.6	47.9	945	9	BC017318 Homo sapi
8	857.8	45.2	1797	10	AB041649 Mus muscu
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13	508.6	26.8	1362	6	AF034633 Homo sapi
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## ALIGNMENTS

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AX136281

LOCUS AX136281

DEFINITION Sequence 203 from Patent EP1067182.

ACCESSION AX136281

VERSION AX136281.1 GI:14272687

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1890)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: EP 1067182-A 203 10-JAN-2001:

Helix Research Institute (JP)

FEATURES Location/Qualifiers

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BASE COUNT 419 a 528 c 533 g 410 t

ORIGIN

Query Match 96.3% Score 1826; DB 6; Length 1890;

Best Local Similarity 99.6% Pred. No. 0;

Matches 1870; Conservative 2; Mismatches 2; Indels 4; Gaps 4;

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VERSION AX358762.1 GI:18675282  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gunney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K., and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0193983-A 15 13-DEC-2001.  
GENETECH Genentech Inc. (US)  
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Oy	1645	CAGGAGGAGAGACAGAGAAAAAAGAAAAACAGCATGAGAAACAGTAATGAAATAAAC	1704
Dh	119545	CAGGAGGAGAGACAGAGAAAAAAGAAAAACAGCATGAGAAACAGTAATGAAATAAAC	119486
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Dh	119485	CATAAATAATTTAGCCCTCTGTTCTGTCTTACTGTGGCCAGGAATGTAACAAATTTTC	119426
Oy	1765	AGTGTGGACATTGACAGCTTTCTTTTGGCCACAGCAGAGAAATTTAAACATGTTTCAA	1824
Dh	119425	AGTGTGGACATTGACAGCTTTCTTTTGGCCACAGCAGAGAAATTTAAACATGTTTCAA	119366
Oy	1825	CCCGGGGAGTGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA	1878
Dh	119365	CCCGGGGAGTGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAGACAGTGA	119312

LOCUS	AX1319944	C	2528 bp	DNA	linear	PAT 14-DEC-2001
DEFINITION	Sequence 3 from Patent WO0181634.					
ACCESSION	AX1319944					
VERSION	AX1319944.1					
KEYWORDS	GI:17901491					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
TITLE	1 Gaivin, K.A. and Rudolph-Owen, L.A.					
JOURNAL	Methods and compositions for the diagnosis and treatment of cardiovascular and tumorigenic disease using 4941 Patent: WO 0181634-A 3 01-NOV-2001;					
FEATURES	Millennium Pharmaceuticals, Inc. (US)					
source	location/Qualifiers					
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BASE COUNT	516 a	766 c	677 g	567 t	2 others
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Best Local Similarity	99.5%; Pred. No. 6.9e-296;				
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Qy	368	TGCTCTCTCCCGGAGTTCATTGTGAATTGACGCGTGAAGCTTCAAGACATGTGTGAGAA	427		
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Qy	428	GAAATGATGAGCAAAAGTGGCGGGATCATATGCCGAATCTCTGTGCATCATCACGGCC	487		
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Qy	788	GTAGGAGCGGAGTCCGTGTTCTTTTCTTCTGTGCAATTAATGAAGAGCTCGGTA	847		
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RESULT 7
LOCUS BC017318 946 bp mRNA linear PRI 09-NOV-2001
DEFINITION Homo sapiens, clone MGC:29643 IMAGE:3641660, mRNA, complete cds.
ACCESSION BC017318
VERSION BC017318.1 GI:16878239
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 946)
Strausberg, R.
Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgtl.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantirpop, S., Thomas, P.J.,
Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

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REMARK  
COMMENT

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IBAI Plate: 39 Row: b Column: 19  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis, Similarity but not identity to protein.  
FEATURES  
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Location/Qualifiers

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BASE COUNT 197 a 292 c 261 g 196 t
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Best Local Similarity 99.9%; Pred. No. 5.6e-200;
Matches 908; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION	Mus musculus brain cDNA, clone MNcb-0671.	linear	ROD 30-JUN-2000
ACCESSION	AB041649		
VERSION	AB041649.1	GI:7670499	
KEYWORDS	file (full insert sequence).		
SOURCE	Mus musculus (Strain:C57BL) adult female cDNA to mRNA, clone_l1b:Sugano mouse brain mncb clone:MNcb-0671.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Osada, N., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Sugano, S. and Hashimoto, K.		
TITLE	Isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method		
JOURNAL	unpublished		
REFERENCE	2 (bases 1 to 1797)		
AUTHORS	Hashimoto, K., Osada, N., Kusuda, J. and Sugano, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-APR-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan		
	(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/, Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)		
COMMENT	URL: http://www.nih.go.jp/yoken/genebank/		
	L1b Name: Sugano mouse brain mncb		
	Lab host: TOP10		
	Vector: pME185-FL3		
	1st strand cDNA was primed with an oligo(dT) primer (ATGCGCCCTTTTCTTTTCTTTT), double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME185-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing ( 5' end primer [CTTGTCTCTTAACCTGCG], 3' end primer [CGACCTGCAGCTCGAGCACAC] ).		
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CDS			

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Best Local Similarity	73.0%:	Pred. No. 3,6e-188:			
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Db	368	GCTTCCAGGCTGGCGCTCAAAATTCAGTGTACAGTGTAGAAATTCAGCTGAACA	427		
OY	363	ACGACTGCTCTCCCGCGATTCAATGTGAATTGACGGGTGAAGCTCAAGCATGTGC	422		
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Qy	1651	GGAGAGCAGAGAAAAAAGAAAAACACAGCATGGAACACACGTAAATGAATAAAA	1703
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LOCUS	BC011449	826 bp	mRNA	linear	PRI 22-AUG-2001
DEFINITION	Homo sapiens, clone IMAGE:4026092, mRNA.				
ACCESSION	BC011449				
VERSION	BC011449.1	GI:15277472			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 826)				
TITLE	Strausberg, R.				
JOURNAL	Direct Submission				
REMARK	Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
COMMENT	NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: ATCC/DCTP				

CDNA Library Preparation: Rubén Labortory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbiology.org>  
contact: [amadan@systemsbiology.org](mailto:amadan@systemsbiology.org)  
Anup Madan, Rachel Dickhoff, Jessica Fahney, Stephanie Ford, Julia  
Greene, Mark Kellman and Anuradha Madan

clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 25 Row: n Column: 18  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES	Location/Qualifiers
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Db 61 GAAACCATTTCTCTGCAGCAGATTGGCTGGTTTCGGCGCTGAG-TGGCTCTAGTGA CT 119

QY 1201 CGAGACTCAATGACTGGGACTTAGACTGGGCTCGGCTCGCTGAAAGTGGTTAGA 1260

Db 120 CGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCCTCGCTGAAAGTGCTTAAGA 179

QY 1261 AAATCTTCTCAGTTCCTTGCGAGGACTGGCGCCGGGACGCGAAGAGCAACGGGGCT 1320

Db 180 AAATCTTCTCAGTTCCTTGCGAGGACTGGCGCCGGGACGGCAAGAGCAACGGGGCT 239

GCACAAAGCGGGCGCTGTCGGTGGTGAAGTGCAGCATGTACGGCGCAGCGCTTCTCGTGT 1321

Db 240 GCACAAAGCGGGCGCTGTCGGTGGTGGAGTGCCGATGTACGCCGAGCGCCTTCTCGTGGT 299

QY 1381 TGGCGTGTGCAGCGACAGGGCGCAGCACAGCACCCTGCACGAACACCCGCCGAACCTGCT 1440

Db 300 TGGCGTGTGCAGCGACAGGGCGAGCACAAGCACCTGCACGAACACCCGCCGAACCTGCT 359

QY 1441 GCGAGGACACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCG 1500

Db 360 GCGAGGACACCGTGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCG 419

QY 1501 AGAAGGGGAGGAGCATGTACGGCCCCGGAAGTAGGACCTCGTCCAGTCGCTTGGGT 1560

Db 420 AGAAGGGGAGGAGTATGTACGCCCGGAAGTAGGACCCTCGTCCAGTCGTGCTTGGGT 479

QY 1561 TGGCCGCAGCCATGATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAATGTCACAA 1620

Db 480 TGGCCGCGCCATGATCCTCGAATCTGTTGGGCATCCAGCATACGGCCAATGTCACAA 539

1621 CAATCAGCCCTGGGCAGACACGAGGAGGAGAGACAGAGAAAAGAAAACACAGCAT 1680

Db 540 CAATCAGCCCTGGGCAGACACGAGCAGGAGGAGAGACAGAGAAAGAAAAACACAGCAT 599

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QY 1801 GAGAGAAATTAACACTGTTTCAACCCGGGAGTGGCTGTGTTAAAGAAAGACATTA 1860
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RESULT 10
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LOCUS Mus musculus chromosome UNK clone RP23-462P13, WORKING DRAFT
DEFINITION
AC124493
SEQUENCE, 5 unordered pieces.
AC124493
AC124493.2 GI:21699722
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULFILLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
2 (bases 1 to 209885)
McPherson,J.D. and Waterston,R.H.
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 209885)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT On Jul 5, 2002 this sequence version replaced gi:21426614.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.edu
Center project name: M_BA0462P13

----- Summary Statistics -----
Sequencing vector: M13: 0%
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990319
Consensus quality: 208484 bases at least Q40
Consensus quality: 208911 bases at least Q30
Consensus quality: 209285 bases at least Q20
Insert size: 206000; agarose-ftp
Insert size: 212112; sum-of-contigs
Quality coverage: 0.00 in Q20 bases; agarose-ftp
Quality coverage: 11.62 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
      I 11331: contig of 11331 bp in length

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* 11332 11431: gap of unknown length
* 11432 28617: contig of 17186 bp in length
* 28618 28717: gap of unknown length
* 28718 49454: contig of 20737 bp in length
* 49455 49554: gap of unknown length
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BASE COUNT 59789 a 44784 c 46164 g 58745 t 403 others
ORIGIN

Query Match 33.9%; Score 643.4; DB 2; Length 209885;
Best Local Similarity 70.8%; Pred. No. 3.1e-138;
Matches 1039; Conservative 2; Mismatches 373; Indels 53; Gaps 12;

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QY 569 CCTCTTGTATACGGGCGGACGCAAGGCAAGAAAGGAGTGTGCTGCGGCGCTGAGGCCA 628
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Db	Sequence	Accession	LOCUS	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
Db	65792	GAGTCAACAGTCTATTTCAGAGACTGCTGCTGGCGTGAAAGTAACCTTTGCTTTTGCGGGAGGG	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1086	GAGGGCCAGTTCCCACTCAAGGCTCCCTGCGTTGACATTCAACTTCATGCTCTCGAANA	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65732	GAGACCCAGTTTGGCTTCAAGGCTTTCGAACTTGGCATTCATATCCCTGCTGTAA	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1146	CCATTCTCTGCAAGCAAAATTGGCTGGTTTCGCGCCGTAGTTGGGCTCTAGTACTCGA	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65672	CTATTTCCTGGGGTGAGACCACACTGGTTTGGTCTCTGAGCCAGTCTGTGCTACTCAG	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1206	CTCAATTGACTGGGACTTAGACTGG---GGCTGGCCCTGCTCTGAAAAGTGGTTAAGAA	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65612	CTCAAGGGCTGGGGCTTAGCCCTTCAGGCTTGGCCCTCAGTCTGAAAAGTGGTTAAGAA	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1263	ATCTTCTCAGTTCTCTCTTTCAGAGGACT-----GGCCGGGAGCGAGCAAGCAAGGG	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65552	ACCTTCTTAGTTCTCTCTGAGGAAGAGTTACTGCCCGGGAGGCTTAGAGAGTAGAGGGG	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1317	CGCTCCACAAAGCGGGCGCTGTGGTGTGAGTGCAGATGATACGCGCAGCGCGCTTCTCG	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65492	CTGGCGGCGTCACTGTGCTCTGCTCTTGGTGAGATGAAAGCGGGCAACGCTGGGCTTCTCT	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1377	TGGTTGGGCTGCTGAGGAGACAGGGGGGCGACAGCAGCAGCTCTGACAGAACCCCGGAAC	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65432	TGGTTGGGCTGCTGAGAGTCTGAGGCTGAGGCGGCGACAGCAGCAGCTCTGACAGAAC	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1437	TGCTCGAGAGCACCCTGATACAGAGCGGGTGTGATGACGAGCTGAGGTAGAAAAAGCTG	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65372	TGCTGAGAGAGACGTTGTAGAGAGAGAGGTTGACACAGAGCTGAGGTAGAGAAAGTA	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1497	TCCGAGAAAGGGAGAGAGATCATGTACGCCGGGAAGTAAGACCTGCTCAGTGGCTTG	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65312	TCAGAGAAAGGGAGAGAGATCATGTATGATCCCTGGAAGTACGTTCTGCTCAGATCATGTTT	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Qy	1557	GCTTGGCGCGCAGCCATATCCCTCGAATCTGTTGGGATCCACATTAAGGCCAATGTC	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Db	65252	GCTTTTCTGTCAGCCATATCTGCTGGATCTGATTTGGGATCTCAACACAGGCCAAGCTC	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
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Qy	1677	GCATGAGAAACAGTAATGA---ATAAACCATTAATATTATTACCCCTCTGTTCTG-T	AX136556	Sequence 478 from Patent EP1067182.	AX136556.1	GI:14272960	human.	1 (bases 1 to 591)	Ota,T., Isogai,T.,

TITLE	Secretory protein or membrane protein			
JOURNAL	Patent: Ep 1067182-A 478 10-JUN-2001;			
FEATURES	Helix Research Institute (JRP)			
source	Location/Qualifiers			
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BASE COUNT	108 a	198 c	173 g	109 t
ORIGIN	3 others			

Query Match	29.0%;	Score 550.4;	DB 6	Length 591;
Best Local Similarity	99.5%;	Pred. No. 6.e-117;		
Matches 562; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1;

FEATURES	LOCATION/Qualifiers
REFERENCE	Galvin, K. A. and Rudolph-Owen, L. A.
AUTHORS	Methods and compositions for the diagnosis and treatment of cardiovascular and tumorigenic disease using 4941
TITLE	Patent: WO 0181634-A 1 01-Nov-2001;
JOURNAL	Millennium Pharmaceuticals, Inc. (US)
Db	16 GCGAATCCGGAGGGGCG -GGTCTGGGCCGGGAGACGGAGAGACAGACACCG 74
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Qy	541 CTCAGTTTGCAATCAGCTGCTGCAAC 565
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DEFINITION	Sequence 1 from Patent WO0181634.
ACCESSION	AX319942
VERSION	AX319942.1 GI:17901489
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



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Db	942	CCAGTCGTGCCTTGGGTTTGCCCGCACACCATGATCTCCGAATCTGGTTGGGATCCAGA	883
OY	1604	TACGGCCAATGTCACAACAATCAGCCCTTGCGGAGA	1638
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LOCUS			
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ACCESSION	Rattus norvegicus clone CH230-286021.	*** SEQUENCING IN PROGRESS	
VERSION	ACLI12072.3	GI:21744373	
KEYWORDS	HTG; HTGS; PHASE1.		
SOURCE	Norway rat.		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 92874) Muzny D.M., Adams C., Adio-Oduola B., All-oman F.R., Allen C., Alsbrooks S.L., Amaralunge H.C., Are J.R., Ayale M., Banks T., Barbatta J., Benton J., Blimage K., Blankenburg K., Bonald N.D., Bouch J., Bowle S., Brileva M., Brown E., Brown M., Bryant L.P., Burnay C., Burch P., Burkett C., Butrell K.L., Byrd N., P., Carroll T.F., Carter M., Cavazos S., R., Chacko J., Chavez D., Chen G., Chen R., Chen Z., Chowdhury I., Christopoulos C., Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R., Dellany M.L., Davis C., Davy-Carroll L., Dederlich D.A., DeLaney K.R., Delgado O., Dem A.L., Ding X., Dim H.H., Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J., Earhart C., Edgar D., Edwards C.C., Elhaj C., Escoto M., Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frantz P., Gabriel A., Gao J., Garcia A., Garner T., Garza N., Gill R., Gorell J.H., Guevara W., Gunaratne P., Hale S., Hamilton K., Harris C., Harris K., Hart M., Havlak P., Hawes A., Hernandez J., Hernandez O., Hodgson A., Hogues M., Holloway C., Hollins B., Homsl F., Howard S., Huber J., Huylk S., Hume J., Jackson L.E., Jacobson B., Jia Y., Johnson R., Jollivet S., Joudah S., Karlsson E., Kelly S., Khan U., King L., Korvah J., Kovac C., Kretovic J., Kureshi A., Landry N., Leal B., Lewis L.C., Lewis L., Li J., Li Z., Lichteberg O., Lieu C., Liu J., Liu W., Louised H., Lozano R.J., Lu X., Lucier A., Lucier R., Luna R., Ma J., Maheshwari M., Mapua P., Martin R., Martindale A., Martinez E., Massey E., Mawhinney E., McLeod M.P., Meador M., Meli G., Metzker M., Miner G., Miner Z., Mitchell T., Mohabbat K., Morgan M., Morris S., Mosser M., Neal D., Newton J., Newton N., Nguyen A., Nguyen N., Nguyen N., Nickerson E., Nwokoko S., Ogulu M., Okunolu G., Orangunye N., Oviedo R., Pace A., Payton B., Peery J., Perez L., Peters L., Pickens R., Primus E., Pu L.L., Quties M., Ren Y., Rives M., Rojas A., Rojudozan I., Rolfe M., Ruiz S., Severy G., Schreier S., Scott G., Shen H., Shooshitari N., Slisson I., Sodergren E., Sonake T., Sparks A., Stanley H., Stone H., Sulton A., Svatek A., Tabors P., Tameris A., Tameris K., Tang H., Tansey J., Taylor C., Taylor T., Telford B., Thomas N., Thomas S., Usmani K., Vasquez L., Vera V., Villalon D., Vinson R., Wang Q., Wang S., Ward-Moore S., Warren R., Washington C., Wallington S., Williams G., Williamson A., Wleczyk R., Wooden S., Worley K., Wu C., Wu Y., Wu Y.F., Zhou J., Zorrilla S., Nelson D., Weinstock G. and Gibbs R.		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 92874)		
REFERENCE	Morley K.C.		
AUTHORS	Direct Submission		
TITLE	Submitted (19-FEB-2002) Human Genome Sequencing Center, Department		

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 92874)  
Worley K.C.  
Direct Submission  
Submitted (17-Jul-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 13, 2002 this sequence version replaced gi:20303189.

----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information -----  
Center project name: GRJD  
Center clone name: CH230-286021  
----- Summary Statistics -----  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 32512 bases at least Q40  
Consensus quality: 34515 bases at least Q30  
Consensus quality: 35930 bases at least Q20  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 50 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
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*	5360	6436:	gap of 1077 bp in length
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*	9012	10370:	contig of 1359 bp in length
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*	11815	12014:	gap of unknown length
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*	25657	26711:	contig of 1055 bp in length
*	26712	26811:	gap of unknown length

of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 92874)  
 Worley,K.C.  
 Direct Submission  
 Submitted (17-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 13, 2002 this sequence version replaced gi:20303189.  
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 Center: Baylor College of Medicine  
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 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
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 Center clone name: CH230-286021  
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 Chemistry: Dye-terminator Big Dye; 100% of reads  
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 \* consists of 50 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
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 \* as soon as it is available and the accession number will  
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ORIGIN

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Matches 880: Conservative 1: Mismatches 368: Indels 41: Gaps 12:

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ACCESSION AXI36698
VERSION AXI36698.1 GI:14273102
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 587)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 620 10-JAN-2001;
Helix Research Institute (JP)
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	1896.2	100.0	1897	24	ABT03284 Human ovarian carc
2	1896.2	100.0	1897	24	ABL40352 Ovarian carcinoma
3	1850.2	97.5	1953	21	AAF23400 Human secreted pro
4	1845.8	97.3	1956	22	AAF64188 Human secreted pro
5	1826	96.3	1890	22	AAF3845 Human cDNA encodin
6	1606.2	84.7	1619	24	ABT03277 Human ovarian carc
7	1606.2	84.7	1619	24	ABT03281 Human ovarian carc
8	1606.2	84.7	1619	24	ABL40345 Ovarian carcinoma
9	1606.2	84.7	1619	24	ABL40349 Ovarian carcinoma

10	1523.2	80.3	1524	24	ABK33543 cDNA encoding huma
11	1405.6	74.1	1608	24	ABO54231 Human ovarian anti
12	1322.2	69.7	2528	22	AAD18630 Human G protein co
13	624	32.9	625	24	ABT03280 Human ovarian carc
14	624	32.9	625	24	ABL40348 Ovarian carcinoma
15	624	32.9	625	24	ABL87898 Human ovarian carc
16	566.4	29.9	1010	24	ABT03282 Human ovarian carc
17	566.4	29.9	1010	24	ABL40350 Human ovarian carc
18	550.4	29.0	591	22	AAF94044 Ovarian carcinoma
19	508.6	26.8	1362	24	ABT03279 Primer specific fo
20	508.6	26.8	1362	24	ABL40347 Human ovarian carc
21	480.4	25.3	587	22	AAF94186 Ovarian carcinoma
22	476.8	25.1	480	24	ABT03283 Primer specific fo
23	476.8	25.1	480	24	ABL40351 Human ovarian carc
24	433.2	22.8	558	24	ABL79397 Human ovarian carc
25	413.4	21.8	444	22	AAH50766 Human tumour assoc
26	396.4	20.9	409	24	ABL81262 Human ovarian carc
27	378.6	20.0	430	24	ABL81273 Human ovarian carc
28	368.8	19.4	396	22	AAF94818 Human ovarian carc
29	368.8	19.4	396	24	ABT03085 Human ovarian carc
30	368.8	19.4	396	24	ABL48768 Ovarian carcinoma
31	365.4	19.3	369	22	AAF95007 Human ovarian carc
32	365.4	19.3	369	24	ABT03274 Human ovarian carc
33	365.4	19.3	369	24	ABL48956 Ovarian carcinoma
34	362	19.1	373	24	ABL78538 Human ovarian carc
35	354	18.7	390	24	ABL78554 Human ovarian carc
36	341.8	18.0	381	24	ABL48484 Human ovarian carc
37	310.2	16.4	349	24	ABL79431 Human ovarian carc
38	175.4	9.2	468	22	AAK54063 Murine transport a
39	171.2	9.0	201	24	ABL85916 Human ovarian carc
40	60	3.2	60	24	ABN41977 Human neurotensin
41	58.2	3.1	1254	17	AAK3127 Non-endogenous hum
42	58.2	3.1	1257	23	ABT98007 DNA encoding novel
43	58.2	3.1	4149	23	AAK76503 Human full-length
44	58	3.1	3609	22	AAK4581 G protein-coupled
45	56.4	3.0	1140	20	AAK83839

## ALIGNMENTS

RESULT 1	
ABT03284	standard; cDNA; 1897 BP.
XX	ABT03284;
XX	05-SEP-2002 (first entry)
XX	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.
DE	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX	cytoskeletal; gene; ss.
XX	Homo sapiens.
XX	WO200239885-A2.
XX	23-MAY-2002.
PD	
XX	13-NOV-2001; 2001WO-US45395.
PF	
XX	14-NOV-2000; 2000US-0713550.
PR	03-APR-2001; 2001US-0825294.
XX	02-OCT-2001; 2001US-0970966.
XX	(CORI-) CORIXA CORP.
PA	
XX	Xu J, Stolk JA, Algate PA, Filing SP, Molesch DA;
PI	WPI; 2002-500186/53.
XX	Novel ovarian cancer polypeptide and polynucleotide; useful for
FT	



ID	ABLA0352 standard; cDNA, 1897 BP.	ABLA0352
AC	ABLA0352;	RESULT 2
AD		ABLA0352
AE	28-JUN-2002 (first entry)	
AF	Ovarian carcinoma O1034C/0591S consensus nucleotide sequence.	
AG	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;	
AH	ss.	
AI	Homo sapiens.	
AK	Key	
AL	Location/Qualifiers	
AM	260..685	
AN	/*tag= "a	
AO	/product= "Ovarian carcinoma protein O1034C/0591S"	
AP	US2002004491-A1.	
AQ	10-JAN-2002.	
AR	03-APR-2001; 2001US-0825294.	
AS	10-SEP-1999; 99US-0394374.	
AT	01-MAY-2000; 2000US-0561778.	
AV	15-AUG-2000; 2000US-0640173.	
AW	07-SEP-2000; 2000US-0656668.	
AX	14-NOV-2000; 2000US-0713550.	
AY	(XUJY) XU J.	
AZ	(STOL) STOLK J A.	
BA	(ALGA) ALGATE P A.	
BB	(FLIN) FLING S P.	
BC	Xu J, Stolk JA, Algate PA, Fling SP;	
BD	WPI; 2002-171027/22.	
BE	P-PSDB; ABB09417.	
BF	Ovarian tumour polypeptide and polynucleotide useful in diagnosis,	
BG	prevention and/or treatment of cancer, especially ovarian cancer -	
BH	Claim 1a; Page 127-128; 131pp; English.	
BI	The invention relates to ovarian tumour polynucleotides and polypeptides	
BJ	that may be utilised in cancer therapy, for example in a vaccine or	
BK	gene therapy. Polypeptides and polynucleotides of the invention are	
BL	useful for detecting a cancer in a patient, for stimulating and/or	
BM	expanding T-cells specific for a tumour protein, and for inhibiting the	
BN	development of a cancer in a patient. They are also useful for	
BO	stimulating an immune response in a patient, and for treating a cancer in	
BP	a patient and for determining the presence of a cancer in a patient.	
BQ	The isolated polynucleotides of the invention are useful for their	
BR	ability to selectively form duplex molecules with complementary stretches	
BS	of the entire desired gene or gene fragments, and for designing and	
BT	preparing ribozyme molecules for inhibiting expression of tumour	
BU	polypeptides in tumour cells. Polypeptides and polynucleotides of the	
BV	invention are also useful in recombinant DNA molecules to direct	
BW	expression of a polypeptide in appropriate host cells. The current	
BX	sequence represents the ovarian carcinoma O1034C/0591S consensus	
BY	nucleotide sequence.	
BZ	Sequence 1897 BP: 435 A: 521 C: 532 G: 407 T: 2 other:	
CA	Query Match	100.0%; Score 1896.2; DB 24; Length 1897;
CB	Best Local Similarity	100.0%; Pred. No. 0;
CC	Matches 1897; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CD	1 GCCACCTCCGAGGCTCTGCTGCTGGCCGGGAGACCGAGCGGAGGACGACGACCCG 60	
CE		

Db	1	GGCAACCTCGGAGGCGTCTGGTGGTCTCGGGCCCGGGAGCGCCAGACCGGAGGAGACAGAGAACCCG	60
Qy	61	CAGCCGGAGACCCGAGCGCGGGCGATGCAAGCTCTCCGGAGCGGACACCTGCGGCTCTCTA	120
Db	61	CAGCCGGAGACCCGAGCGCGGGCGATGCAAGCTCTCCGGAGCGGACACCTGCGGCTCTCTA	120
Qy	121	AGCTACGACCGCTCTCTCCGGGGAGAGAGGGGGGCCCCAGACGCTCGGACAGCCACAGC	180
Db	121	AGCTACGACCGCTCTCTCCGGGGAGAGAGGGGGGCCCCAGACGCTCGGACAGCCACAGC	180
Qy	181	CGCTACACCGGGGAGAGCTCCGCTGCTGTCGGCTCCTCGATGGCGCTTGGCCCTCCCG	240
Db	181	CGCTACACCGGGGAGAGCTCCGCTGCTGTCGGCTCCTCGATGGCGCTTGGCCCTCCCG	240
Qy	241	GGCCCGGGAGCTCCGGGAGATGTGGTCTTAGGCATCGCGGCAACTTTTGGCGATGT	300
Db	241	GGCCCGGGAGCTCCGGGAGATGTGGTCTTAGGCATCGCGGCAACTTTTGGCGATGT	300
Qy	301	CTTGCTTCCAGGCTTTGGGCTGCAATTCACGTGCTACCACTGTGAAGATTCCAGCTGA	360
Db	301	CTTGCTTCCAGGCTTTGGGCTGCAAAATCACGTGCTACCACTGTGAAGATTCCAGCTGA	360
Qy	361	CAACACACTGCTCTCCCGGAGTTGATTTGAATTTGACAGGTAAAGTTCAAGACATGTG	420
Db	361	CAACACACTGCTCTCCCGGAGTTGATTTGAATTTGACAGGTAAAGTTCAAGACATGTG	420
Qy	421	TCGAGAAGAAGTGAATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTCTGTGATCATC	480
Db	421	TCGAGAAGAAGTGAATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTCTGTGATCATC	480
Qy	481	AGCGGCGTGTCTCATCGGCTTGGCGGGTACAGTCTTCTGCTCCCAAGGAACTGAA	540
Db	481	AGCGGCGTGTCTCATCGGCTTGGCGGGTACAGTCTTCTGCTCCCAAGGAACTGAA	540
Qy	541	CTCAGTTTGCATTCAGCTGCTGCAACACCCCTTTTGAACGGGCCCAAGGCCCAAGAAAG	600
Db	541	CTCAGTTTGCATTCAGCTGCTGCAACACCCCTTTTGAACGGGCCCAAGGCCCAAGAAAG	600
Qy	601	GGGAAGTTCTGCTCGCGCCCTCAAGGCGCGGACCGCACACACATCTTCTCAAAAT	660
Db	601	GGGAAGTTCTGCTCGCGCGCCCTCAAGGCGCGGACCGCACACACATCTTCTCAAAAT	660
Qy	661	AGCCTCTTCTTCGGCACACTGCTGAGAGTGAAGATGCCACACCCCTCTGCAATGTTC	720
Db	661	AGCCTCTTCTTCGGCACACTGCTGAGAGTGAAGATGCCACACCCCTCTGCAATGTTC	720
Qy	721	TTCCAGGCCCTGGCCCCAACCCCCACCTCCCGAGTAGTTCTTCTGGGCTGCTTTT	780
Db	721	TTCCAGGCCCTGGCCCCAACCCCCACCTCCCGAGTAGTTCTTCTGGGCTGCTTTT	780
Qy	781	ATTCTGGGTAGGAGACGGAGATCCGTTTCTTTTGTTCCTGTGCAAATTAATGAAGAG	840
Db	781	ATTCTGGGTAGGAGACGGAGATCCGTTTCTTTTGTTCCTGTGTGAATTAATGAAGAG	840
Qy	841	CTCGTAAAGCATTTCTGAATTAATTCAGCTGACTGAATTTTCAGTATGTACTGAAGA	900
Db	841	CTCGTAAAGCATTTCTGAATTAATTCAGCTGACTGAATTTTCAGTATGTACTGAAGA	900
Qy	901	AGGAGGTGAGTGAAGGTACCCCCATGTCGTGTGTAACCGGAGTCAAGGCCAGGCTGGC	960
Db	901	AGGAGGTGAGTGAAGGTACCCCCATGTCGTGTGTAACCGGAGTCAAGGCCAGGCTGGC	960
Qy	961	AGAGTCGCTCTTGAAGTCACTGAGTGGGCAATCGCTTTTGTAAAGCTCCAGGTGC	1020
Db	961	AGAGTCGCTCTTGAAGTCACTGAGTGGGCAATCGCTTTTGTAAAGCTCCAGGTGC	1020
Qy	1021	CATTCATCCTGTATGGGGGCAATGTTTGAAGTCAAGTCAAGAGTGAAGTCAAGTTCCTT	1080
Db	1021	CATTCATCCTGTATGGGGGCAATGTTTGAAGTCAAGTCAAGAGTGAAGTCAAGTTCCTT	1080
Qy	1081	GGCTGGAGGGCAATTCGCACTAAGGCTCCCGCTTACAACTTCATGCTCTCT	1140
Db	1081	GGCTGGAGGGCAATTCGCACTAAGGCTCCCGCTTACAACTTCATGCTCTCT	1140



QY 241 GCCCGGAGCTCCGGAGAAATGGGTCTAGGCATCGCGCACTTTTGGCGATTGTT 300  
| | | | |  
Db 1713 GCCCGGAGCTCCGGAGAAATGGGTCTAGGCATCGCGCACTTTTGGCGATTGTT 1654  
QY 301 CTTCGTTCCAGGCTTGGCTGCAAAATCCAGTGTACAGTGTGAAGAAATTCACATGAA 360  
| | | | |  
Db 1653 CTTCGTTCCAGGCTTGGCTGCAAAATCCAGTGTACAGTGTGAAGAAATTCACATGAA 1594  
QY 361 CAACGACTGCTCTCCCGGAGTTCATTGTGAATTCACAGTGAAGCTTCAAGACATGTG 420  
| | | | |  
Db 1593 CAACGACTGCTCTCCCGGAGTTCATTGTGAATTCACAGTGAAGCTTCAAGACATGTG 1534  
QY 421 TCAGAAAGAGATGATGAGCAAAAGTCCGGGATCATGTACCCGAAGTCTGTGCATCATC 480  
| | | | |  
Db 1533 TCAGAAAGAGATGATGAGCAAAAGTCCGGGATCATGTACCCGAAGTCTGTGCATCATC 1474  
QY 481 AGCGGCTGTCTCATGCTGTGCGGGGTACCAAGTCTCTCTCCCGGAGAACTGAA 540  
| | | | |  
Db 1473 AGCGGCTGTCTCATGCTGTGCGGGGTACCAAGTCTCTCTCCCGGAGAACTGAA 1414  
QY 541 CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCAAGGCCCAAGAAAG 600  
| | | | |  
Db 1413 CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCAAGGCCCAAGAAAG 1354  
QY 601 GGGAAATTTGCTGCTGCGCCCTCAGGCGCAGGCTCCGACACCATCTGTCTCTCAATT 660  
| | | | |  
Db 1353 GGGAAATTTGCTGCTGCGCCCTCAGGCGCAGGCTCCGACACCATCTGTCTCTCAATT 1295  
QY 661 AGCCCTCTCTGCGGACACTGCTGTAAGCTGAAGAGATGCCACCCCTCCCTCATTTGTC 720  
| | | | |  
Db 1294 AGCCCTCTCTGCGGACACTGCTGTAAGCTGAAGAGATGCCACCCCTCCCTCATTTGTC 1235  
QY 721 TTCACGCTCTGCGCCCAACCCCAACCTCCCTGAGTGAATTTCTTGGGTCTCTTTT 780  
| | | | |  
Db 1234 TTCACGCTCTGCGCCCAACCCCAACCTCCCTGAGTGAATTTCTTGGGTCTCTTTT 1175  
QY 781 ATTCTGGGAGGAGGAGGAGTCCGTTCTCTTTGTTCTCTGTCGAATTAATGAAGAG 840  
| | | | |  
Db 1174 ATTCTGGGAGGAGGAGGAGTCCGTTCTCTTTGTTCTCTGTCGAATTAATGAAGAG 1115  
QY 841 CTCGGTAAGCAATTCGTAATTAATTCAGCTGATGATGTAATTTTCAATGTAAGGA 900  
| | | | |  
Db 1114 CTCGGTAAGCAATTCGTAATTAATTCAGCTGATGATGTAATTTTCAATGTAAGGA 1055  
QY 901 AGGAGTGGAGTGAAGATTCACCCCATGCTGTGTAAACCGGAGTCAAGGCCAGGCTGAC 960  
| | | | |  
Db 1054 AGGAGTGGAGTGAAGATTCACCCCATGCTGTGTAAACCGGAGTCAAGGCCAGGCTGAC 995  
QY 961 AGAGTGMGTCTTAAAGTCACTGAGTGGGATCTGCTTTTGTAAAGCTTCCAGTGTG 1020  
| | | | |  
Db 994 AGAGTGMGTCTTAAAGTCACTGAGTGGGATCTGCTTTTGTAAAGCTTCCAGTGTG 935  
QY 1021 CATTCCATCCCTGATGAGGAGGATGATTGAGACTCAGAGTGAAGTGAAGTCTTCTTAG 1080  
| | | | |  
Db 934 CATTCCATCCCTGATGAGGAGGATGATTGAGACTCAGAGTGAAGTGAAGTCTTCTTAG 875  
QY 1081 GGCTGGAGGCGCAAGTTCCTCAATCAAGGCTCCCTGCTTGACATTAATTCATCTCTCT 1140  
| | | | |  
Db 874 GGCTGGAGGCGCAAGTTCCTCAATCAAGGCTCCCTGCTTGACATTAATTCATCTCTCT 815  
QY 1141 GAAACCATTTCTGACAGAGAAATGGCTGCTTGGCGCTAGTGGGCTTAACTGACT 1200  
| | | | |  
Db 814 GAAACCATTTCTGACAGAGAAATGGCTGCTTGGCGCTAGTGGGCTTAACTGACT 755  
QY 1201 CGAGACTCAATGACTGAGACTGAGTGGGCTCGGCTCGCTGGAAGAGTGAAGGA 1260  
| | | | |  
Db 754 CGAGACTCAATGACTGAGACTGAGTGGGCTCGGCTCGCTGGAAGAGTGAAGGA 695  
QY 1261 AAATCTTCTCAATGCTCTCTGAGAGAGTGGCGCGGAGCGGAAGAGCAAGCGGCGCT 1320  
| | | | |  
Db 694 AAATCTTCTCAATGCTCTCTGAGAGAGTGGCGCGGAGCGGAAGAGCAAGCGGCGCT 635  
QY 1321 GCACAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

Db 634 GCACAAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575  
QY 1381 TGGGCTGCTGAGGAGACAGCGGCGGAGACACACACCTCTCAGCAACACCCCGGAACTGCT 1440  
| | | | |  
Db 574 TGGGCTGCTGAGGAGACAGCGGCGGAGACACACACCTCTCAGCAACACCCCGGAACTGCT 515  
QY 1441 GCGAGACACCGTGTACAGAGACCGGCTTGAATGACGAGCTGAGTGAAGAAACCTCTCCG 1500  
| | | | |  
Db 514 GCGAGACACCGTGTACAGAGACCGGCTTGAATGACGAGCTGAGTGAAGAAACCTCTCCG 455  
QY 1501 AGAAGGAGAGAGATCATGTAGCCCGGAGAGTGAAGACCTCTGCTCACTGCTTGGGTT 1560  
| | | | |  
Db 454 AGAAGGAGAGAGATCATGTAGCCCGGAGAGTGAAGACCTCTGCTCACTGCTTGGGTT 395  
QY 1561 TGGCGGACGCTATCTCTCCGAATCTGCTTGGGCTATCCAGCATACGCGCAATGTCAAA 1620  
| | | | |  
Db 394 TGGCGGACGCTATCTCTCCGAATCTGCTTGGGCTATCCAGCATACGCGCAATGTCAAA 335  
QY 1621 CAATCAGCCCTGCGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
| | | | |  
Db 334 CAATCAGCCCTGCGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 275  
QY 1681 GAGAACACAGTAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740  
| | | | |  
Db 274 GAGAACACAGTAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 215  
QY 1741 GCCAGGAATGTATACCAATTTTCACTGTTGAGCTTGAACAGCTCTTTTGGCAACAA 1800  
| | | | |  
Db 214 GCCAGGAATGTATACCAATTTTCACTGTTGAGCTTGAACAGCTCTTTTGGCAACAA 155  
QY 1801 GAGAGAAATTAACACTGTTTCAAAACCGGAGAGTGGCTGTGTTAAAGAACATTA 1860  
| | | | |  
Db 154 GAGAGAAATTAACACTGTTTCAAAACCGGAGAGTGGCTGTGTTAAAGAACATTA 95  
QY 1861 AATGCTTTAGACAGTGA 1878  
| | | | |  
Db 94 AATGCTTTAGACAGTGA 77  
  
RESULT 4  
AAF64188/c  
ID AAF64188 standard; cDNA; 1956 BP.  
XX  
AC AAF64188;  
XX  
DT 06-Apr-2001 (first entry)  
XX  
DE Human secreted protein gene I3 SEQ ID NO:23.  
XX  
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
KW antiproliferative; cytoskeletal; cardiant; vasotropic; cerebroprotective;  
KW neurologic; neuroprotective; antibacterial; virucide; fungicide;  
KW ophthalmological; vulvenerary; autoimmune disease; cardiovascular disorder;  
KW hyperproliferative disorders; cerebrovascular disorder; wound healing;  
KW nervous system disorder; ocular disorder; skin aging; chemotaxis;  
KW food additive; ss.  
XX  
OS Homo sapiens.  
XX  
PN M0200077026-A1.  
XX  
PD 21-Dec-2000.  
XX  
PE 01-JUN-2000; 2000MO-US14973.  
XX  
PR 11-JUN-1999; 9905-0138630.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
PI Rosen CA, Ruben SM, Komatsoulis GA;  
XX







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Db 853 CTCGGTAAGCATCTGTAATTAATTCAGCTTGACTGAATTTTCACTATGACTTGAAGA 912
Qy 901 AGGAGGTGGAGTGAAGATTACACCCCATGTCTGTAAACCGAGTCAAGGCGAGCTGGC 960
Db 913 AGGAGGTGGAGTGAAGATTACACCCCATGTCTGTAAACCGAGTCAAGGCGAGCTGGC 972
Qy 961 AGAGTGMGTCTTGAAGATCACTGAGGTGGGATCGCTTTTGTAAAGCCCTCAGTGTG 1020
Db 973 AGAGTGMGTCTTGAAGATCACTGAGGTGGGATCGCTTTTGTAAAGCCCTCAGTGTG 1032
Qy 1021 CATTCATCCCTGATGAGGCGCATAGTTTGAGACTGCAGAGTGAAGTGAAGCTTTTCTAG 1080
Db 1033 CATTCATCCCTGATGAGGCGCATAGTTTGAGACTGCAGAGTGAAGTGAAGCTTTTCTAG 1092
Qy 1081 GGTGGAGGCGCAAGTCCCACTCAAGGCTCCCTCGCTTGACTTAAACTTATCTCTCT 1140
Db 1093 GGTGGAGGCGCAAGTCCCACTCAAGGCTCCCTCGCTTGACTTAAACTTATCTCTCT 1152
Qy 1141 GAAACCATTCCTGAGAGAAATGGGCTGGTTGGCGCTGATGGGCTGATGACT 1200
Db 1153 GAAACCATTCCTGAGAGAAATGGGCTGGTTGGCGCTGATGGGCTGATGACT 1212
Qy 1201 CGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCTCGCTTGAAAGTCTTAAGA 1260
Db 1213 CGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCTCGCTTGAAAGTCTTAAGA 1272
Qy 1261 AATCTTCTCAATGCTT-CCTTGAGAGACTGGCGCGGAGCGGAGAGCAAGCGGCGC 1319
Db 1273 AATCTTCTCAATGCTT-CCTTGAGAGACTGGCGCGGAGCGGAGAGCAAGCGGCGC 1332
Qy 1320 TGCACAAACCGGGCGCTGTCCGTTGGTGGAGTGGCGCATGACGCGAGGCGCTTCCTG 1379
Db 1333 TGCACAAACCGGGCGCTGTCCGTTGGTGGAGTGGCGCATGACGCGAGGCGCTTCCTG 1392
Qy 1380 TTGGCTGTGTCAGCAGCAGGCGGCGAGCAGACACTGTCAGCAACACCCCGGAAACTGC 1439
Db 1393 TTGGCTGTGTCAGCAGCAGGCGGCGAGCAGACACTGTCAGCAACACCCCGGAAACTGC 1452
Qy 1440 TGGGAGACACCGTGTACAGAGGCGGTTGATGACCGAGCTGAGGTAAGAAACCTCTCC 1499
Db 1453 TGGGAGACACCGTGTACAGAGGCGGTTGATGACCGAGCTGAGGTAAGAAACCTCTCC 1512
Qy 1500 GAGAAAGGAGAGAGATCATGTACGCCGGAAGTAGAGACTGTCAGTCTGTGGGT 1559
Db 1513 GAGAAAGGAGAGAGATCATGTACGCCGGAAGTAGAGACTGTCAGTCTGTGGGT 1572
Qy 1560 TTGGCCGAGCCATGATCTCTCGAATCTGTGGGCAATCAGCATACGCGCAATGTACA 1619
Db 1573 TTGGCCGAGCCATGATCTCTCGAATCTGTGGGCAATCAGCATACGCGCAATGTACA 1632
Qy 1620 ACAATAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679
Db 1633 ACAATAGCCCTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1692
Qy 1680 TGAGAACACAGTAAATGAATTAACCATTAATTTAGCCCTCTGTCTGTGCTTACT 1739
Db 1693 TGAGAACACAGTAAATGAATTAACCATTAATTTAGCCCTCTGTCTGTGCTTACT 1752
Qy 1740 GGGCAGAAATGGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAAGCA 1799
Db 1753 GGGCAGAAATGGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAAGCA 1812
Qy 1800 AGAGAAATTTAACTGTTTAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCAAT 1859
Db 1813 AGAGAAATTTAACTGTTTAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCAAT 1872
Qy 1860 AATGCTTTAGACAGTGT 1877
Db 1873 AATGCTTTAGACAGTGT 1890

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ABT03277
ID ABT03277 standard; cDNA; 1619 BP.
XX
AC ABT03277:
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.
XX
KW Human: ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW cytosolic; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
PR 03-APR-2001; 2001US-0825294.
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX
DR WPI; 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT
PS Claim 2; Page 189-190; 197pp; English.
PS
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;
XX
Query Match 84.7%; Score 1606.2; DB 24; Length 1619;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
Qy 280 GCAACTTTTGGGATTTGTTCTTGTCCAGGCTTGGCTGCAAAATCAGTGTACCA 339
Db 1 GCAAACTTTTGGGATTTGTTCTTGTCCAGGCTTGGCTGCAAAATCAGTGTACCA 60
Qy 340 GTGTAAGAAATTTCCAGTGAACAGACTGCTCTCCCGGAGTTCATTTGTGAATTCAC 399
Db 61 GTGTAAGAAATTTCCAGTGAACAGACTGCTCTCCCGGAGTTCATTTGTGAATTCAC 120
Qy 400 GGTGAACCTTCAAGACATGTGTCAAGAAAGATGAGAGCAAAAGTCCGGATCATGTA 459
Db 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGATGAGAGCAAAAGTCCGGATCATGTA 180
Qy 460 CCGCAAGTCTGTGCATCATCAGCGGCTGTGTGATGAGCTGTGCGGGTACAGTCTTT 519
Db 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTGTGATGAGCTGTGCGGGTACAGTCTTT 240
Qy 520 CTGCTCCCGCAGGAAACTGAATTCAGTTTGATAGCTGTGTGCAACACCCCTCTTTGTA 579
Db 241 CTGCTCCCGCAGGAAACTGAATTCAGTTTGATAGCTGTGTGCAACACCCCTCTTTGTA 300
Qy 580 CGGGCAAGGCCCAAGAAAGGGAAGTTGCTCGGCTCGGCTCGAGGAGGCTCCGAC 639
Db 301 CGGGCAAGGCCCAAGAAAGGGAAGTTGCTCGGCTCGGCTCGAGGAGGCTCCGAC 360
Qy 640 CACCATCTGTTCTCAATTAATAGCCCTTCTCGGCACTGTGAAGTGAAGAGATG 699

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RESULT 6

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|||||
Db 361 CACATCCCTGTCCTCAATATAGCCCTCTTCGCGACACTGCTAGAGTGAAGAGATG 420
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Qy 700 CCACCCCTCCGCAATGTTCTTCACGCCCTGGCCCCCAACCCCTCCTCTAGTGA 759
|||
Db 421 CCACCCCTCCGCAATGTTCTTCACGCCCTGGCCCCCAACCCCTCCTCTAGTGA 480
|||
Qy 760 GTTCTCTGCGGTCTCTTATCTGCGGTAGGAGCGGAGTCCGTGTTCTTCTTGT 819
|||
Db 481 GTTCTCTGCGGTCTCTTATCTGCGGTAGGAGCGGAGTCCGTGTTCTTCTTGT 540
|||
Qy 820 CCTGTGCAATATATGAAGAGCTCGTAAAGCATCTGATTAATTAATCACTGAT 879
|||
Db 541 CCTGTGCAATATATGAAGAGCTCGTAAAGCATCTGATTAATTAATCACTGAT 600
|||
Qy 880 TTTTCAGTATGTTCTGGAAGAGAGGTGAGTGAAGTCAACCCCTCATGCTGTGTAAC 939
|||
Db 601 TTTTCAGTATGTTCTGGAAGAGAGGTGAGTGAAGTCAACCCCTCATGCTGTGTAAC 660
|||
Qy 940 CGAGTCAAGGCCAGGCTGGCAGAGTCTGCTTGAAGTCACTAGGTGGCATCTGCTCC 999
|||
Db 661 CGAGTCAAGGCCAGGCTGGCAGAGTCTGCTTGAAGTCACTAGGTGGCATCTGCTCC 720
|||
Qy 1000 TTTTGTAAAGCTCCAGTGTCTCATTCATCCCTGATGGGGGCATAGTTTGAAGTGCAGA 1059
|||
Db 721 TTTTGTAAAGCTCCAGTGTCTCATTCATCCCTGATGGGGGCATAGTTTGAAGTGCAGA 780
|||
Qy 1060 GTGAGTACAGCTTTTCTTAGGGCTGAGGGGCGAGTCCCATCAAGGCTCCCTGCTTG 1119
|||
Db 781 GTGAGTACAGCTTTTCTTAGGGCTGAGGGGCGAGTCCCATCAAGGCTCCCTGCTTG 840
|||
Qy 1120 ACATTCAAACTTCATGCTCTGTAAGAAATCTTCTGACAGCAAAATGGCTGGTTCGCGC 1179
|||
Db 841 ACATTCAAACTTCATGCTCTGTAAGAAATCTTCTGACAGCAAAATGGCTGGTTCGCGC 900
|||
Qy 1180 CTGAGTGGGCTCTAGTACTCTGAACTCAATGACTGGGACTTAGACTGGGGCTGGGCT 1239
|||
Db 901 CTGAGTGGGCTCTAGTACTCTGAACTCAATGACTGGGACTTAGACTGGGGCTGGGCT 960
|||
Qy 1240 CGCTCTGAAAAGTCTGTTAAGAAATCTTCTGACAGCAAAATGGCTGGTTCGCGC 1299
|||
Db 961 CGCTCTGAAAAGTCTGTTAAGAAATCTTCTGACAGCAAAATGGCTGGTTCGCGC 1020
|||
Qy 1300 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCTGGTGTGAGTGGCGCATGA 1359
|||
Db 1021 ACGCAAGAGCAAGCGGCGCTGACAAAGCGGCGCTGCTGGTGTGAGTGGCGCATGA 1080
|||
Qy 1360 CGCGAGGCGCTCTGAGTGGGCTGCTGAGAGCAAGCGGCGAGCAAGCACC-TGC 1418
|||
Db 1081 CGCGAGGCGCTCTGAGTGGGCTGCTGAGAGCAAGCGGCGAGCAAGCACC-TGC 1140
|||
Qy 1419 ACGAAGACCCCGCGAAGTGTGCGAGAGCAACCGTGTACAGAGGCGGTTATGACCGAG 1478
|||
Db 1141 ACGAAGACCCCGCGAAGTGTGCGAGAGCAACCGTGTACAGAGGCGGTTATGACCGAG 1200
|||
Qy 1479 CTGAGGTGAAAAGCTCTCCGAGAAGGGAGAGATCATGTACCCCGGAAGTAGGAC 1538
|||
Db 1201 CTGAGGTGAAAAGCTCTCCGAGAAGGGAGAGATCATGTACCCCGGAAGTAGGAC 1260
|||
Qy 1539 CTGCGACAGTGTGCTGGGTTGGCGCAGCAGCATCTCCGAATGTGGTGGGCTATC 1598
|||
Db 1261 CTGCGACAGTGTGCTGGGTTGGCGCAGCAGCATCTCTCCGAATGTGGTGGGCTATC 1330
|||
Qy 1599 CAGCATACGGCCATGTCAACAATATGAGCCCTGGCGAGACAGCAGGAGGAGAGAC 1658
|||
Db 1321 CAGCATACGGCCATGTCAACAATATGAGCCCTGGCGAGACAGCAGGAGGAGAGAC 1380
|||
Qy 1659 AGAGAAAAGAAAACACAGCATGTGAGACACAGTAATGATTAATTAATTTAG 1718
|||
Db 1381 AGAGAAAAGAAAACACAGCATGTGAGACACAGTAATGATTAATTAATTTAG 1440
|||
Qy 1719 CCGCTCTGTCTGTGCTACGTGCGCAGGAATGGTACCAATTTTCAGTGTGACACTTGA 1778
|||

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Db 1441 CCGCTGTCTGTGCTTACTGCGCCAGGAATGTTACCAATTTTTCAGTGTGACTTGA 1500
|||
Qy 1779 CAGCTTCTTTTGGCCACAAGCAGAGAGAATTTAACTGTTTCAAAACCGGGGAGTTGG 1838
|||
Db 1501 CAGCTTCTTTTGGCCACAAGCAGAGAGAATTTAACTGTTTCAAAACCGGGGAGTTGG 1560
|||
Qy 1839 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGAATTAATTAATTAATTAATTAAT 1897
|||
Db 1561 CTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGAATTAATTAATTAATTAATTAAT 1619
|||

RESULT 7
ABF03281
ID ABF03281 standard; cDNA; 1619 bp.
XX
AC ABF03281;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW cytosolic; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2001; 2000US-0713550.
PR 03-APR-2001; 2001US-0825284.
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;
XX
DR WPI: 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
PS Claim 2; Page 195; 197pp; English.
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
SQ Sequence 1619 bp; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 84.7%; Score 1606.2; DB 24; Length 1619;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```



CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumor  
 CC polypeptides in tumor cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the extended cDNA sequence of ovarian carcinoma  
 CC isolate 57887 given in record ABL48956.

XX  
 SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 84.7%; Score 1606.2; DB 24; Length 1619;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1616; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```

Oy 280 GGCACCTTTTCCGATGTTCTTCTCCAGGCTTTCGCGCAATTCAGTGTACCA 339
Db 1 GGCACCTTTTCCGATGTTCTTCTCCAGGCTTTCGCGCAATTCAGTGTACCA 60
Oy 340 GTTGAGAAATTCAGTGAACACAGACGTCCTCCCGAGTTCAATGTAATTCAC 399
Db 61 GTTGAGAAATTCAGTGAACACAGACGTCCTCCCGAGTTCAATGTAATTCAC 120
Oy 400 GGTGAACGTTCAAGCATGTGTCAAGAAAGAGTGTGAGCAAAAGTCCGGGATCAGTA 459
Db 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGAGTGTGAGCAAAAGTCCGGGATCAGTA 180
Oy 460 CCGCAAGTCCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGGTACAGTCTT 519
Db 181 CCGCAAGTCCTGTGATCATCAGCGGCTGTCTCATGCTCTGCGGGGTACAGTCTT 240
Oy 520 CTGCTCCCGAGGAAATGAACTGATGTCATGCTGTCGCAACACCCCTTTTGTAA 579
Db 241 CTGCTCCCGAGGAAATGAACTGATGTCATGCTGTCGCAACACCCCTTTTGTAA 300
Oy 580 GGGGCAAGGCGCCAGAAAGGGAGTTCCTGCGGCTCCAGGCGGAGGCTCCGAC 639
Db 301 GGGGCAAGGCGCCAGAAAGGGAGTTCCTGCGGCTCCAGGCGGAGGCTCCGAC 360
Oy 640 CACCATCTGTTCTCAATTAAGCCCTCTCTGCGCACATGCTGAAGAGATG 699
Db 361 CACCATCTGTTCTCAATTAAGCCCTCTCTGCGCACATGCTGAAGAGATG 420
Oy 700 CCACCCCTCTCGCATTTTCTTCCAGCCCTCGCCCAACCCCACTCTCTGAATGA 759
Db 421 CCACCCCTCTCGCATTTTCTTCCAGCCCTCGCCCAACCCCACTCTCTGAATGA 480
Oy 760 GTTCTCTGGGTGTCCTTTATCTGAGTGAAGGCGGAGTCCGTCTCTTTTGT 819
Db 481 GTTCTCTGGGTGTCCTTTATCTGAGTGAAGGCGGAGTCCGTCTCTTTTGT 540
Oy 820 CCTGTCAAAATATGAAAGACCTCGTAAACATTTCTGAATTAATTCAGTGTGAT 879
Db 541 CCTGTCAAAATATGAAAGACCTCGTAAACATTTCTGAATTAATTCAGTGTGAT 600
Oy 880 TTTCAGTATGACTTGAAGAGAGAGTGTGAGTGAAGTCAACCCCATGCTGTGTAA 939
Db 601 TTTCAGTATGACTTGAAGAGAGAGTGTGAGTGAAGTCAACCCCATGCTGTGTAA 660
Oy 940 CGGAGTCAAGGCGAGGCGGAGAGTGTGAGTGAAGTCAACCCCATGCTGTGTAA 999
Db 661 CGGAGTCAAGGCGAGGCGGAGAGTGTGAGTGAAGTCAACCCCATGCTGTGTAA 720
Oy 1000 TTTTGTAAAGGCTCCAGTGTCCATTCCTGATGGGGCATAGTTGAGATGACAGA 1059
Db 721 TTTTGTAAAGGCTCCAGTGTCCATTCCTGATGGGGCATAGTTGAGATGACAGA 780
Oy 1060 GTGAGAGTGAAGTGTCTTGAAGGCTGAGGCGCAGTTCACCTAAGGCTCCCTGCTG 1119
Db 781 GTGAGAGTGAAGTGTCTTGAAGGCTGAGGCGCAGTTCACCTAAGGCTCCCTGCTG 840
Oy 1120 ACATTCAAACTTCATGCTCTGAAAGACATTCCTGCGAGCAATTTGGCTTTCCGCG 1179

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Db 841 ACATTCAAACTTCATGCTCTGAAAGACATTCCTGCGAGCAATTTGGCTTTCCGCC 900
Oy 1180 CTGAGTTGGGCTCTAGTACTCCAGATCATATGACTGAGGCTTAGACTGGGCTCCGCT 1239
Db 901 CTGAGTTGGGCTCTAGTACTCCAGATCATATGACTGAGGCTTAGACTGGGCTCCGCT 960
Oy 1240 CGGCTGAAAAAGTCTTAAATAATCTTCTCAGTTCCTCTGAGAGAGTGTGCGCGGG 1299
Db 961 CGGCTGAAAAAGTCTTAAATAATCTTCTCAGTTCCTCTGAGAGAGTGTGCGCGGG 1020
Oy 1300 ACAGGAGAGCAACGAGGCGCTGCACAAAGCGGCGCTGTGCTGTGAGTGTGAGTGTG 1359
Db 1021 ACAGGAGAGCAACGAGGCGCTGCACAAAGCGGCGCTGTGCTGTGAGTGTGAGTGTG 1080
Oy 1360 CGGCGAGGCGCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1418
Db 1081 CGGCGAGGCGCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1140
Oy 1419 ACAGAACCCGCGGAAACTCTGCGAGACACCGTGTACAGAGCGGCTGTGATGACCGAG 1478
Db 1141 ACAGAACCCGCGGAAACTCTGCGAGACACCGTGTACAGAGCGGCTGTGATGACCGAG 1200
Oy 1479 CTGAGTGAAGAAAAAGTCTCCGAGAGAGGAGAGATCATGTACCCCGGAAATGAGAC 1538
Db 1201 CTGAGTGAAGAAAAAGTCTCCGAGAGAGGAGAGATCATGTACCCCGGAAATGAGAC 1260
Oy 1539 CTGCTCCAGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1598
Db 1261 CTGCTCCAGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1320
Oy 1599 CAGCATACGCGCAATGTACAGACATATGAGGCTGTGCGAGACAGAGAGGAGAGAGAC 1658
Db 1321 CAGCATACGCGCAATGTACAGACATATGAGGCTGTGCGAGACAGAGAGGAGAGAGAC 1380
Oy 1659 AGAGAAAAAGAAAAACACAGCATGAGAACACATGAATGAATTAATTAATTAATTAAT 1718
Db 1381 AGAGAAAAAGAAAAACACAGCATGAGAACACATGAATGAATTAATTAATTAATTAAT 1440
Oy 1719 CCCCTGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1778
Db 1441 CCCCTGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1500
Oy 1779 CAGCTTCTTTTGCACAGAGAGAGATTTAAACATGTTTAAACCCGCGGAGTGTG 1838
Db 1501 CAGCTTCTTTTGCACAGAGAGAGATTTAAACATGTTTAAACCCGCGGAGTGTG 1560
Oy 1839 CTGCTTAAAGAAAAAGCAATTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAAT 1897
Db 1561 CTGCTTAAAGAAAAAGCAATTAATGCTTTAGACAGTGTAAAAAATTAATTAATTAAT 1619

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RESULT 9  
 ABL40349  
 ID ABL40349 standard; cDNA; 1619 BP.

XX ABL40349;  
 AC 28-JUN-2002 (first entry)

XX Ovarian carcinoma O591S nucleotide sequence.  
 DE Ovarian cancer; cancer therapy; vaccine; gene therapy; tumor; cancer;  
 KW ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.  
PR 15-AUG-2000; 2000US-0640173.  
PR 07-SEP-2000; 2000US-0656668.  
PR 14-NOV-2000; 2000US-0713550.

PA (XUJJ/) XU J.  
PA (STOL/) STOLK J A.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.

PI Xu J, Stolk JA, Algate PA, Fling SP;  
XX  
DR WPI; 2002-171027/22.

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
PT prevention and/or treatment of cancer, especially ovarian cancer

PS Claim 1a; Page 125-126; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides  
CC that may be utilised in cancer therapy, for example in a vaccine or  
CC gene therapy. Polypeptides and polynucleotides of the invention are  
CC useful for detecting a cancer in a patient, for stimulating and/or  
CC expanding T-cells specific for a tumour protein, and for inhibiting the  
CC development of a cancer in a patient. They are also useful for  
CC stimulating an immune response in a patient, and for treating a cancer in  
CC a patient and for determining the presence of a cancer in a patient.  
CC The isolated polynucleotides of the invention are useful for their  
CC ability to selectively form duplex molecules with complementary stretches  
CC of the entire desired gene or gene fragments, and for designing and  
CC preparing ribozyme molecules for inhibiting expression of tumour  
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
CC invention are also useful in recombinant DNA molecules to direct  
CC expression of a polypeptide in appropriate host cells. The current  
CC sequence represents the ovarian carcinoma 05915 nucleotide sequence.

50 Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match	84.7%	Score 1606.2	DB 24	Length 1619
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1616; Conservative	2	Mismatches	0	Indels 1; Gaps 1;

OY	280	GGAACTTTTGGGAAATGTTCTTGCTCCAGAGCTTTGGCGCTGGCAAAATCCAGAGCTACCA	33.9
Db	1	GGCAACTTTTGGCGAATTTGTTCTTGCTCCAGAGCTTTGGCGCTGGCAAAATCCAGAGCTACCA	60
OY	340	GTTGGAAAGATTCAGCTGAACAACGAGCTGCTCCCTCCCGAGTTCAATTGTGAATTCAC	39.9
Db	61	GTTGGAAAGATTCAGCTGAACAACGAGCTGCTCCCTCCCGAGTTCAATTGTGAATTCAC	120
OY	400	GSTGAAGCTTCAAGCATGCTGCAGAAAGAAAGTATGAGCAAAAGTCCCGGATCAGTA	43.9
Db	121	GSTGAAGCTTCAAGCATGCTGCAGAAAGAAAGTATGAGCAAAAGTCCCGGATCAGTA	180
OY	460	CCGCAAGTCTGTGCATCATCAGGGGCTGTCTATGAGCTCTGACCGGTAACAGTCTTT	51.9
Db	181	CCGCAAGTCTGTGCATCATCAGGGGCTGTCTATGAGCTCTGACCGGTAACAGTCTTT	240
OY	520	CTGCTCTCCCAAGGAAACTGAACCTAGTTTGATAGCTGCTGCACAACCCCTCTTTGTAA	57.9
Db	241	CTGCTCTCCCAAGGAAACTGAACCTAGTTTGATAGCTGCTGCACAACCCCTCTTTGTAA	300
OY	580	CGGGCCAAAGGCCCAAGAAAGAGGGAGTTTGCTCGGACCTTCAGGGCAGAGGGCTCCGCAC	63.9
Db	301	CGGGCCAAAGGCCCAAGAAAGAGGGAGTTTGCTCGGACCTTCAGGGCAGAGGGCTCCGCAC	360
OY	640	CACCATCTGTTCTCTCAAAATTAGCCCTCTTCTCGGCACACTGCTGAAGCTGAAGAGATG	69.9
Db	361	CACCATCTGTTCTCTCAAAATTAGCCCTCTTCTCGGCACACTGCTGAAGCTGAAGAGATG	420
OY	700	CCACCCCTCTCTGCATTTGTTCTTCGACAGCCTTCGGCCCCCAACCCCCCACTCCCTGAAGTGA	75.9
Db	421	CCACCCCTCTCTGCATTTGTTCTTCGACAGCCTTCGGCCCCCAACCCCCCACTCCCTGAAGTGA	480

QY	760	GTTCCTCTGGGTCGTCCTTTATCTCGGGTAGGAGACGGGAGATCCGTCGTCCTTTGGT	813
Db	481	GTTCCTCTGGGTCGTCCTTTATCTCGGGTAGGAGACGGGAGATCCGTCGTCCTTTGGT	540
QY	830	CCGTGCAAAATAAATGAAGAAGCTCGGTAAAGCAATTCGTGAATTAATTCAGCTYGAAGT	879
Db	541	CCGTGCAAAATAAATGAAGAAGCTCGGTAAAGCAATTCGTGAATTAATTCAGCTYGAAGT	600
QY	880	TTTCAGTATGTACTTGAAGAGAGAGGTGAGTGAAGTTCAACCCCATGTCGTGTAC	939
Db	601	TTTCAGTATGTACTTGAAGAGAGAGGTGAGTGAAGTTCAACCCCATGTCGTGTAC	660
QY	940	CGGAGTCAAGGCCCGGCTGGCAGAGTCWGTCTTAACAATCACTAGAGTGGGACTCTGCC	999
Db	661	CGGAGTCAAGGCCCGGCTGGCAGAGTCAGTCTTGAABAATCACTAGAGTGGGCACTGCC	720
QY	1000	TTTTGTAAAGCTTCAAGTGTCCATTCCTCATCCGTATGGGGGCAATGTTGAGACTGCAGA	1059
Db	721	TTTTGTAAAGCTTCAAGTGTCCATTCCTCATCCGTATGGGGGCAATGTTGAGACTGCAGA	780
QY	1060	GTGAGAGTACGCTTCTTGAAGGCTGGAGGGCCAGTCTCCACTCAAGGCTCCCTGCGTGG	1119
Db	781	GTGAGAGTACGCTTCTTGAAGGCTGGAGGGCCAGTCTCCACTCAAGGCTCCCTGCGTGG	840
QY	1120	ACATTCAAACTTCATGCTCTCTGTAANAACCAATTCCTCTGACAGACAATTTGGCTGGTTCCGCGC	1179
Db	841	ACATTCAAACTTCATGCTCTCTGTAANAACCAATTCCTCTGACAGACAATTTGGCTGGTTCCGCGC	900
QY	1180	CTGAGTTGGGCTCTAATGAGTCTCGAGACTCAATATCTGGGAACTTAACATCGGGCTCGGCT	1239
Db	901	CTGAGTTGGGCTCTAATGAGTCTCGAGACTCAATATCTGGGAACTTAACATCGGGCTCGGCT	960
QY	1240	CGCTCTGAAAGTCTTAAAGAAATCTTTCATATTCCTCTCAGAGACTGGCCGCCGG	1299
Db	961	CGCTCTGAAAGTCTTAAAGAAATCTTTCATATTCCTCTCAGAGACTGGCCGCCGG	1020
QY	1300	ACGGAGAGACCAACGGGCGCTGCACAAACGGGGCGCTGTCCGTGTTGAATGTCGATGTA	1359
Db	1021	ACGGAGAGACCAACGGGCGCTGCACAAACGGGGCGCTGTCCGTGTTGAATGTCGATGTA	1080
QY	1360	CGCGAGGCGGTTCTCGTGGTGGCGGTGCTGCAGCAGACAGGGCGGCACACACACC-7GC	1418
Db	1081	CGCGAGGCGGTTCTCGTGGTGGCGGTGCTGCAGCAGCAGGGCGGCACACACACCTTCC	1140
QY	1419	ACGAACACCCCGCGAAATCTCTCGAGAGACCCGTGTACAGAGCGGGTGTGATGCCGAG	1478
Db	1141	ACGAACACCCCGCGAAATCTCTCGAGAGACCCGTGTACAGAGCGGGTGTGATGCCGAG	1200
QY	1479	CTGAGGTGAAGAAACGTCTCCGAGAAAGGGAGAGGATATGACGCCCGGAAAGTAGAC	1538
Db	1201	CTGAGGTGAAGAAACGTCTCCGAGAAAGGGAGAGGATATGATGACGCCCGGAAAGTAGAC	1260
QY	1539	CTCGTCAGTGTGCTTGGGTTTGGCGCAGCCATGATCCTCCGAATCTGTTGGGCAATC	1598
Db	1261	CTCGTCAGTGTGCTTGGGTTTGGCGCAGCCATGATCCTCCGAATCTGTTGGGCAATC	1320
QY	1599	CAGCATACGGCCATGTGCACAACAATCACCCCTGGGCAACACAGGAGAGGAGAGAC	1658
Db	1321	CAGCATACGGCCATGTGCACAACAATCACCCCTGGGCAACACAGGAGAGGAGAGAC	1380
QY	1659	AGAGAAAAGAAAACACACAGATGAGAACACAGTAAATGAAATAAACATAAATATTTTGG	1718
Db	1381	AGAGAAAAGAAAACACACAGATGAGAACACAGTAAATGAAATAAACATAAATATTTTGG	1440
QY	1719	CCCCCTGTGTTCTGTACTGCGCAGAGAAATGTACCAATTTTTCAGTGTGCACTTGA	1778
Db	1441	CCCCCTGTGTTCTGTACTGCGCAGAGAAATGTACCAATTTTTCAGTGTGCACTTGA	1500
QY	1779	CAGCTCTTTTGGCACAAGCAGAAGGAAATTTAACTCTTTTCAAAACCGGGGGAGTTGG	1838
Db	1501	CAGCTCTTTTGGCACAAGCAGAAGGAAATTTAACTCTTTTCAAAACCGGGGGAGTTGG	1560

QY 1839 CTGTGTTAAAGAACCATTAATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAAAA 1897  
 |||  
 DB 1561 CTGTGTTAAAGAACCATTAATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAAAA 1619

RESULT 10  
 ID ABRK33543 standard; cDNA: 1524 BP.  
 XX  
 AC ABRK33543;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE cDNA encoding human PRO protein, Seq ID No 15.  
 XX  
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200208288-A2.  
 PD 31-JAN-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-US21066.  
 XX  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220585P.  
 PR 25-JUL-2000; 2000US-220605P.  
 PR 25-JUL-2000; 2000US-220607P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220638P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 25-JUL-2000; 2000US-220666P.  
 PR 26-JUL-2000; 2000US-220893P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-233646P.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001WO-US17092.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Desnoyers L, Gerltsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 XX  
 DR WPI: 2002-172001/22.  
 DR P-PSDB: AAU83599.  
 XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumours  
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
 PT tumour or liver tumour -  
 XX  
 PS Claim 2; Figure 15; 3599P; English.  
 XX  
 CC The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating

CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. ABRK33536-ABRK33567 represent human  
 CC PRO protein coding sequences of the invention.  
 XX

SO Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;

Query Match 80.3%; Score 1523.2; DB 24; Length 1524;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1522; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 140 GCGGCAGACGCGCGGGCCCCAGCAGCCTCGGACCCAGCCAGCCCGCTGCAGCCGGGAGCC 199  
 DB 1 GCGGCAGACGCGCGGGCCCCAGCAGCCTCGGACCCAGCCAGCCCGCTGCAGCCGGGAGCC 60

QY 200 TCCGCTGCTGCGGCTCCTGATGCGGCTTGCCCTCCCGGGCCGCGGACTCCGGGAGA 259  
 |||  
 DB 61 TCCGCTGCTGCGGCTCCTGATGCGGCTTGCCCTCCCGGGCCGCGGACTCCGGGAGA 120

QY 260 ATGTGGGTCTAGGACATCGCGGCACTTTTTCGCGATTTCTTCCAGGCTTTGCG 319  
 |||  
 DB 121 ATGTGGGTCTAGGACATCGCGGCACTTTTTCGCGATTTCTTCCAGGCTTTGCG 180

QY 320 CTGCAAAATCCAGTCTACCACTGTGAAGAAATTCACAGTGAACAACGACTCTCTCCCC 379  
 |||  
 DB 181 CTGCAAAATCCAGTCTACCACTGTGAAGAAATTCACAGTGAACAACGACTCTCTCCCC 240

QY 380 GAGTTCATTGGAATTCAGAGGTGACAGTCAAGACATGTCAGAAAGAAAGATGAGAG 439  
 |||  
 DB 241 GAGTTCATTGGAATTCAGAGGTGACAGTCAAGACATGTCAGAAAGAAAGATGAGAG 300

QY 440 CAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTCTCATCGCC 499  
 |||  
 DB 301 CAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTCTCATCGCC 360

QY 500 TCTCGCGGGTACCACTCTCTGTCTCCCAAGGAACTGAACATCATCATCACTGCG 559  
 |||  
 DB 361 TCTCGCGGGTACCACTCTCTGTCTCCCAAGGAACTGAACATCATCATCACTGCG 420

QY 560 TGCACACACCCCTTTTGAACGGGCAAGGCCAAGAAAGGGAAGTTGCTGCTGGCC 619  
 |||  
 DB 421 TGCACACACCCCTTTTGAACGGGCAAGGCCAAGAAAGGGAAGTTGCTGCTGGCC 480

QY 620 CTCAGGCGAGGGTCCGACACCATCTGTCTCAAAATTAAGCCCTCTCTGCGCACAC 679  
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 DB 481 CTCAGGCGAGGGTCCGACACCATCTGTCTCAAAATTAAGCCCTCTCTGCGCACAC 540

QY 680 TGTGGAAGCTGAAGAGATGCGACACCCCTCTGCAATTTCTTCCAGCCCTGCCCCAA 739  
 |||  
 DB 541 TGTGGAAGCTGAAGAGATGCGACACCCCTCTGCAATTTCTTCCAGCCCTGCCCCAA 600

QY 740 CCCCCACCTCCCTGAGTGAAGTTCTTCTGAGTGTCTTTTATTTGAGGAGAGGAGG 799  
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 DB 601 CCCCCACCTCCCTGAGTGAAGTTCTTCTGAGTGTCTTTTATTTGAGGAGAGGAGG 660

QY 800 AGTCCGTTCTCTTTTGTTCCTGTGCAAAATGAAGAGCTCGTGAAGCATTTGAA 859  
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 DB 661 AGTCCGTTCTCTTTTGTTCCTGTGCAAAATGAAGAGCTCGTGAAGCATTTGAA 720

QY 860 TAAATTCAGCTGACCTGAATTTTCAATATGATGATGGAAGAGAGGTGAGTGAAGTT 919  
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 DB 721 TAAATTCAGCTGACCTGAATTTTCAATATGATGATGGAAGAGAGGTGAGTGAAGTT 780

QY 920 CACCCCATCTCTGTGAACCGAGTGAAGGAGGCTGAGAGTGCCTTAGAAGT 979  
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QY 980 CACTGAGGTGGGATCTGCTTTTGAAGCTTCAGATGTCATTCATCCCTGATGGG 1039  
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```

Oy 685 AAGCTAAGAGATGCGACCCCTCCTGATGTTCTTCAGCCCTCGGCCCAACCC 744
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Oy 745 CACCTCCCGAGTGAATTTCTTCTGGGTGCTCTTTATTTCTGGGTAGGAGGCGGAGTCC 804
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Db 399 CACCTCCCGAGTGAATTTCTTCTGGGTGCTCTTTATTTCTGGGTAGGAGGCGGAGTCC 458
Oy 805 GTTGTCTCTTTTGTTCCTGTCATAATGAAGAGCTCGTAAGCAATTCGATTAAT 864
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Oy 865 TCAGCTGACATAATTTTGTATGATGACTTGAAGAGAGAGTGAAGATTCCACC 924
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Db 519 TCAGCTGACATAATTTTGTATGATGACTTGAAGAGAGAGTGAAGATTCCACC 578
Oy 925 CCATGCTGTGTACCGGAGTCAAGGCCGCTGGAGAGTGMWCTTGAAGTCACTG 984
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Db 579 CCATGCTGTGTACCGGAGTCAAGGCCGCTGGAGAGTGMWCTTGAAGTCACTG 638
Oy 985 AAGTGGGATCTGCTTTTGTAAAGCCTCAGTGTCCATTCCTCCATCCCTGATGGGACATA 1044
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Db 639 AAGTGGGATCTGCTTTTGTAAAGCCTCAGTGTCCATTCCTCCATCCCTGATGGGACATA 698
Oy 1045 GTTTGAGACTGCAAGTGAAGTGAAGTGTCTTAGGGCTGAGGGCCCATTTCCACTCA 1104
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Db 699 GTTTGAGACTGCAAGTGAAGTGAAGTGTCTTAGGGCTGAGGGCCCATTTCCACTCA 758
Oy 1105 AAGCTCCCTCGCTTGAACATTCATTCCTGTAAGAAACATTCCTGAGCAGAT 1164
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Db 759 AAGCTCCCTCGCTTGAACATTCATTCCTGTAAGAAACATTCCTGAGCAGAT 818
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Oy 1225 ACTGGGGCTCGGCTCGCTGTAAAGTCTTAAGAAATCTTCTCACTGTTCTTGCAG 1284
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Db 999 TGGAGTGGCGATGTACGGCGAGCGCGCTTCTCGTGGTTGGCGTGTGACGACGAGCGCG 1058
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Oy 1465 GGTGTATGACCGAGGTGAGGTGAGAAAGGTCTCCGAGAGGGGAGGAGATCATGTACG 1524
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Oy 1525 CCCGGAAGTAGGACTCTGTCAGTGTGCTTGGGTTGGCCGACCATGATCTCCGAA 1584
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Oy 1585 TGTGGTGGGATTCAGATACGGCCATGTACAAACAATCAGCCCTGGCAGACAGAG 1644
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Oy 1645 CAGGAGGAGACAGAGAAAAAAGAACACAGCATGGAACACAGTAATGAATGAATAAAC 1704
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Db 1359 CATTAATAATTTTATGCCCCCTGTGCTTGTGCTTACTGCGCAGAGAAATGTACCAATTTTTC 1418
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```

```

Db 1419 AGTGTGACTTGACAGCTTCTTTGCCACAGCAAGAGAAATTAACACTGTTCAA 1478
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Db 1479 CCGGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGA 1532
    |||

RESULT 12
AADI8690/c
ID AADI8690 standard; cDNA: 2528 BP.
AC
AC AADI8690;
AC
AC 18-DEC-2001 (first entry)
DE
DE Human G protein coupled receptor (GPCR) 4941 cDNA.
XX
XX
XX Human; cardiovascular; tumorigenic disorder; aberrant angiogenesis;
XX gene therapy; aberrant vascularisation; atherosclerosis; ovarian cancer;
XX ischaemia/reperfusion injury; hypertension; arterial inflammation;
XX psoriasis; endothelial cell disorder; diabetic retinopathy; restenosis;
XX myocardial infarction; Grave's disease; G protein coupled receptor;
XX GPCR 4941; vasotropic; hypotensive; anti-inflammatory; cytostatic;
XX antidiabetic; antipsoriatic; leukaemia; ss.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
XX CDS 42..1403
XX /*tag= a
XX /product= "Human GPCR 4941"
XX /note= "The CDS is specifically claimed in claim 1 of
XX the specification"
XX
XX WO200181634-A2.
XX
XX 01-NOV-2001.
XX
XX 25-APR-2001; 2001MO-US13788.
XX
XX 26-APR-2000; 2000US-199908P.
XX 09-AUG-2000; 2000US-0635521.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Galvin KA, Rudolph-owen LA;
XX
XX WPI: 2001-611743/70.
XX P-PSDB: AAE11751.
XX
XX Identifying nucleic acids for the diagnosis and treatment of
XX cardiovascular and tumorigenic disorders, comprises identifying G
XX protein coupled receptor (GPCR)-4941 -
XX
XX Example 1; Fig 1; 118pp; English.
XX
XX The present invention relates to a method for identifying a nucleic acid
XX molecule (G protein coupled receptor gene, GPCR 4941) associated with a
XX cardiovascular or tumorigenic disorder. The method comprising contacting
XX a sample containing a nucleic acid molecule with a hybridisation probe or
XX amplification primers and detecting the presence. The invention is used
XX in gene therapy. The method of the invention is used for identifying
XX nucleic acids or polypeptides associated with a cardiovascular or
XX tumorigenic disorder such as aberrant angiogenesis, aberrant
XX vascularisation, atherosclerosis, or ovarian cancer, ischaemia/
XX reperfusion injury, hypertension, restenosis, arterial inflammation,
XX endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial
XX infarction, Grave's disease and leukaemia. The methods can also detect
XX mRNA or genomic DNA in a sample. The present sequence is G protein
XX coupled receptor (GPCR) 4941 cDNA.
XX
XX Sequence 2528 BP; 516 A; 766 C; 677 G; 567 T; 2 other;
SQ

```





QY 1811 AACACTGTTTCACAAACCCGGGGAGTTGGCTGTTTAAAGAACACATTAAATGCTTAG 1870  
 DB 541 AACACTGTTTCACAAACCCGGGGAGTTGGCTGTTTAAAGAACACATTAAATGCTTAG 600  
 QY 1871 ACAGTGTAAAAAAGAAAAA 1895  
 DB 601 ACAGTGTAAAAAAGAAAAA 625

965

RESULT 15  
 ABL87898  
 ID ABL87898 standard; DNA; 625 BP.  
 AC ABL87898;

DT 17-MAY-2002 (first entry)

DE Human ovarian cancer related DNA clone seq ID NO:10876.

XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.

OS Homo sapiens.

PN WO200192581-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001WO-US17756.

PR 26-MAY-2000; 2000US-207484P.

PA (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

DR WPI; 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide

PS Claim 1; SEQ ID 10876; 489bp; English.

XX The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (S1) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient. Where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumour protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
 CC and proteins in tumour cells; and to isolate a full length gene from a  
 CC suitable library e.g., a tumour cDNA library using well known  
 CC techniques.

SQ Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;

Query Match 32.9%; Score 624; DB 24; Length 625;  
 Best Local Similarity 99.8%; Pred. No. 1.5e-145;  
 Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1271 AGTTCTCTTCGACAGACAGTGGCCGGGACGACGAGAACGACGAGGCGCTGCACAAAGCG 1330  
 DB 1 AGTTCTCTTCGACAGACAGTGGCCGGGACGACGAGAACGACGAGGCGCTGCACAAAGCG 60  
 QY 1331 GGCCTGTGCGTGTGTGAGTGGCATGTACGCGCAGGCGCTTCTCGTGTGTGGCTGTG 1390  
 DB 61 GGCCTGTGCGTGTGTGAGTGGCATGTACGCGCAGGCGCTTCTCGTGTGTGGCTGTG 120  
 QY 1391 CAGCGACAGGGGGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1450  
 DB 121 CAGCGACAGGGGGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 180  
 QY 1451 CGTGTACAGAGAGCGGTTGATGACGAGCTGAGTAGAAAAAGCTTCCGAGAGGGGAG 1510  
 DB 181 CGTGTACAGAGAGCGGTTGATGACGAGCTGAGTAGAAAAAGCTTCCGAGAGGGGAG 240  
 QY 1511 GAGGATCATGTACGCGCGGAGAGTACGCTGTGCTGCTGTGGCTTGGCCGACG 1570  
 DB 241 GAGGATCATGTACGCGCGGAGAGTACGCTGTGCTGCTGTGGCTTGGCCGACG 300  
 QY 1571 CATGATCTCCGAATCTGTGGGATGACGATGACGATGACGATGACGATGACGATGACG 1630  
 DB 301 CATGATCTCCGAATCTGTGGGATGACGATGACGATGACGATGACGATGACGATGACG 360  
 QY 1631 TGGGACAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1690  
 DB 361 TGGGACAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 QY 1691 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTGTCTGTCTGTCTGT 1750  
 DB 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTGTCTGTCTGTCTGT 480  
 QY 1751 GGTACCAATTTTTCAGTGTGTGACCTTGACCTTCTTTTGCACAGCAAGAGAAATT 1810  
 DB 481 GGTACCAATTTTTCAGTGTGTGACCTTGACCTTCTTTTGCACAGCAAGAGAAATT 540  
 QY 1811 AACACTGTTTCACAAACCCGGGGAGTTGGCTGTTTAAAGAACACATTAAATGCTTAG 1870  
 DB 541 AACACTGTTTCACAAACCCGGGGAGTTGGCTGTTTAAAGAACACATTAAATGCTTAG 600  
 QY 1871 ACAGTGTAAAAAAGAAAAA 1895  
 DB 601 ACAGTGTAAAAAAGAAAAA 625

Search completed: November 7, 2002, 10:10:41  
 Job time : 384.511 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 17:54:48 ; Search time 2541.81 Seconds  
(without alignments)  
12086.984 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897  
Sequence: 1 gcccaaccgcgagcctctg.....aaaaaaaaaaaaaaaaaaaa 1897

Scoring table: OLIGO-NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 10

Total number of hits satisfying chosen parameters: 20126099

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	647	34.1	704 13	BI919074 603180881
2	631	33.3	888 14	BQ689771 AGENCOURT
3	627	33.1	702 14	BQ006545 UI-H-E11-
4	597	31.5	747 10	BI917149 603181571
5	587	30.9	676 10	BE385990 601276636
6	586	30.9	696 13	BM547680 AGENCOURT

7	585	30.8	987 14	B068420	B068420 AGENCOURT
C 8	556	29.3	591 12	A1844686	A1844686 w183407. x
C 9	552	29.1	606 12	BF439382	BF439382 nab3306.
C 10	552	29.1	948 14	B0882838	B0882838 AGENCOURT
C 11	546	28.8	678 9	A1936826	A1936826 w69910. x
C 12	545	28.7	627 13	BM669397	BM669397 UI-E-DML-
C 13	537	28.3	537 12	BF594242	BF594242 7n10d03. x
C 14	530	27.9	616 9	A1990500	A1990500 w40d07. x
C 15	517	27.3	649 10	AM590950	AM590950 h51e12. x
C 16	500	26.4	551 12	BE858216	BE858216 7919g07. x
C 17	498	26.3	608 13	BI554034	BI554034 603235426
C 18	489	25.8	508 12	BF939693	BF939693 nac80b12.
C 19	484	25.5	578 9	A1742092	A1742092 w938h03. x
C 20	479	25.3	534 10	BE350014	BE350014 h67g12. x
C 21	476	25.1	527 10	AM338938	AM338938 ha68h04. x
C 22	476	25.1	707 13	BI913989	BI913989 603180565
C 23	473	24.9	530 12	BF726459	BF726459 by06h03. y
C 24	472	24.9	920 9	AL538562	AL538562 AL538562
C 25	471	24.8	879 14	B0689033	B0689033 AGENCOURT
C 26	464	24.5	515 9	A1336858	A1336858 xf40h05. x
C 27	444	23.4	690 10	AM149665	AM149665 UI-E-DMD-
C 28	440	23.2	538 13	BM667957	BM667957 xb24e07. x
C 29	439	23.1	500 10	AM075598	AM075598 601570968
C 30	426	22.5	794 12	BE731003	BE731003 601570755
C 31	426	22.5	1134 12	BE730800	BE730800 601570755
C 32	425	22.4	467 9	A1150931	A1150931 qb53c04. x
C 33	425	22.4	480 10	BE336607	BE336607 bb68e04. y
C 34	424	22.4	759 12	BF125050	BF125050 601762888
C 35	424	22.4	843 12	BF125134	BF125134 601762356
C 36	423	22.3	571 14	BM709964	BM709964 UI-E-CO1-
C 37	415	21.9	537 9	A1018769	A1018769 ov32e04. x
C 38	408	21.5	688 13	BI544761	BI544761 603242028
C 39	408	21.5	690 13	BI669845	BI669845 603293440
C 40	404	21.3	743 10	BE395797	BE395797 601310028
C 41	396	20.9	366 9	AA613995	AA613995 n086c08. s
C 42	394	20.8	452 9	A1391683	A1391683 gy93f04. x
C 43	390	20.6	366 9	A1499630	A1499630 t003b07. x
C 44	383	20.2	654 12	BE746601	BE746601 601580186
C 45	380	20.0	456 9	A1765236	A1765236 w172n08. x

## ALIGNMENTS

RESULT 1  
BI919074  
LOCUS  
DEFINITION  
603180881F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5244956 5', mRNA sequence.  
ACCESSION  
BI919074  
VERSION  
BI919074.1 GI:16200128  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 704)  
NIH-MGC http://mgs.nci.nih.gov/  
TITLE  
Unpublished (1999)  
JOURNAL  
National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1618 row: a column: 21  
High quality sequence start: 4  
High quality sequence stop: 702.  
Location/Qualifiers

## FEATURES



QY 1291 GCGCCGCGGAGCCGGAAGCAACGCGGCTGCACAAAGCGGCGCTGTGCTGTGAGT 1350  
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 Db 442 GCGCGCGGAGCCCGGAAGCAACGCGGCGCTGCACAAAGCGGCGCTGTGCTGTGAGT 501  
 |||||||  
 QY 1351 GCGCATGTACGGCGGCGCTGTGCTGTGCGGTGCGACGACAGCGGCGGACACA 1410  
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 Db 502 GCGCATGTACGGCGGCGCTGTGCTGTGCGGTGCGACGACAGCGGCGGACACA 561  
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 QY 1411 GCACGTGCAGCAACCCCGCAAACTGCTGCAGACACCTGTACAGAGAGCGGATTGA 1470  
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 Db 562 GCACGTGCAGCAACCCCGCAAACTGCTGCAGACACCTGTACAGAGAGCGGATTGA 621  
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 QY 1471 TCACGAGCTGAGGTGAGAAAACGTCTCCGAGAGGGGAGAGATCATGTACGCCGGA 1530  
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 Db 682 AGTAGACCTGCTCCAGTGTG 703  
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RESULT 3  
 B0006545/c  
 LOCUS 702 bp mRNA linear EST 26-MAR-2002

DEFINITION UT-H-E11-aza-n-21-0-UI-s1 NCI-GAP\_E11 Homo sapiens cDNA clone  
 IMAGE:5846228 3', mRNA sequence.

ACCESSION B0006545

VERSION B0006545.1 GI:19731445

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 702)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncigap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

TITLE Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Seq primer: M13 FORWARD

POLY-A-Tes

FEATURES  
 Location/Qualifiers

1..702

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5846228"

/clone\_1lb="NCI-GAP\_E11"

/tissue\_type="Chondrosarcoma"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)

with a modified polylinker site; 1: Ecor I; site 2: Not I;

NCI-GAP\_E11 is a normalized cDNA library containing the

following tissue(s): Chondrosarcoma. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an Ecor I

adaptor, digested with Not I, and cloned directionally

into pT73-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

ACACTGCAC.

TAG-LIB-UT-H-E11

TAG-TISSUE-chondrosarcoma

BASE COUNT 137 a 200 c 163 g 202 t  
 ORIGIN

Query Match 33.1%; Score 627; DB 14; Length 702;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 677; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1218 GACCTTAGACCTGGGCGCTGGGCGCTGCTGAAAGTGTAAAGAAATCTTCAGTTCTC 1277  
 |||||||  
 Db 678 GACTTAGACCTGGGCGCTGGGCGCTGCTGAAAGTGTAAAGAAATCTTCAGTTCTC 619  
 |||||||  
 QY 1278 CTTCAGAGACTGCGCGCGGAGCGCAAGAGCAACGCGGCTGCACAAAGCGGCGCTG 1337  
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 Db 618 CTTCAGAGAGACTGCGCGCGGAGCGCAAGAGCAACGCGGCTGCACAAAGCGGCGCTG 559  
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 QY 1338 TCGGTGTGAGAGTGGCATGTACGCCGCTCTCTGCTGTGTTGGCTGCTGACGGAC 1397  
 |||||||  
 Db 558 TCGGTGTGAGAGTGGCATGTACGCCGCTCTCTGCTGTGTTGGCTGCTGACGGAC 499  
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QY 1398 AGCGGCGAGCAGACACCTGCGAGACACCGCGCAAGTGTGCGAGACCGCTGTAC 1457  
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 Db 498 AGCGGCGAGCAGACACCTGCGAGACACCGCGCAAGTGTGCGAGACCGCTGTAC 439  
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QY 1458 AGGAGCGGTTGATGACCGAGCTGAGGTAGAAAACGCTCTCCGAGAGGAGAGGATC 1517  
 |||||||  
 Db 438 AGGAGCGGTTGATGACCGAGCTGAGGTAGAAAACGCTCTCCGAGAGGAGAGGATC 379  
 |||||||

QY 1518 ATGTACGCGCGGAAAGTACGACCTGCTCAGTGTGCTGTGTTGGCTGCGACCGCATGATC 1577  
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 Db 378 ATGTACGCGCGGAAAGTACGACCTGCTCAGTGTGCTGTGTTGGCTGCGACCGCATGATC 319  
 |||||||

QY 1578 CTCGGAATCTGTTGGGCGATCCAGCATACGCGCAATGTCACAAATCAGCCCTGGGCGAG 1637  
 |||||||  
 Db 318 CTCGGAATCTGTTGGGCGATCCAGCATACGCGCAATGTCACAAATCAGCCCTGGGCGAG 259  
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QY 1638 ACACGAGCAGAGGAGAGAGACAGAGAAAAGAAAACACAGCATGAGAACAGTAATGA 1697  
 |||||||  
 Db 258 ACACGAGCAGAGGAGAGAGACAGAGAAAAGAAAACACAGCATGAGAACAGTAATGA 199  
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QY 1698 ATAAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGGCCAGGAATGTACCA 1757  
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 Db 198 ATAAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGGCCAGGAATGTACCA 139  
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QY 1758 ATTTTTCAGTTGTGACCTGACAGCTCTTTTGGCACAAGAGAGATTTAAACCTG 1817  
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 Db 138 ATTTTTCAGTTGTGACCTGACAGCTCTTTTGGCACAAGAGAGATTTAAACCTG 79  
 |||||||

QY 1818 TTTCAAACCCGCGGAGTGGCTGTGTTAAAGAAAGCAATTAATGCTTTAGACAGTGT 1877  
 |||||||  
 Db 78 TTTCAAACCCGCGGAGTGGCTGTGTTAAAGAAAGCAATTAATGCTTTAGACAGTGT 19  
 |||||||

QY 1878 AAAAAAAAAAAAAAAAAA 1895  
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 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 4  
 LOCUS B1917149 747 bp mRNA linear EST 16-OCT-2001

DEFINITION 603181571F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5245648 5',

mRNA sequence.

ACCESSION B1917149

VERSION B1917149.1 GI:16181111

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 747)

NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

TITLE

AUTHORS

REFERENCE

NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

TITLE

AUTHORS

REFERENCE

NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

TITLE





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Db 301 CAGCACCCTGACAGAACCCCGGAAACTGTCGAGGACACCGTGTACAGAGGGGTT 360
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Qy 1469 GATGACCCGAGCTAGAGTAAACCTCTCCGAGAAGGAGAGATCATGTACGCCG 1528
    |||
Db 361 GATGACCCGAGCTAGAGTAAACCTCTCCGAGAAGGAGAGATCATGTACGCCG 420
    |||
Qy 1529 GAAGTAGAAGCTGTCTCACTGCTGTGGGTTGGCCGAGCCATGATCTCCGATCTG 1588
    |||
Db 421 GAAGTAGAAGCTGTCTCACTGCTGTGGGTTGGCCGAGCCATGATCTCCGATCTG 480
    |||
Qy 1589 GTTGGGATCCAGCATAGAGCCCAATGTCTCAACATTCAGCCCTGGGACAGACGAGCAG 1648
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Db 481 GTTGGGATCCAGCATAGAGCCCAATGTCTCAACATTCAGCCCTGGGACAGACGAGCAG 540
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Qy 1649 AGGAGAGACAGAGAAAGAAACACAGCATGAGAACAGCTAAAT 1695
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Db 541 AGGAGAGACAGAGAAAGAAACACAGCATGAGAACAGCTAAAT 587
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RESULT 6
BM547680 696 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6507108 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727798
DEFINITION 5', mRNA sequence.
ACCESSION BM547680
VERSION BM547680.1 GI:18781656
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 696)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM12722 row: h column: 07
High quality sequence stop: 641.
Location/Qualifiers
1. 696
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5727798"
/clone.lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-Sport6; site_1: EcoRV
(destroyed); site_2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

BASE COUNT 188 a 160 c 197 g 134 t 17 others
ORIGIN
Query Match 30 9%; Score 586; DB 13; Length 696;
Best Local Similarity 99.8%; Fred. No. 0;
Matches 636; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1210 ATGACTGAGCTTAACTGAGGCTCGCTCGTGAAGAAATGCTTAAAGAAATCTTCT 1269
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Db 4 ATGACTGAGCTTAACTGAGGCTCGCTCGCTCGTGAAGAAATGCTTAAAGAAATCTTCT 63

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Qy 1270 CAGTTCTCCTTGCAGAGAGACTGGCCCGGAGACCGAAGACAGGGCGCTGCACAAAGC 1329
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Db 64 CAGTTCTCCTTGCAGAGAGACTGGCCCGGAGACCGAAGACAGGGCGCTGCACAAAGC 123
    |||
Qy 1330 GGGCGCTGTCCGTGTGTGAGTGCATGTACGCGCAGGCGCTTCTGTGTGTGCGTGTCT 1389
    |||
Db 124 GGGCGCTGTCCGTGTGTGAGTGCATGTACGCGCAGGCGCTTCTGTGTGTGCGTGTCT 183
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Qy 1390 GCAGGACAGGCGGACAGACAGCACTGCACAGAACCCCGCAACTGCTGCGAGACACA 1449
    |||
Db 184 GCAGGACAGGCGGACAGACAGCACTGCACAGAACCCCGCAACTGCTGCGAGACACA 243
    |||
Qy 1450 CCGTGTACAGAGGCGGCTGTGATGACCCGAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGGA 1509
    |||
Db 244 CCGTGTACAGAGGCGGCTGTGATGACCCGAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGGA 303
    |||
Qy 1510 GGAGGATCATGTACGCCCCGGAAGTAGACCTGTCCAGTGTGTGGTTGGCCGAG 1569
    |||
Db 304 GGAGGATCATGTACGCCCCGGAAGTAGACCTGTCCAGTGTGTGGTTGGCCGAG 363
    |||
Qy 1570 CCATGATCCTCCGAATCTGTTGGGCAATCCGATACGGCCCAATGTCAACAATCAGCC 1629
    |||
Db 364 CCATGATCCTCCGAATCTGTTGGGCAATCCGATACGGCCCAATGTCAACAATCAGCC 423
    |||
Qy 1630 CTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1689
    |||
Db 424 CTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
    |||
Qy 1690 GTAAATGATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1749
    |||
Db 484 GTAAATGATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 543
    |||
Qy 1750 TGGTACCAATTTTTCAGGTGTGAGCTGACAGCTTCTTTGCCAAGAGAGAGAT 1809
    |||
Db 544 TGGTACCAATTTTTCAGGTGTGAGCTGACAGCTTCTTTGCCAAGAGAGAGAT 603
    |||
Qy 1810 TAACACTGTTTCAAAACCGGGGAGATTGGCTGTGT 1846
    |||
Db 604 TAACACTGTTTCAAAACCGGGGAGATTGGCTGTGT 640
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RESULT 7
B0668420 987 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT_8301981 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275121
DEFINITION 5', mRNA sequence.
ACCESSION B0668420
VERSION B0668420.1 GI:21778667
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 987)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rublin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2457 row: m column: 10
High quality sequence stop: 583.
Location/Qualifiers
1. 987
/organism="Homo sapiens"
/db_xref="taxon:9606"

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